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<p>(54) Title: HUMAN CANCER ASSOCIATED GENE SEQUENCES AND POLYPEPTIDES</p> <p>(57) Abstract</p> <p>This invention relates to newly identified tissue specific cancer associated polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "cancer antigens", and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such tissue specific cancer antigens for detection, prevention and treatment of tissue specific disorders, particularly the presence of cancer. This invention relates to the cancer antigens as well as vectors, host cells, antibodies directed to cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing tissue specific disorders, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.</p>		

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Human Cancer Associated Gene Sequences and Polypeptides

5 *Field of the Invention*

This invention relates to newly identified tissue specific cancer associated polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "cancer antigens," and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such cancer antigens for detection, 10 prevention and treatment of tissue specific diseases, particularly cancers. This invention relates to the cancer antigens as well as vectors, host cells, antibodies directed to cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to tissue specific diseases, including cancer, and therapeutic methods for treating such 15 disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

20 *Background of the Invention*

Cell growth is a carefully regulated process which responds to specific needs of the body. Occasionally, the intricate, and highly regulated controls dictating the rules for cellular division break down. When this occurs, the cell begins to grow and divide independently of its homeostatic regulation resulting in a condition commonly referred to as 25 cancer. In fact, cancer is the second leading cause of death among Americans aged 25-44.

Cancers or malignant tumors are characterized by continuous cell proliferation and cell death. Cancer cells have been shown to exhibit unique gene expression, and dozens of cancer-specific genetic markers, tumor antigens, have been identified. P35B, a tumor rejection antigen, was first identified in mouse. A point mutation in the P35B gene elicits a 30 cytolytic T lymphocyte response but no detectable antibody response (Szikora, J. P. et al. (1990) EMBO J. 9:1041-1050). A human homolog of P35B, FX, is a homodimeric

NADP(H)-binding protein of 68 kDa. FX acts as a combined epimerase and NADPH-dependent reductase in converting GDP-4-keto-6-D-deoxymannose to GDP-L-fucose (Tonetti, M. et al. (1996) J. Biol. Chem. 271: 27274-27279). GDP-L-fucose is the substrate of several fucosyl-transferases involved in the biosynthesis of blood group ABH antigenic determinants. GDP-L-fucose is also utilized in synthesizing fucosylated glycoproteins and glycolipids which function in cell adhesion and recognition (Springer, T. A. and Lasky, L. A. (1991) Nature 329: 196-197; Brandley, B. K. et al. (1990) Cell 63: 861-863; and Feizi, T. and Childs, R. A. (1987) Biochem. J. 245: 1-11).

Thus, there is a need for the identification and characterization of novel tissue specific polynucleotides and polypeptides which modulate activation and differentiation of cells, both normally and in disease states. In particular, there is a need to isolate and characterize additional molecules that mediate apoptosis, DNA repair, tumor-mediated angiogenesis, genetic imprinting, immune responses to tumors and tumor antigens and, among other things, that can play a role in detecting, preventing, ameliorating or correcting dysfunctions or diseases.

Summary of the Invention

The present invention includes isolated nucleic acid molecules comprising, or alternatively, consisting of, a cancer associated polynucleotide sequence disclosed in the sequence listing (as SEQ ID NOs:1 to 842) and/or contained in a human cDNA clone described in Tables 1, 2 and 5 and deposited with the American Type Culture Collection ("ATCC"). Fragments, variant, and derivatives of these nucleic acid molecules are also encompassed by the invention. The present invention also includes isolated nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide encoding a cancer polypeptide. The present invention further includes cancer polypeptides encoded by these polynucleotides. Further provided for are amino acid sequences comprising, or alternatively consisting of, cancer polypeptides as disclosed in the sequence listing (as SEQ ID Nos: 843 to 1684) and/or encoded by a human cDNA clone described in Tables 1, 2 and 5 and deposited with the ATCC. Antibodies that bind these polypeptides are also encompassed by the invention. Polypeptide fragments, variants, and derivatives of these amino acid sequences are also encompassed by the invention, as are polynucleotides encoding these polypeptides and antibodies that bind these polypeptides. Also provided are diagnostic methods for diagnosing

and treating, preventing, and/or prognosing disorders related to cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention.

5 *Detailed Description*

Tables

Table 1 summarizes some of the cancer antigens encompassed by the invention (including contig sequences (SEQ ID NO:X) and the cDNA clone related to the contig sequence) and further summarizes certain characteristics of the cancer polynucleotides and the polypeptides encoded thereby. The first column shows the "SEQ ID NO:" for each of the 842 cancer antigen polynucleotide sequences of the invention. The second column provides a unique "Sequence/Contig ID" identification for each cancer associated sequence. The third column, "Gene Name," and the fourth column, "Overlap," provide a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database and the database accession no. for the database sequence having similarity, respectively. The fifth and sixth columns provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity), respectively, observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence. The ninth column provides a unique "Clone ID" for a cDNA clone related to each contig sequence. The tenth column shows the tissue in which each SEQ ID NO:X is predominantly expressed.

Table 2 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, fifteen or more of any one or more of these public EST sequences are optionally excluded from certain embodiments of the invention.

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in most of the cancer associated polynucleotides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl.

Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). Cancer associated polypeptides (e.g., SEQ ID NO:Y, polypeptides encoded by SEQ ID NO:X, or polypeptides encoded by the cDNA in the referenced cDNA clone) may possess one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown in column two of Table 4 correspond to the amino acid sequences for most cancer associated polypeptide sequence shown in the Sequence Listing.

Table 5 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X (as described in column 1 of Table 1) or the related cDNA clone (as described in column 9 of Table 1 and contained within a library deposited with the ATCC). For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence.

Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

5 In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown in column 9 of Table 1, each clone is identified by a cDNA Clone ID. Each Clone ID is unique to an individual clone and the
10 Clone ID is all the information needed to retrieve a given clone from the HGS library. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 5 provides a list of the deposited cDNA libraries. One can use the Clone ID to determine the library source by reference to Tables 2 and 5. Table 5 lists the deposited
15 cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone ("Clone ID") isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1 correlates the Clone ID names with SEQ ID NOs. Thus, starting with a SEQ ID NO, one can use Tables 1, 2 and 5 to determine the corresponding Clone ID,
20 from which library it came and in which ATCC deposit the library is contained. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for
25 the purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), and/or sequences contained in the
30 related cDNA clone within a library deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH

7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also included within "polynucleotides" of the present invention are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

The polynucleotides of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the

polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

"SEQ ID NO:X" refers to a tissue specific cancer antigen polynucleotide sequence described in Table 1. SEQ ID NO:X is identified by an integer specified in column 1 of Table 1. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. There are 842 cancer antigen polynucleotide sequences described in Table 1 and shown in the sequence listing (SEQ ID NO:1 through SEQ ID NO:842). Likewise there are 842 polypeptide sequences shown in the sequence listing, one polypeptide sequence for each of the polynucleotide sequences (SEQ ID NO:843 through SEQ ID NO:1684). The polynucleotide sequences are shown in the sequence listing immediately followed by all of the polypeptide sequences. Thus, a polypeptide sequence corresponding to polynucleotide sequence SEQ ID NO:1 is the first polypeptide sequence shown in the sequence listing. The second polypeptide sequence corresponds to the polynucleotide sequence shown as SEQ ID NO:2, and so on. In otherwords, since there are 842 polynucleotide sequences, for any polynucleotide sequence SEQ ID NO:X, a corresponding polypeptide SEQ ID NO:Y can be determined by the formula $X + 842 = Y$. In addition, any of the unique "Sequence/Contig ID" defined in column 2 of Table 1, can be linked to the corresponding polypeptide SEQ ID NO:Y by reference to Table 4.

The polypeptides of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

The cancer polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple
5 histidine residues, or an additional sequence for stability during recombinant production.

The cancer polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-
10 step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

15 By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to
20 a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

"A polypeptide having functional activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular assay, such as, for example, a biological
25 assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than
30 about three-fold less activity relative to the polypeptide of the present invention).

The functional activity of the cancer antigen polypeptides, and fragments, variants derivatives, and analogs thereof, can be assayed by various methods.

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length polypeptide of the present invention for binding to an antibody to the full length polypeptide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques
5 such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays,
10 immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an
15 immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See
20 generally, Phizicky, E., et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, physiological correlates polypeptide of the present invention binding to its substrates (signal transduction) can be assayed.

In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present invention and
25 fragments, variants derivatives and analogs thereof to elicit polypeptide related biological activity (either in vitro or in vivo). Other methods will be known to the skilled artisan and are within the scope of the invention.

30 Cancer Associated Polynucleotides and Polypeptides of the Invention

It has been discovered herein that the polynucleotides described in Table 1 are expressed at significantly enhanced levels in human cancer tissues as shown in column 10 of

Table 1. Accordingly, such polynucleotides, polypeptides encoded by such polynucleotides, and antibodies specific for such polypeptides find use in the prediction, diagnosis, prevention and treatment of tissue specific disorders, including cancer as more fully described below.

Table 1 summarizes some of the polynucleotides encompassed by the invention
5 (including contig sequences (SEQ ID NO:X) and the related cDNA clones) and further summarizes certain characteristics of these tissue specific cancer associated polynucleotides and the polypeptides encoded thereby.

Table 1

Seq ID Contig ID No.	Sequence/ Gene Name	Overlap	HGS Nucleotide		Clone ID	Tissue(s)
			Start	End		
1	507291 uvomorulin [Homo sapiens] >sp Q15855 Q15855 UVOMORULIN PRECURSOR (E-CADHERIN) (ARC-1/UVOMORULIN). >gi 930046 uvomorulin (140 AA) [Homo sapiens] {SUB 168-307; Length = 878	gi 340185	2	475	HCHAU23	Pancreas, Breast/Ovarian
2	508000 HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >gi 179345 HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >pir B35098 B35098 MHC class III histocompatibility antigen HLA-B- associated transcript 2 - human >sp P48634 BAT2_HUMAN LARGE PROLINE- RICH P	gi 179339	100	1902	HWAAK36	Lung, Breast/Ovarian
3	518325		110	310	HHFCP36	Lung, Pancreas, Colon, Breast/Ovarian
4	523111 Sm D2 [Homo sapiens] >pir 138861 138861 small nuclear ribonucleoprotein chain D2 - human Length = 118	gi 600748	233	670	HATAE67	Lung, Breast/Ovarian
5	526869 (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis thaliana] >sp O49289 O49289 SIMILAR ATP-DEPENDENT RNA HELICASE. Length = 845	gi 2829912	1	552	HT4P57	Pancreas, Breast/Ovarian
6	532211 retinoic acid-binding protein [Bos taurus] Length = 138	gi 162906	2	481	HHGCV63	Lung, Breast/Ovarian

7	532247		160	384		HEBCC47	Pancreas, Breast/Ovarian Lung, Breast/Ovarian
8	537932	alcohol dehydrogenase [Homo sapiens] >gil178134 alcohol dehydrogenase 3 [Homo sapiens] >pirJH0789 DEHUC2 alcohol dehydrogenase (EC 1.1.1.1) 5 - human >sp P11766 ADHX_HUMAN ALCOHOL DEHYDROGENASE CLASS III CHI CHAIN (EC 1.1.1.1) (GLUTATHIONE- DEPENDENT FOR	gil178130	1	1149	92	HUSIB86
9	540117		174	635		HRGBU25	Lung, Breast/Ovarian
10	547710	transketolase [Homo sapiens] Length = 623	gil1297297	2	1189	92	HIMUAZ27
11	551747	rtvp-1 [Homo sapiens] >pir JC5308 JC5308 testis- specific, vespid, and pathogenesis-related protein 1 - human >sp P48060 GLIP_HUMAN GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN). Length = 266	gil1030053	26	931	91	HTDAE10
12	552799	delta- aminolevulinate synthase (housekeeping) [Homo sapiens] >pir S13682 SYHUAL 5- aminolevulinate synthase (EC 2.3.1.37) 1 precursor - human >sp P13196 HEM1_HUMAN 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA-AM	gil28583	104	814	100	HHECX90

13	553243	RING7 [Homo sapiens] >gij557702 HLA-DMB [Homo sapiens] >gij512472 HLA-DMB [Homo sapiens] >gij1054742 DMB [Homo sapiens] >pirj37533j37533 MHC class II histocompatibility antigen HLA-DM beta chain precursor - human Length = 263	gij313002	202	1017	93	93	HUKD144	Lung, Pancreas
14	553368	(AF053944) aortic carboxypeptidase-like protein ACLP [Homo sapiens] >spjG3288916jG3288916 AORTIC CARBOXYPEPTIDASE-LIKE PROTEIN ACLP. >gnlP1Dj1013781 AEBP1 [Homo sapiens] (SUB 314-1158) Length = 1158	gij3288916	1	459	96	96	HADGE84	Lung, Pancreas
15	554349	immunoglobulin heavy chain [Homo sapiens] Length = 152		3	776			HUSCK19	Lung, Pancreas
16	558491	dj6802.2 [Homo sapiens] >spj35579jMYSN_HUMAN MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN, TYPE A) (NMIMHC-A). >gij553596 cellular myosin heavy chain [Homo sapiens] (SUB 1-1337) Length = 1960	gij567128	1	429	98	100	HUFEN61	Lung, Pancreas, Colon
17	558983		gnlP1Dj1294465	219	623	100	100	HC01BM82	Pancreas, Breast/Ovarian
18	572943			367	522			HBAMC47	Pancreas, Breast/Ovarian
19	585892	epithelial tumor antigen precursor, membrane-bound form - human Length = 515	pirjS10572jS10572	3	965	89	89	HUKAL69	Lung, Pancreas, Colon, Breast/Ovarian

20	589390	C1 inhibitor [Homo sapiens] >gil29535 C1 inhibitor [Homo sapiens] >pir51386[THUC1 complement C1 inhibitor precursor - human >sp05155[CI_HUMAN PLASMA PROTEASE C1 INHIBITOR PRECURSOR (C1 INH). >gnl PID c3783 C1 inhibitor (AA 155-478) (1 is 2nd base i	gnl PID c222400	3	983	96	96	HSRAB10	Lung, Pancreas
21	596882			800	1057			IIMCEP91	Lung, Pancreas, Colon
22	616289	nucleoporin p58 [Rattus norvegicus] >sp P70581 P70581 NUCLEOPORIN P58. Length = 385	gil1537068	1	390	67	70	HAJCB44	Lung, Pancreas
23	622140	selenophosphate synthetase 2 [Homo sapiens] >sp Q99611 Q99611 SELENOPHOSPHATE SYNTHETASE 2. Length = 448	gil1815622	92	325	97	97	HEONC67	Pancreas, Breast/Ovarian
24	623566	karyopherin aliph 3 [Homo sapiens] >sp O00505 IMA3_HUMAN IMPORTIN ALPHA-3 SUBUNIT (KARYOPHERIN ALPHA-3 SUBUNIT). Length = 521	gnl PID d1021210	66	1652	99	99	HDJPP20	Lung, Breast/Ovarian
25	647714			1	711			HSSE129	Pancreas, Breast/Ovarian
26	647752	ubiquitin conjugating-protein [Oryctolagus cuniculus] >gil184046 HHR6B (Human homologue of yeast RAD 6); putative [Homo sapiens] >gil30954 E2 protein [Homo sapiens] >gil207555 ubiquitin conjugating-protein [Rattus norvegicus] >gnl PID c233515 HR6B gene pr	gil165780	3	590	100	100	HD1DH46	Lung, Colon

27	651774	P58 [Homo sapiens] >pir[S68363]S68363 protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor - human >sp P30101 ER60_HUMAN PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD) MICROSOMAL PROTEIN (P58) (GRP58) (ERP57). Length	gil1147739	1	1632	96	96	HDPAA15	Lung, Pancreas, Breast/Ovarian
28	651995	collagen [Mus musculus] >pir[S21779]S21779 collagen alpha 1(VIII) chain - mouse >sp Q00780 CA18_MOUSE COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR. >bbs J34935 alpha 1-VIII collagen [rats, mesangial cell, Peptide Partial, 172 aa] [Rattus sp.] (SUB 399-570) Leng	gnl PIDc245912	3	335	90	95	11B1AD44	Lung, Pancreas
29	652156	phospholipid hydroperoxide glutathione peroxidase [Homo sapiens] >sp O43381 O43381 GSHH_HUMAN (EC 1.11.1.9) (GLUTATHIONE PEROXIDASE). >gil3399677 (AC005390) GSSH_HUMAN, partial CDS [Homo sapiens] (SUB 149-197) Length = 197	gil825667	262	633	94	94	HOEBK80	Lung, Breast/Ovarian
30	653010	von Willebrand factor [Homo sapiens] >pir A34480 VWHU von Willebrand factor precursor - human >gil553810 von Willebrand factor [Homo sapiens] (SUB 990-1947) >gnl PIDc22518 von Willebrand factor [Homo sapiens] (SUB 1-178) >gil340316 von Willebrand antige	gil340356	79	183	96	96	HSRAA58 HSEBB94	Lung, Pancreas Lung, Breast/Ovarian
31	655904			632	1891				
32	657852			70	522			HCHAL14	Colon, Breast/Ovarian
33	666414			1	285			HOSEK18	Lung, Pancreas

34	667847	ribosomal protein S9 [Rattus norvegicus] >pir N0587 S21497 ribosomal protein S9 - rat Length = 194	gi 57143	1	714	98	98	HCFLJ62	Lung, Pancreas, Breast/Ovarian
35	670188	G protein gamma-10 subunit [Homo sapiens] >pir J39158 J39158 GTP-binding regulatory protein gamma-10 chain - human >sp P50151 GBGA_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-10 SUBUNIT. Length = 68	gi 995919	2	238	100	100	I1WADR30	Lung, Pancreas
36	670279	ribosomal protein S24 [Homo sapiens] >gi 517222 ribosomal protein S24 [Homo sapiens] >gi 49652 ribosomal protein S19 (AA 1 - 133) [Mesocricetus auratus] >gi 57838 ribosomal protein S24 [Rattus norvegicus] >gi 57722 ribosomal protein S24 (AA 1-133) [Rattus	gi 337506	96	503	87	87	HSAYG46	Lung, Pancreas, Breast/Ovarian
37	670729	acidic ribosomal phosphoprotein (P1) [Homo sapiens] >pir B27125 RGHUP1 acidic ribosomal protein P1 - human Length = 114	gi 190234	74	496	100	100	H2CBM17	Lung, Pancreas, Colon, Breast/Ovarian
38	674123	collagen type VI, alpha 3 chain [Homo sapiens] >sp E1292418 E1292418 COLLAGEN TYPE VI, ALPHA 3 CHAIN. Length = 3176	gn P1D1e1292418	40	438			I1YACJ55	Lung, Pancreas
39	676496		gn P1D1e1292418	250	1029	98	98	HSLIC82	Lung, Pancreas
40	678162	TAXREB107 [Homo sapiens] >pir J51803 J51803 TAXREB107 - human Length = 288	gn P1D1d1005017	528	974	100	100	HBJJA02	Lung, Pancreas, Breast/Ovarian

41	678248	dolichol-phosphate-mannose synthase [Homo sapiens] >sp O60762 O60762 DOLICHOL-PHOSPHATE-MANNOSE SYNTHASE. >gnl PID d1026578 dolichol-phosphate-mannose synthase [Homo sapiens] {SUB 1-120} Length = 260	gnl PID d1026577	3	770	100	100	HMTAK71	Lung, Pancreas
42	683668	alpha 1 (I) chain propeptide [Homo sapiens] >gi 180380 alpha-1 type I collagen [Homo sapiens] {SUB 64-201} Length = 1040	gi 180392	566	1912	94	94	HWHGV07	Lung, Pancreas, Breast/Ovarian
43	693172	Q1Z 7F5 [Homo sapiens] >gi 189266 may code for Wilms' tumor-related protein [Homo sapiens] >gi 190814 Wilms' tumor-related protein [Homo sapiens] >gi 1203971 QM gene product [Homo sapiens] >bbs 135740 QM [human, nontumorigenic Wilms' microcell hybrid c	gi 184407	23	214	97	100	HNHIW05	Lung, Pancreas, Breast/Ovarian
44	694303			2824	3219			HOGAV47	Lung, Breast/Ovarian
45	695042	Description: KRAB zinc finger protein; this is a splicing variant that contains a stop codon and frame shift between the KRAB box and the zinc finger region; Method: conceptual translation supplied by author [Homo sapiens] >sp Q13359 Q13359 KRAB ZINC FING	gi 1049295	471	680	74	91	IIISBX26	Pancreas, Breast/Ovarian
46	699799	lipocortin (AA 1-346) [Homo sapiens] >pir A03080 LUHU annexin I - human >sp P04083 ANX1_HUMAN ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE; A2 INHIBITORY PROTEIN). {SUB 2-346} Length = 346	gi 34388	3	1121	100	100	HNDAA51	Lung, Breast/Ovarian

47	702216	dihydrodiol dehydrogenase [Homo sapiens] >gi487135 hepatic dihydrodiol dehydrogenase [Homo sapiens] >gi181549 dihydrodiol dehydrogenase [Homo sapiens] >pirA33436/A53436 3-alpha- hydroxysteroid/dihydrodiol dehydrogenase (EC 1.1.1.-) - human >sp Q04828 DB	gi452484	41	1048	95	95	HNALC11	Lung, Pancreas
48	703015	latent transforming growth factor-beta-binding protein - human Length = 1820	pirA55494/A55494	3	587	100	100	HGCOX28	Lung, Pancreas
49	706391	vacuolar H+ ATPase proton channel subunit [Homo sapiens] >pirA39367/A39367 H+-transporting ATPase (EC 3.6.1.35) chain PKD1 - human Length = 155	gi189676	29	622	85	85	HMA6L73	Lung, Breast/Ovarian
50	706892	copper transport protein HAH1 [Homo sapiens] >sp O00244 O00244 COPPER TRANSPORT PROTEIN HAH1. Length = 68	gi1945365	3	287	82	82	HUFDS83	Lung, Breast/Ovarian
51	706924			2847	3215			HRAEB20	Lung, Breast/Ovarian
52	707642	ribosomal protein L8 [Homo sapiens] >gi157704 ribosomal protein L8 [Rattus rattus] >gi1527178 ribosomal protein L8 [Mus musculus] >pirJU0177/R5RTL8 ribosomal protein L8, cytosolic - rat >pirJN0923/JN0923 ribosomal protein L8, cytosolic - human >gi3851	gi433899	1	516	94	94	HSRDJ44	Lung, Pancreas, Colon, Breast/Ovarian
53	710369			99	611			HSPA181	Lung, Pancreas, Breast/Ovarian
54	718826			581	877			HSIFK68	Lung, Breast/Ovarian

55	719790	lipocortin II [Homo sapiens] >pir A23942 LUHU36 annexin II - human >sp P07355 ANX2_HUMAN ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV). (SUB 2-339) >sp G545587 G545587	gnl PID d1000439	3	869	98	98	HKADK62	Lung, Pancreas
56	720222	homology with 16.7 KD putative viral protein YU1B1_NPVAC [Caenorhabditis elegans] Length = 250	gnl PID e1346018	34	729	45	60	HSKEP04	Lung, Pancreas, Breast/Ovarian
57	724033			1	654			HPJUV92	Lung, Pancreas, Breast/Ovarian
58	724767	epsilon isoform of 61kDa regulatory subunit of PP2A [Homo sapiens] >gi 1478070 protein phosphatase B56-epsilon [Homo sapiens] >sp Q16537 Q16537_EPSILON_ISOFORM OF 61KDA REGULATORY SUBUNIT OF PP2A. >gi 1022892 protein phosphatase PP2A0 B' subunit delta is	gnl PID e220196	71	526	100	100	HKABH59	Lung, Breast/Ovarian
59	727065	ATPase [Homo sapiens] Length = 617	gi 291868	228	1010	99	99	HELGY15	Lung, Pancreas
60	727246	(AB009282) cytochrome b5 [Homo sapiens] >sp O43169 O43169_CYTOCHROME B5 (FRAGMENT). Length = 146	gnl PID d1024640	3	509	96	98	HCFMH52	Lung, Colon
61	727932			41	199			HLJDO53	Lung, Breast/Ovarian
62	731167	Sec23 protein [Homo sapiens] Length = 765	gnl PID e236013	1	987	99	99	HDTEM51	Lung, Pancreas

63	732514	lysophosphatidic acid acyltransferase-alpha [Homo sapiens] >gil2253613 putative lysophospholipid acyltransferase [Homo sapiens] >gnl P D e286645 l-acylglycerol-3-phosphate O-acyltransferase. [Homo sapiens] >sp Q99943 PLCA_HUMAN l-ACYL-SN-GLYCEROL-3-PHOSPHA	gil2155238	3	794	99	99	HLDBX26	Pancreas, Prostate
64	734080			1	567			HF1BK44	Lung, Breast/Ovarian
65	734288	cysteinyl-tRNA synthetase [Homo sapiens] Length = 595	gil927229	154	2067	99	99	HKA1BU01	Lung, Pancreas
66	739448	Nascent polypeptide associated complex alpha subunit [Homo sapiens] >gil4092060 (AF054187) alpha NAC [Homo sapiens] >pir S49326 S49326 Nascent polypeptide associated complex alpha chain - human >sp Q13765 Q13765 NASCENT POLYPEPTIDE ASSOCIATED COMPLEX ALPHA	gil556642	441	1184	82	82	HKGA131	Lung, Breast/Ovarian
67	739668			2	484			HAPTL07	Lung, Pancreas
68	740060	Diff33 gene product [Homo sapiens] >sp Q13530 Q13530 PLACENTAL PROTEIN DIFF33. Length = 494	gil293563	76	1536	94	94	HMEGB82	Lung, Pancreas
69	741560			3	296			HCGM112	Lung, Colon
70	742543	human gamma-glutamyl hydrolase [Homo sapiens] >sp Q92820 Q92820 HUMAN GAMMA-GLUTAMYL HYDROLASE (EC 3.4.22.12). Length = 318	gil2951931	187	804	99	100	HE2BG62	Lung, Colon, Breast/Ovarian
71	742831			25	297			HCIDAL47	Pancreas, Colon

72	745327	channel-like integral membrane protein [Homo sapiens] >gi1314304 channel-like integral membrane protein [Homo sapiens] >pirA41616/A41616 erythrocyte integral membrane protein 28K - human >sp 29972 AQP1_HUMAN AQP1/PORIN-C11IP (WATER CHANNEL PROTEIN FOR RE	gi180501	1	534	98	98	HWHPM73	Lung, Pancreas
73	745695	Mac-2 binding protein [Homo sapiens] >gi1483474 90K gene product [Homo sapiens] >pirA47161/A47161 Mac-2-binding glycoprotein precursor - human >sp Q08380 Q08380 MAC-2 BINDING PROTEIN PRECURSOR. Length = 585	gi307153	886	2016	98	98	HOIPBN02	Lung, Pancreas
74	750316	(AF029890) hepatitis B virus X interacting protein [Homo sapiens] >sp O43504 O43504 HEPATITIS B VIRUS X INTERACTING PROTEIN. Length = 91	gi2745883	99	398	100	100	IKMLD65	Lung, Pancreas, Breast/Ovarian
75	750522			172	906			HUKFI58	Lung, Pancreas, Colon, Breast/Ovarian
76	750583			58	189			IIHJH66	Lung, Breast/Ovarian
77	751020			1	480			HEBAE80	Lung, Breast/Ovarian
78	752196			1	120			HL1AL67	Pancreas, Prostate
79	753084	UGTrel1 [Homo sapiens] >pir JC5024 JC5024 UDP-galactose transporter related isozyme 1 - human >sp P78383 P78383 UGTREL1. Length = 322	gi1669560	53	1168	87	87	HDPKG74	Lung, Pancreas
80	754957	The ha1237 gene product is related to S.pombe rad21 gene product. [Homo sapiens] Length = 631	gn P1D1008135	242	1330	94	94	HWBGB01	Lung, Pancreas

81	756557	myosin I heavy chain [Rattus norvegicus] >pir A45439 A45439 myosin I heavy chain - rat >sp Q05096 Q05096 MYOSIN HEAVY CHAIN I. Length = 1136	gi 56733	1	888	94	94	HE8AF67	Lung, Pancreas, Colon, Breast/Ovarian
82	756712	5-lipoxygenase activating protein [Homo sapiens] >pir A39824 A39824 5-lipoxygenase-activating protein - human >sp P20292 P1_LAP_11 MAN 5- LIPXYGENASE ACTIVATING PROTEIN (FLAP) (MK-886-BINDING PROTEIN). Length = 161	gi 182658	1457	1729	99	100	HISYBW76 HCABA08	Lung, Pancreas Lung, Colon
84	757614	tetrapeptide repeat protein [Homo sapiens] >sp Q99614 Q99614 TETRAPETRICPEPTIDE REPEAT PROTEIN. Length = 292	gi 1688074	83	991	100	100	HMEJS13	Lung, Pancreas, Breast/Ovarian
85	757815	(AF038604) contains similarity to Drosophila ovarian tumor locus protein (GB:X13693) [Caenorhabditis elegans] >sp O44438 O44438 B0546.2 PROTEIN. Length = 346	gi 2702370	2	988	58	81	HCHOL74	Lung, Breast/Ovarian
86	759878	nuclear pore complex protein NUP107 [Rattus norvegicus] >pir A54142 A54142 nucleoporin NUP107 - rat >sp P52590 N107_RAT NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105). Length = 926	gi 510717	526	1833	86	88	HNTAP78	Lung, Breast/Ovarian
87	760227	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana] >sp O80459 O80459 PUTATIVE NICOTINATE PHOSPHORIBOSYLTRANSFERASE. Length = 574	gi 3242705	2	484	52	71	HCHMM71	Pancreas, Breast/Ovarian

88	760312	chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide [Homo sapiens] >sp P13611 PGCV_HUMAN VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (GLIAL HYALURONATE-BINDIN	gil608515	993	3215	99	99	IIMVDD07	Lung, Pancreas
89	766051			1	627			HMAFA79	Lung, Breast/Ovarian
90	767593			327	497			HCECT76	Pancreas, Colon
91	768053	(AF039688) antigen NY-CO-3 [Homo sapiens] >sp Q60525 Q60525 ANTIGEN NY-CO-3 (FRAGMENT). Length = 192	gil3170176	251	625	99	99	ITTP11171	Pancreas, Breast/Ovarian
92	768055	ATP synthase gamma-subunit [Homo sapiens] >gnl P1D1d1004512 ATP synthase gamma-subunit [Homo sapiens] >pir A49108/A49108 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain - human >sp P36542 ATPG_HUMAN ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR	gnl P1D1d1004511	32	949	100	100	HAAJAQ70	Lung, Pancreas
93	769685	src-like tyrosine kinase (put.); putative [Homo sapiens] Length = 537	gil338228	1005	1409	100	100	HIRADN48	Lung, Pancreas, Colon, Breast/Ovarian
94	771920	F36D4.2 gene product [Caenorhabditis elegans] >sp Q20100 Q20100 COSMID F36D4. Length = 224	gil245686	711	1562	58	77	HAIDT44	Lung, Pancreas
95	772790	cell division inhibitor [Synechocystis sp.] >pir S77404 S77404 cell division inhibitor - Synechocystis sp. (PCC 6803) >sp P73467 P73467 CELL DIVISION INHIBITOR. Length = 339	gnl P1D1d1018240	145	1158	35	54	HCEOT95	Lung, Breast/Ovarian

96	772916	similar to human ZFY protein. [Homo sapiens] >sp Q92610 Q92610 MYELOBLAST KIAA0211. Length = 1267	gn P ID J101389	3	965	99	99	HCEIT26	Lung, Pancreas
97	773225			52	504			HCLB178	Lung, Pancreas
98	773632	hrs [Homo sapiens] >gi 2731383 HGF receptor substrate Hrs [Homo sapiens] >sp O14964 O14964 HRS, COMPLETE CDS. Length = 777	gn P ID J1024245	1	309	98	98	HCEVQ60	Pancreas, Prostate, Breast/Ovarian
99	774364	(AF080361) SYT interacting protein SIP [Homo sapiens] >sp O75932 O75932 SYT INTERACTING PROTEIN SIP. Length = 669	gi 3746787	1	408	100	100	HCHAR77	Pancreas, Breast/Ovarian
100	775355			1599	1781			HD1BY31	Lung, Pancreas
101	775844	rtp transforming protein [Homo sapiens] >pi A28101 TVHURF ret finger protein - human >gn P ID J308255 RFP [Homo sapiens] [SUB 250- 513] Length = 513	gi 337372	138	1877	92	92	HISCU10	Lung, Pancreas
102	777760	(AF015040) NUMB protein [Homo sapiens] >sp G4102705 G4102705 NUMB PROTEIN. >gi 4050088 (AF109907) S171 [Homo sapiens] [SUB 79-603] >gi 887362 ORF1 putative [Homo sapiens] [SUB 469-603] Length = 603	gi 4102705	62	1372	88	88	HMSIHK67	Pancreas, Breast/Ovarian
103	779837	tazarotene-induced gene 2 [Homo sapiens] >sp Q99969 Q99969 TAZAROTENE-INDUCED GENE 2. Length = 163	gi 1848264	88	567	97	98	HSWBV38	Lung, Pancreas
104	780769	(AF084259) bromodomain-containing protein BP75 [Mus musculus] >sp O88665 O88665 BROMODOMAIN-CONTAINING PROTEIN BP75. Length = 651	gi 3493162	100	762	35	58	HUJLS08	Lung, Pancreas
105	781445			496	1443			HMVAP52	Pancreas, Breast/Ovarian

106	781531	lumican [Homo sapiens] Length = 338	gi 699577	1	486	100	100	HCHAF71	Pancreas, Breast/Ovarian
107	783018	ovary2 [Drosophila melanogaster] >sp Q27924 Q27924 OVARY2. >gi 1208729 ovary2 [Drosophila melanogaster] [SLR_386-515] Length = 545	gi 1208732	120	674	58	76	HTPCZ45	Pancreas, Breast/Ovarian
108	783097	myogenic repressor 1-mf [Homo sapiens] >sp Q99750 Q99750 MYOGENIC REPRESSOR 1- MF. Length = 246	gi 1763615	413	919	85	85	HMWGR19	Lung, Colon
109	784198	(AJ005893) JM26 [Homo sapiens] >sp O60828 O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)). Length = 265	gn IPID c1289747	80	943	81	81	HNTNB85	Lung, Pancreas, Breast/Ovarian
110	784868	WW-domain binding protein 1 [Mus musculus] >sp P97764 P97764 WW-DOMAIN BINDING PROTEIN 1. Length = 305	gi 1777577	1	969	77	85	HNTNQ08	Lung, Pancreas, Breast/Ovarian
111	785428	translation initiation factor 5 [Homo sapiens] >sp P55010 P5_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF- 5). Length = 431	gi 1229140	308	1606	87	87	IIPMC114	Lung, Pancreas, Breast/Ovarian
112	785845			67	1350			HCGBE06	Lung, Colon, Breast/Ovarian
113	785854			3	509			HUSXJ65	Lung, Pancreas
114	786705			64	180			HBJB89	Lung, Pancreas, Breast/Ovarian
115	787186			319	975			HUKBB89	Lung, Pancreas
116	787279	proteasome subunit z [Homo sapiens] >sp Q99436 Q99436 PROTEASOME SUBUNIT Z. Length = 277	gn IPID d1007816	80	856	94	94	HKAJZ91	Lung, Breast/Ovarian
117	789002			178	402			HATBM56	Lung, Pancreas, Breast/Ovarian

118	789008	1.8 kb mRNA (AA 1-84) [Homo sapiens] >pir S03384 S03384 hypothetical protein (IGF-II 3' region) - human >sp P09565 IG2R_HUMAN PUTATIVE INSULIN-LIKE GROWTH FACTOR II ASSOCIATED PROTEIN. Length = 84	gij33000	1354	1737	100	100	100	HISCN20	Lung, Pancreas
119	789555	(AL035247) hypothetical trp-asp repeat protein [Schizosaccharomyces pombe] Length = 760	gnl PID e1371207	124	1815	42	66		HTTFCB23	Pancreas, Breast/Ovarian
120	789631			192	320				IIIJCN93	Lung, Pancreas, Colon
121	789779			1	396				HCHMS40	Colon, Breast/Ovarian
122	790387			3	527				HLMNA32	Colon, Breast/Ovarian
123	790461	(AF008445) phospholipid scramblase [Homo sapiens] >gnl PID d1033532 (AB006746) hMmTRA1b [Homo sapiens] >gij4092081 (AF098642) phospholipid scramblase; plasma membrane phospholipid scramblase [Homo sapiens] >sp O15162 O15162 PHOSPHOLIPID SCRAMBLASE. >sp G4	gij2282601	105	1193	99	99		HTGAV10	Lung, Pancreas, Breast/Ovarian
124	790931			2	394				HIBCA030	Pancreas, Breast/Ovarian
125	791176	(AB002107) hPer [Homo sapiens] >gij2435507 (AF022991) Rigui [Homo sapiens] >sp O15534 O15534 RIGUI. Length = 1290	dbj AB002107_1	3	1034	90	90		IINFC167	Lung, Pancreas
126	791983			637	837				HIBJLE45	Lung, Pancreas, Colon, Breast/Ovarian

127	792339	(AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens] >sp O14801 O14801 EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT. Length = 320	gi 2460200	94	1068	94	94	HDPPX89	Lung, Pancreas, Breast/Ovarian
128	792749	protein arginine N-methyltransferase [Rattus norvegicus] >sp Q63009 ANM1_RAT PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-). Length = 353	gi 1390025	34	1104	95	96	HQOEP64	Lung, Breast/Ovarian
129	792961	(AF036249) polymerase I-transcript release factor; PTRF [Mus musculus] >sp O54724 O54724 POLYMERASE I AND TRANSCRIPT RELEASE FACTOR (POLYMERASE I-TRANSCRIPT RELEASE FACTOR). Length = 392	gi 2674195	778	1305	85	86	HMEKG25	Lung, Breast/Ovarian
130	793206	dj1409.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens] >sp O76058 O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE). Length = 606	gn pID c1311294	889	1365	99	99	11TWFN71	Lung, Pancreas
131	793249	proliferation associated gene (pag) gene product [Homo sapiens] >pir A46711 A46711 proliferation associated gene (pag) protein - human Length = 199	gi 287641	3	701	100	100	HJAAE81	Lung, Pancreas, Breast/Ovarian
132	793626	alpha mannosidase II isozyme [Homo sapiens] >sp P49641 MAZX_HUMAN ALPHA-MANNOSIDASE IIX (EC 3.2.1.114) (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX). Length = 1139	gn pID d1010153	119	640	99	99	HWABS13	Lung, Pancreas

133	794417	(AF047470) malate dehydrogenase precursor [Homo sapiens] >sp O43682 O43682 MALATE DEHYDROGENASE (EC 1.1.1.37) PRECURSOR (EC 1.1.1.37). Length = 338	gil2906146	3	1142	99	99	11F1BK03	Lung, Pancreas, Breast/Ovarian
134	795197			82	888			HDPT26	Lung, Breast/Ovarian
135	795251	GAP SH3 binding protein [Homo sapiens] >sp Q13283 Q13283 GAP SH3 BINDING PROTEIN. Length = 466	gil1051170	101	1531	91	91	HE8FJ92	Pancreas, Breast/Ovarian
136	795752			2	1018			HWBDR92	Lung, Pancreas
137	796261	ubiquitin carrier protein E2 - human >gil181916 ubiquitin carrier protein [Homo sapiens] (SUB 23- 247) Length = 247	pir B42856 B42856	3	851	87	87	HCHPQ06	Colon, Breast/Ovarian
138	796933	lumican [Homo sapiens] Length = 338	gil699577	49	1107	94	94	HPMSD56	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
139	799424			525	1553			HEONK47	Lung, Pancreas, Breast/Ovarian
140	799698			1	426			HCLIAM08	Colon, Breast/Ovarian
141	800351	DNAJ homolog [Homo sapiens] >gil127833 heat shock protein hsp40 homolog [Homo sapiens] >pir G02272 G02272 heat shock protein hsp40 homolog - human >sp Q13431 Q13431 HEAT SHOCK PROTEIN HSP40 HOMOLOG. Length = 178	gil1518918	282	860	83	84	HEMFP05	Pancreas, Breast/Ovarian

142	800573	26S protease subunit [Sus scrofa] >gi 3193258 (AF069053) proteasome subunit SUG1 [Bos taurus] >gnl PID d1012606 proteasomal ATPase (rat SUG1) [Rattus norvegicus] >gnl PID d1023806 (AB000491) proteasome p45/SUG [Rattus norvegicus] >gnl PID c199326 mSUG1 pr	gnl PID c235521	178	1383	93	93	HCEVS28	Lung. Breast/Ovarian
143	805815			15	1055			HCI1AP80	Lung. Colon. Breast/Ovarian
144	806445			711	1028			HTELC67	Lung. Pancreas
145	810309	(AF098482) transcriptional coactivator p52 [Homo sapiens] >sp G4050034 G4050034 TRANSCRIPTIONAL COACTIVATOR P52. Length = 333	gi 4050034	226	741	61	75	HNTDX22	Lung. Pancreas
146	811022			168	881			HISEA13	Lung. Pancreas
147	811023			13	234			HLWAW17	Lung. Pancreas. Colon. Breast/Ovarian
148	811143	cytokine-inducible SH2-containing protein [Mus musculus] >pir S55551 S55551 cytokine-inducible protein CIS - mouse >sp Q62225 Q62225 CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN (SH2 DOMAIN CONTAINING PROTEIN INDUCED BY MULTIPLE CYTOKINES, SIC). Length = 257	gnl PID d1007285	3	887	90	92	IIDQP1A25	Lung. Breast/Ovarian
149	811381	FIN14 gene product [Mus musculus] >sp Q61077 F14_MOUSE FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14). Length = 61	gi 1353711	1338	1511	86	91	HLYEK93	Colon. Breast/Ovarian

150	811595	CIRP [Homo sapiens] >gi 2924760 (AC004258) CIRP [Homo sapiens] >gi 2541973 (AF021336) DNA damage-inducible RNA binding protein [Homo sapiens] >sp Q1401 Q1401.1 GLYCINE- RICH RNA BINDING PROTEIN CIRP. Length = 172	gn P D d 0111874	1	609	100	100	100	HDTLA92	Pancreas, Breast/Ovarian
151	813000	Tera [Mus musculus] >sp P70361 P70361 TERA. Length = 277	gi 1573505	95	850	84	86	86	HDPVZ64	Pancreas, Breast/Ovarian
152	813288	fau gene product [Homo sapiens] >gi 31305 (fau 1 gene product [Homo sapiens] >pir C1278 C1278 ubiquitin-like protein / ribosomal protein S30, cytosolic - human Length = 133	gi 31303	1	510	86	86	86	IICIMQ63	Pancreas, Lung, Breast/Ovarian
153	813431	DAP-1 [Homo sapiens] >pir 37274 37274 death- associated protein 1 - human >sp P51397 DAP1_HUMAN DEATH- ASSOCIATED PROTEIN 1 (DAP-1). Length = 102	gi 434845	3	470	89	89	89	HWHQS70	Lung, Pancreas
154	813450	PISSLRE gene product [Homo sapiens] >pir S49330 S49330 serine/threonine kinase (EC 2.7.1.1-) pisslre - human >pir 38116 38116 gene PISSLRE protein - human >sp Q15131 Q15131 PISSLRE MRNA. Length = 360	gi 556651	1	651	100	100	100	HCEEJ73	Lung, Pancreas
155	813478	retinoblastoma-binding protein mRbAp48 [Mus musculus] >pir 49366 49366 retinoblastoma- binding protein mRbAp48 - mouse Length = 461	gi 1016275	1	1398	99	100	100	HAJDH20	Lung, Pancreas, Breast/Ovarian
156	813505	ribosomal protein L23a [Homo sapiens] >gi 306549 homology to rat ribosomal protein L23 [Homo sapiens] {SUB 10-156} Length = 156	gi 404015	2	496	100	100	100	IIDAHR53	Lung, Pancreas

157	815552	(A011497) Claudin-9 [Homo sapiens] >sp E1363658 E1363658 CLAUDIN-9. Length = 211	gnl P D e1363658	317	898	95	96	HUFEI129	Lung, Colon
158	815606	Ki-1/57 intracellular antigen [Homo sapiens] >sp O75804 O75804 Ki-1/57 INTRACELLULAR ANTIGEN (FRAGMENT). Length = 299	gi 3403154	218	1303	90	95	HDPRY63	Lung, Pancreas, Breast/Ovarian
159	816048	neutral protease alpha subunit [Homo sapiens] >gi 35328 protease small subunit (aa 1-268) [Homo sapiens] >gi 1905903 (AD001527) calcium-dependent protease, small (regulatory) subunit (calpain) (calcium-activated neutral proteinase) (CANP) [Homo sapiens] >	gi 179909	24	644	95	96	HTLCZ60	Lung, Breast/Ovarian
160	822978	(AF003130) similar to Achlya ambisexualis antheridiol steroid receptor (NID: g166306) [Caenorhabditis elegans] >sp O01757 O01757 SIMILAR TO ACHLYA AMBISEXUALIS ANTHERIDIOL STEROID RECEPTOR. Length = 1043	gi 2088668	94 1449 992	156	60	78	HODEM46	Lung, Pancreas
161	823616				1775			HCEME79	Pancreas, Colon
162	823981				2617			HWHQH79	Lung, Breast/Ovarian
163	824364	drebrin E2 [Homo sapiens] >gnl P D J1005005 drebrin E [Homo sapiens] >pi N0809 N0809 drebrin E (clone gDhh13) - human >sp Q16643 DREB_HUMAN DREBRIN E. Length = 649	gi 392890	1	606	84	84	HCHPR34	Colon, Breast/Ovarian

164	824423	UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase [Homo sapiens] >pirjC4223/jC4223 polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human >sp Q10472 PAGT_HUMAN POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP	gi 971459	61	1743	100	100	HPWDL83	Lung, Pancreas
165	825279			36	602			H6EDN61	Lung, Pancreas
166	825442			1	900			HTODA45	Colon, Breast/Ovarian
167	825548	ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus] >sp P70295 P70295 ANCIEN UBQUITOUS PROTEIN PRECURSOR (AUP1). Length = 410	gi 1517822	473	1504	81	84	HLUDB77	Lung, Breast/Ovarian
168	825725	hNop56 [Homo sapiens] >sp O00567 NO56_HUMAN NJC1.EOLAR PROTEIN NOP56. Length = 602	gnl PID e1188703	25	723	99	99	HMWIV57	Lung, Pancreas
169	826639	H.sapiens mRNA for rat translocon-associated protein delta homolog [Homo sapiens] >gnl PID e212192 translocon-associated protein delta subunit precursor [Homo sapiens] >gnl PID e220312 translocon-associated protein delta subunit precursor [Homo sapiens] >	gi 1071681	1	561	100	100	HPTVX93	Lung, Colon, Breast/Ovarian
170	827079	(AL009171) 62D9.a [Drosophila melanogaster] >sp E1198294 E1198294 62D9.A. Length = 1305	gnl PID e1198294	53	2176	71	85	HDAAD02	Lung, Breast/Ovarian

171	827153	pancreatitis-associated protein [Homo sapiens] >gil312807 preprotein [Homo sapiens] >bsl121222 PAP-H=pancreatitis-associated protein [human, pancreas, 175 aa] [Homo sapiens] >gilPID1003233 PAP homologous protein [Homo sapiens] >pir149616/A49	gil482909	54	602	90	90	HI.QHS95	Pancreas, Colon, Breast/Ovarian
172	827351			1	639			HSKJ135	Colon, Breast/Ovarian
173	827503	(AC004003) serine/threonine kinase RICK; match to protein AF027706 (PID:g3123887) and mRNA AF027706 (NID:g3123886) [Homo sapiens] >gil3290172 (AF064824) CARD-containing ICE associated kinase [Homo sapiens] >gil3342910 (AF078530) receptor interacting prote	gil3264574	255	1886	98	98	HLAAB36	Lung, Breast/Ovarian
174	827563	rhophilin [Mus musculus] >spQ61085/Q61085 GTP-RHO BINDING PROTEIN 1 (RHOPHILIN). Length = 643	gil1176422	6	776	81	91	IIBGDH11	Colon, Breast/Ovarian
175	827565	serine protease [Homo sapiens] Length = 492	gil2507613	1	744	55	68	HCHAK72	Lung, Pancreas, Colon, Breast/Ovarian
176	827893	homology with GTP binding protein; putative [Caenorhabditis elegans] >pirS44605/S44605 C02F5.3 protein - Caenorhabditis elegans Length = 573	gil289610	165	836	62	75	HMSOT38	Lung, Pancreas
177	828072			1147	1305			HTECA53	Lung, Pancreas, Breast/Ovarian
178	828228			1105	1314			HW1.A1178	Prostate, Colon

179	828241	cathepsin O [Homo sapiens] >pir A55090 A55090 cathepsin O (EC 3.4.-.-) precursor - human >sp P43234 CATO_HUMAN CATHEPSIN O PRECURSOR (EC 3.4.22.-). Length = 321	gil574804	2	1012	93	93	HWBBP30	Lung, Pancreas, Prostate
180	828287	histone (H2A.Z) [Bos taurus] >gil410 histone H2A.Z (AA 1-127) [Bos taurus] >gil184060 histone (H2A.Z) [Homo sapiens] >gil31975 histone H2A.Z (AA 1-127) [Homo sapiens] >gil3649600 histone [Homo sapiens] >gil204599 histone (H2A.Z) [Rattus norvegicus] >gil57	gil163150	171	572	100	100	HUSIS02	Lung, Pancreas, Prostate, Breast/Ovarian
181	828364			663	1340			HWHGT17	Pancreas, Breast/Ovarian
182	828371	complement component C1s [Homo sapiens] >gil179648 complement subcomponent C1s precursor [Homo sapiens] >gil763110 complement protein C1s precursor [Homo sapiens] >pir A40496 C1HUS complement subcomponent C1s (EC 3.4.21.42) precursor - human >sp P09871 C1	gil179646	4	2283	97	97	HLQCQ12	Lung, Pancreas, Colon, Breast/Ovarian
183	828403	DNA-binding protein [Homo sapiens] >pir A44478 A44478 probable cell growth or differentiation regulator (alternatively spliced type I transcript) - human >sp Q02833 Q02833 PUTATIVE TRANSCRIPTIONAL REGULATORY PROTEIN HRC1. Length = 373	gil184390	1	648	98	98	HDTHL82	Lung, Pancreas, Colon
184	828501	(AF056302) c1f-2alpha kinase [Drosophila melanogaster] >sp O61651 O61651 EIF-2ALPHA KINASE. Length = 1589	gil3046551	1	1812	36	58	IIBMDG73	Lung, Colon, Breast/Ovarian

185	828520	(A1010840) ATP-dependent RNA helicase [Homo sapiens] >sp E1321519 E1321519 ATP-DEPENDENT RNA HELICASE (FRAGMENT). Length = 420	gn P1D1e1321519	445	1821	91	91	HRG1B47	Prostate, Breast/Ovarian
186	828527			723	926			HSKQ05	Lung, Pancreas, Prostate, Breast/Ovarian
187	828538			332	976			HPWDF55	Lung, Prostate, Breast/Ovarian
188	828541	pre-pump-1 proteinase (AA -17 to 250) [Homo sapiens] >gi 35803 PUMP [Homo sapiens] >pir B28816 KCHUM matrilysin (EC 3.4.24.23) precursor - human >sp P09237 COG7_HUMAN MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRI	gi 35799	43	933	100	100	HRACJ32	Pancreas, Prostate, Colon
189	828549	thrombospondin 2 [Homo sapiens] >pir A47379 TSHUP2 thrombospondin 2 precursor - human Length = 1172	gi 307506	26	1738	94	94	HF1AL22	Pancreas, Colon
190	828562			1	342			HPWBR24	Pancreas, Prostate
191	828576			3	731			HPTVU91	Pancreas, Prostate, Colon
192	828602			1050	1568			HPRAT58	Lung, Prostate
193	828628	tumor-associated antigen [Homo sapiens] >pir A36056 A36056 tumor-associated antigen CO-029 - human >sp P19075 CO02_HUMAN TUMOR-ASSOCIATED ANTIGEN CO-029. Length = 237	gi 180926	307	1029	94	94	HPRCM33	Pancreas, Prostate, Colon

194	828667	cytochrome c-1 [Homo sapiens] >sp P08574 CY1_HUMAN CYTOCHROME C1, HEME PROTEIN PRECURSOR. >gil181238 cytochrome c1 [Homo sapiens] {SUB 99-325; length = 325}	gil181240	2	1006	85	85	HKAOB02	Pancreas, Breast/Ovarian
195	828684	p55CDC [Homo sapiens] >pirA56021A56021 probable cell division control protein p55CDC - human >sp Q12834 Q12834 P55CDC. Length = 499	gil468032	41	1573	92	92	HPIJAE35	Pancreas, Prostate
196	828727	(AF044954) NADH:ubiquinone oxidoreductase PDSW subunit [Homo sapiens] >gil4165091 (AF088991) NADH:ubiquinone oxidoreductase PDSW subunit [Homo sapiens] Length = 172	gil4164442	3	629	93	93	HMCBB12	Lung, Prostate, Breast/Ovarian
197	828734	homologue of Drosophila Fat protein [Homo sapiens] >sp Q14517 Q14517 CADHERIN- RELATED TUMOR SUPPRESSOR HOMOLOG PRECURSOR (FAT PROTEIN HOMOLOG). >gnl PID d1022418 cadherin [Homo sapiens] {SUB 993-1132; length = 4590	gil1107687	1	657	99	99	HSRAB84	Pancreas, Colon, Breast/Ovarian
198	828750	(AF035940) similar to mago nashi [Homo sapiens] >gil2330011 (AF007862) mm-Mago [Mus musculus] >gil2909828 (AF035939) similar to mago nashi [Mus musculus] >sp O35169 O35169 MM-MAGO. >sp G2909830 G2909830 MAGOH. >sp P50606 MGN_HUMAN MAGO NASHI PROTEIN HOMOL	gil2909830	13	546	100	100	HPIAC11	Pancreas, Prostate, Breast/Ovarian

199	828842	(AB007191) AMY-1 [Homo sapiens] >gnl PID d1009980 c-myc binding protein [Homo sapiens] >sp Q99417 Q99417 C-MYC BINDING PROTEIN. Length = 103	gnl PID d1023271	1	363	98	100	HOUGA12	Pancreas, Prostate, Breast/Ovarian
200	828843	p48 [Homo sapiens] >sp P50502 HIP_HUMAN .HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN). >gil 1857033 SCN6 gene product [Homo sapiens] {SUB 99-369} Length = 369	gil 904032	3	761	99	100	HOVBK85	Lung, Pancreas, Prostate
201	828851	(AF054284) spliceosomal protein SAP 155 [Homo sapiens] >sp G4033735 G4033735 SPLICEOSOMAL PROTEIN SAP 155. >gil 3387899 (AF070540) putative nuclear protein [Homo sapiens] {SUB 101-1304} Length = 1304	gil 4033735	1	1029	98	98	HOSGA73	Pancreas, Prostate
202	828856	thymidine kinase (EC 2.7.1.21) [Homo sapiens] >gil 339719 thymidine kinase [Homo sapiens] >pir A27318 KHUT thymidine kinase (EC 2.7.1.21), cytosolic - human >sp P04183 KITH_HUMAN THYMIDINE KINASE, CYTOSOLIC (EC 2.7.1.21). >gil 339713 thymidine kinase [Homo sapiens]	gil 339709	1	804	99	100	HOHEN75	Prostate, Breast/Ovarian
203	828862	tyrosine kinase receptor [Homo sapiens] >pir B41527 B41527 transforming protein (axl(-)) - human Length = 885	gil 292870	1	417	98	98	HOHB190	Prostate, Breast/Ovarian
204	828870	TRAM protein [Homo sapiens] >pir S30034 S30034 translocating chain-associating membrane protein - human >sp Q15629 Q15629 TRAM PROTEIN. Length = 374	gil 37265	32	1279	94	94	HOEKU65	Lung, Pancreas, Colon

205	828873	precursor polypeptide (AA -31 to 1139) [Homo sapiens] >gi 538354 thrombospondin [Homo sapiens] {SUB 1-397} >gi 339669 thrombospondin [Homo sapiens] {SUB 1028-1170} >gi 532689 thrombospondin-1p180 [Homo sapiens] {SUB 364-422} Length = 1170	gi 37465	1	1398	100	100	100	HOHCJ26	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
206	828892	keratin [Homo sapiens] >sp Q14533 Q14533 KERATIN (HAIR TYPE II BASIC KERATIN) (KERATIN LIKE). >gn P1D1 18093 hair type II basic keratin [Homo sapiens] {SUB 81-505} >gi 951272 keratin like [Homo sapiens] {SUB 249-505} >hbs 161491 type II hair keratin {cl}	gn P1D1 e321549	3	653	90	91	91	HOGAA83	Lung, Prostate, Breast/Ovarian
207	828893	ESX [Homo sapiens] >gi 1841523 ESE-1b [Homo sapiens] >gi 2338756 AF017307 Ets-related transcription factor [Homo sapiens] >gi 2384740 AF016295 Ets transcription factor [Homo sapiens] >gi 2459797 epithelial-specific ets protein [Homo sapiens] >sp P78545	gi 1754538	36	1253	86	86	86	HOGAS09	Pancreas, Prostate, Colon, Breast/Ovarian
208	828897	prolactin [Homo sapiens] >gi 862305 prolactin [Homo sapiens] >pir A57014 A57014 prolactin (EC 3.4.21.-) precursor - human >sp G565130 G565130 PROLACTIN=SERINE PROTEINASE (N-TERMINAL); {SUB 45-64} Length = 343	gi 1143194	59	811	92	92	92	HBCAY53	Pancreas, Colon, Breast/Ovarian

209	828910	light chain 3 subunit of microtubule-associated proteins 1A and 1B [Rattus norvegicus] >pirA53624 A53624 microtubule-associated protein 1 light chain 3 - rat >sp Q62625 MPL3_RAT MICROTUBULE-ASSOCIATED PROTEINS 1A/1B LIGHT CHAIN 3 (MAP1A/MAP1B LC3). {SUB	gi 455109	28	540	96	98	HOIIDY41	Prostate, Colon
210	828927	cytochrome c oxidase subunit Va [Homo sapiens] >pirJT0342 OTHUSA cytochrome-c oxidase (EC 1.9.3.1) chain Va precursor - human >sp P20674 COXA_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR (EC 1.9.3.1). >gi 3859864 (AF067635) cytochrome c oxidase su	gi 693360	1	567	99	99	HHFJM88	Lung, Breast/Ovarian
211	828932	80K-11 protein [Homo sapiens] >gi 1293640 protein kinase C substrate 80K-H [Homo sapiens] >pir A32469 A32469 80K protein H precursor - human >sp P14314 G19P_HUMAN PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, HEAVY CHAIN (PKCSH) (80K-H PROTEIN). Length = 527	gi 182855	82	1026	83	83	INTAC57	Lung, Pancreas, Prostate, Breast/Ovarian
212	828933	Csa-19 [Homo sapiens] Length = 217	gi 531171	439	852	97	98	HEMCA07	Lung, Pancreas, Breast/Ovarian
213	828941	ORF YJL115w [Saccharomyces cerevisiae] >gi 171091 ASF1 [Saccharomyces cerevisiae] >pir S30766 S30766 ASF1 protein - yeast (Saccharomyces cerevisiae) >sp P32447 ASF1_YEAST ANTI-SILENCING PROTEIN 1. Length = 279	gi 1008304	1	729	59	74	HMGJB25	Lung, Pancreas, Colon, Breast/Ovarian

214	828957	F3IC3.5 [Caenorhabditis elegans] >sp O62193 O62193 F3IC3.5 PROTEIN. Length = 180	gnl P1D1e1346411	3	635	37	68	HMWHG54	Prostate, Breast/Ovarian
215	828963	house-keeping protein [Mus musculus] >pir S27870 S27870 house-keeping protein - mouse >sp Q61669 Q61669 HOUSE-KEEPING PROTEIN 1. Length = 396	gi 193871	73	1293	55	77	HMWB1191	Lung, Prostate, Colon, Breast/Ovarian
216	828964			639	905			HMWFZ60	Pancreas, Prostate, Colon, Breast/Ovarian
217	828966	S-adenosylhomocysteine hydrolase [Homo sapiens] >pir A43629 A43629 adenosylhomocysteinease (EC 3.3.1.1) - human Length = 432	gi 178279	2	1372	98	98	HMWV34	Lung, Pancreas, Prostate, Breast/Ovarian
218	828967	putative tRNA synthetase-like protein [Homo sapiens] >gi 4104935 (AF042347) putative phenylalanyl-tRNA synthetase alpha-subunit; PheHa [Homo sapiens] >sp E317305 E317305 PUTATIVE tRNA SYNTHETASE-LIKE PROTEIN. >sp G2102679 G2102679 PUTATIVE tRNA SYNTHETASE	gi 2102679	3	1535	98	98	HMUB112	Pancreas, Prostate, Breast/Ovarian
219	828977	insulin-like growth factor binding protein 2 [Homo sapiens] >bbs 106618 insulin-like growth factor binding protein-2, IGFBP-2 [human, placenta, Peptide, 328 aa] [Homo sapiens] >pir A41927 A41927 insulin-like growth factor-binding protein 2 precursor - hum	gi 179477	2	685	100	100	HMVAW27	Lung, Pancreas, Prostate, Breast/Ovarian

220	828978	annexin IV (placental anticoagulant protein II) [Homo sapiens] >gnl PID d1011889 annexin IV (carbohydrate-binding protein p33/41) [Homo sapiens] >pir A42077 A42077 annexin IV - human >sp P0925 ANX4_HUMAN ANNEXIN IV (LIPOCORTIN IV) (ENDONEXIN I) (CHROMOB	gi 178699	213	1184	100	100	HNTMH78	Lung, Pancreas, Prostate
221	828979			16	1080			IIMUB053	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
222	829001			1621	1959			IIMSJR30	Lung, Pancreas, Prostate, Breast/Ovarian
223	829003	plasma gelsolin [Homo sapiens] >pir A03011 FAHUP gelsolin precursor, plasma - human >sp P06396 GELS_HUMAN GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL). >gnl PID e20365 plasma gelsolin (AA 49-117) [Homo sapiens] [SUB 49-11	gi 736249	635	2536	99	99	HMSKA53	Lung, Pancreas, Prostate
224	829016	(AB006625) The human homolog of a mouse imprinted gene, Peg3. [Homo sapiens] >sp P78418 P78418 KIAA0287 (PEG3) (FRAGMENT). >gi 1899244 PEG3 [Homo sapiens] [SUB 518-1132] Length = 1132	dbj AB006625_1	409	759	87	87	IIMIA173	Prostate, Breast/Ovarian
225	829027	ras-like protein [Homo sapiens] >pir D34788 TVHUC4 transforming protein ras (teratocarcinoma clone TC10) - human Length = 213	gi 190881	2	577	100	100	IIMIBE59	Prostate, Colon

226	829028	RnudC gene product [Rattus norvegicus] >pir A55897 A55897 prolactin-induced T cell protein c15 - rat >sp Q63525 Q63525 C15 MRNA. Length = 332	gil619907	31	1110	95	98	HMG1Q56	Pancreas, Prostate, Breast/Ovarian
227	829031	protocadherin X [Mus musculus] >sp G4099553 G4099553 PROTOCADHERIN X. Length = 928	gil4099553	116	637	90	93	HMG1H69	Lung, Pancreas, Prostate, Breast/Ovarian
228	829034			28	1362			HME1Y69	Pancreas, Prostate
229	829036	Similar to B. subtilis Poly(A) polymerase (SW:PAPS_BACSU) [Caenorhabditis elegans] >sp Q93795 Q93795 F55B12.4 PROTEIN. Length = 440	gn P D e 347205	114	1151	67	81	HME1J75	Pancreas, Prostate
230	829049	UDP-Gal:GlcNAc galactosyltransferase [Homo sapiens] >sp O60910 O60910 UDP-GAL:GLCNAC GALACTOSYLTRANSFERASE. Length = 393	gn P D e 283714	233	1444	94	94	HMEFQ33	Prostate, Colon
231	829073			193	843			HLYCD85	Pancreas, Prostate
232	829075			2	484			HMAAD66	Lung, Pancreas, Prostate, Breast/Ovarian
233	829076			3	665			HADDC41	Lung, Pancreas, Breast/Ovarian
234	829080			3	500			IIMABG80	Prostate, Breast/Ovarian
235	829087	small GTP-binding protein [Oryctolagus cuniculus] >pir A48500 A48500 small GTP-binding protein Rab25 - rabbit Length = 213	gil436001	157	873	95	97	HLWBY67	Pancreas, Prostate, Breast/Ovarian

236	829092	UDP-galactose translocator [Homo sapiens] >pir JC4903 JC4903 UDP-galactose transporter, splice form 1 - human Length = 393	gnl PID d1013353	1	513	85	85	HLWBC74	Pancreas, Prostate
237	829095			3	425			HLWBM89	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
238	829096	antiquitin=26g turgor protein homolog [human, kidney, Peptide, 511 aa] [Homo sapiens] >pir A54676 A54676 antiquitin - human >sp P49419 DHAX_HUMAN ANTIQUITIN (EC 1.2.1.-). Length = 511	bbs 158840	552	1628	97	97	HLWAO28	Prostate, Breast/Ovarian
239	829118	nuclear autoantigen fo 14 kDa [Homo sapiens] >sp O43805 O43805 NUCLEAR AUTOANTIGEN FO 14 KDA. Length = 119	gnl PID c322419	2	415	99	99	HLSDA35	Lung, Prostate
240	829152	unknown protein precursor [Homo sapiens] >pir JN0596 JN0596 fibrinogen-related protein II(FRII)-I precursor - human >sp Q08830 Q08830 FIBRINOGEN-LIKE PROTEIN I PRECURSOR. Length = 312	gnl PID d1003846	215	1231	95	95	HLIC182	Lung, Pancreas, Prostate
241	829160	ubiquitin-conjugating enzyme UbcH6 [Homo sapiens] Length = 193	gij 1064914	2	769	83	83	HLFB156	Lung, Pancreas, Prostate, Colon
242	829163			403	930			HSPBG80	Lung, Pancreas, Breast/Ovarian
243	829176	C4b-binding protein alpha chain [Homo sapiens] >gij 190502 C4b-binding protein alpha chain (Homo sapiens) >pir A33568 NBHUC4 C4b-binding protein alpha chain precursor - human >sp P04003 C4BP_HUMAN C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PRO	gij 190500	3	662	100	100	HLQBR92	Lung, Pancreas
244	829204			515	913			HLISB22	Prostate, Breast/Ovarian

245	829207		111	977		HL1SA66	Prostate, Breast/Ovarian
246	829228		1	2508		HKGBQ77	Lung, Prostate, Colon
247	829252		96	1322		HKAP121	Pancreas, Prostate
248	829254		1	483		HKFB196	Lung, Pancreas, Prostate, Breast/Ovarian
249	829269		121	474		HKAE196	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
250	829277		3	596		HJPC91	Lung, Prostate
251	829290		100	207		HJBDL52	Lung, Pancreas, Prostate, Breast/Ovarian
252	829294		3	1847		HISDU47	Pancreas, Prostate
253	829299		3	794		HISEC32	Lung, Pancreas, Prostate
254	829308	dJ1409.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens] >sp O76058 O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE). Length = 606	207	938	47	111BCN93	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
255	829349	ribosomal protein S15a [Rattus norvegicus] >pir JC2234 JC2234 ribosomal protein S15a - rat Length = 130	152	547	100	HICAF44	Lung, Pancreas, Prostate, Breast/Ovarian
256	829354	RAD4 gene product [Saccharomyces cerevisiae] Length = 730	1	1113	44	HJBD51	Lung, Pancreas, Breast/Ovarian

257	829388	DNase protein [Homo sapiens] >gi 1620214 XIB [Homo sapiens] >pir C4633 C4633 DNase I-like endonuclease (EC 3.1.-.-) - human >sp P49184 DRNL_HUMAN MUSCLE-SPECIFIC DNASE I-LIKE PRECURSOR (EC 3.1.21.-) (DNASE X) (XIB). Length = 302	gi 929628	319	1281	94	94	HUVCJ22	Lung, Pancreas, Colon, Breast/Ovarian
258	829540			258	437			HAPOU28	Lung, Pancreas, Colon, Breast/Ovarian
259	829626	mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - rabbit (fragment) >gi 474282 mannosyl-oligosaccharide alpha-1,2-mannosidase [Oryctolagus cuniculus] (SUB 12-480) Length = 480	pir B54408 B54408	3	764	75	88	HCEES14	Lung, Pancreas, Colon, Breast/Ovarian
260	829730	underexpressed in thyroid tissue after TSH stimulation [Canis familiaris] >sp Q28283 Q28283 C5FW PROTEIN. Length = 343	gnl PID e252512	455	1153	62	75	HAJBK53	Pancreas, Breast/Ovarian
261	829892	(AF053651) cellular apoptosis susceptibility protein [Homo sapiens] >sp O75432 O75432 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN. Length = 971	gi 3598795	64	1053	85	85	HAMFJ43	Lung, Prostate
262	829933	(AF035606) calcium binding protein [Homo sapiens] >sp O75340 O75340 CALCIUM BINDING PROTEIN. Length = 191	gi 3342794	1	540	86	86	HAICT76	Pancreas, Prostate
263	829938	(AF067855) geminin [Homo sapiens] >sp O75496 O75496 GEMININ. Length = 209	gi 3249005	230	952	93	93	HAIBS55	Pancreas, Prostate
264	829969			551	814			HACCB64	Lung, Pancreas, Prostate, Breast/Ovarian

265	829982	(AF020352) NADH:ubiquinone oxidoreductase 15 kDa IP subunit [Homo sapiens] >gil2911482 (AF047434) NADH-ubiquinone oxidoreductase 15kDa subunit; CI-15 protein [Homo sapiens] >sp O43920 NIPM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 15 KD SUBUNIT (EC 1.6.5.3) (E	gil2655055	28	399	100	100	11A1BK1:25	Prostate, Breast/Ovarian
266	830007	catechol-O-methyltransferase [Homo sapiens] >gil403304 catechol O-methyltransferase [Homo sapiens] >pir S37406 A38459 catechol O-methyltransferase (EC 2.1.1.6) - human >sp P21964 COMT_HUMAN CATECHOL O-METHYLTRANSFERASE; MEMBRANE-BOUND FORM (EC 2.1.1.6) (M	gil180920	110	1006	99	99	H6EDW66	Lung, Prostate, Breast/Ovarian
267	830019	(AF030249) putative dienoyl-CoA isomerase [Homo sapiens] >gil564065 peroxisomal enoyl-CoA hydratase-like protein [Homo sapiens] >pir 38882 38882 peroxisomal enoyl-CoA hydratase-like protein - human >sp Q13011 ECH1_HUMAN PROBABLE PEROXISOMAL ENOYL-COA HY	gil2623168	77	976	94	96	112MAC92	Prostate, Breast/Ovarian
268	830073			1	690			HBWBK27	Lung, Pancreas, Breast/Ovarian
269	830130			1	177			H2LAD55	Lung, Prostate, Breast/Ovarian
270	830134			16	1290			H2CIBP53	Lung, Pancreas, Prostate, Colon, Breast/Ovarian

271	830135	neutrophil gelatinase associated lipocalin [Homo sapiens] >sp P80188 NGAL_HUMAN NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (25 KD ALPHA-2-MICROGLOBULIN-RELATED SUBUNIT OF MMP-9) (LIPOCALIN-2) (ONCOGENE 24P3). Length = 198	gij929657	2	763	100	100	H2MAC06	Pancreas, Prostate, Breast/Ovarian
272	830148	snRNP polypeptide B [Homo sapiens] >sp Q15182 Q15182 SNRNP POLYPEPTIDE B. Length = 285	gij190247	96	839	79	79	HAICK77	Lung, Prostate, Breast/Ovarian
273	830149	threonyl-tRNA synthetase [Homo sapiens] >pir A38867 YSHUT threonine--tRNA ligase (EC 6.1.1.3) - human Length = 712	gij1464742	3	2333	95	95	H2CBC04	Lung, Pancreas, Prostate
274	830154	spectrin SH3 domain binding protein 1 [Homo sapiens] >sp O76049 O76049 SPECTRIN SH3 DOMAIN BINDING PROTEIN 1. Length = 508	gij3165429	2	1081	100	100	HYAAC49	Lung, Pancreas
275	830183	heat shock protein 84 - mouse >pir B34461 B34461 heat shock protein 90 beta - rabbit (fragment) (SUB 1-25) >sp P30947 HS9B_RABBIT HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (FRAGMENT). (SUB 2-25) >pir S13268 S13268 heat shock protein, 90K - bovine (fragment)	pir A35569 HHMS84	92	338			HWLQF08	Pancreas, Breast/Ovarian
276	830194			3	1043	100	100	HLDCP20	Lung, Pancreas, Breast/Ovarian
277	830207	(AF016437) contains similarity to a C2H2-type zinc finger [Caenorhabditis elegans] >sp O16350 O16350 F13H6.1 PROTEIN. Length = 631	gij2315332	173	1051	45	63	HWLMF07	Pancreas, Colon
278	830242			85	654			HWLUF58	Lung, Pancreas

279	830328	putative cyclin G1 interacting protein [Homo sapiens] >sp O43257 O43257 PUTATIVE CYCLIN G1 INTERACTING PROTEIN. Length = 154	gi 2668505	304	954	81	81	HWLEL26	Lung, Colon, Breast/Ovarian
280	830340	putative cell surface antigen [Rattus norvegicus] >sp P97881 P97881 PUTATIVE CELL SURFACE ANTIGEN. Length = 347	gi 1890275	1	336	63	81	HWLEG68	Pancreas, Colon
281	830341	peroxisomal acyl-coenzyme A oxidase, AOX [human, liver, Peptide, 661 aa] [Homo sapiens] Length = 661	bbs 144907	1	648	100	100	HSIAI179	Lung, Pancreas
282	830351			3	656			HWHQ721	Colon, Breast/Ovarian
283	830358			456	716			HSUAE53	Lung, Colon, Breast/Ovarian
284	830390	platelet membrane glycoprotein IIb beta subunit [Homo sapiens] >sp O15495 O15495 PLATELET MEMBRANE GLYCOPROTEIN IIIA BETA SUBUNIT. Length = 784	gi 2443452	2	523	90	90	HWGQA69	Pancreas, Colon
285	830400	phosphate carrier protein [Homo sapiens] >pir B53737 B53737 phosphate carrier protein, form B - human Length = 361	gi 38262	2	1078	99	100	IHW11P1Y68	Lung, Pancreas, Breast/Ovarian
286	830437	IgG Fc receptor 1 [Homo sapiens] >gi 292169 Fc gamma receptor 1 [Homo sapiens] >pir A39878 A39878 Fc gamma (IgG) receptor 1-A (high affinity) precursor - human >sp Q92663 Q92663 FC GAMMA RECEPTOR 1. Length = 374	gi 180279	3	1199	91	91	HWABG32	Lung, Colon

287	830458	HBp15/L22 [Sus scrofa] >gnlPID d1005074 HBp15/L22 [Mus musculus] >pirJC212 JC2121 heparin-binding protein 15 - pig >pirJC2119 JC2119 heparin-binding protein 15 - mouse Length = 128	gnlPID d1005075	1	441	70	70	HDQMF96	Lung, Pancreas
288	830466	tenascin X [Homo sapiens] >spIP78530 P78530		988	1260			HOEEZ61	Lung, Colon
289	830497	TENASCIN X (TENASCIN-X). >gil2347137 (AF019413) tenascin X [Homo sapiens] {SUB 2593-4289} >pirA42175 A42175 tenascin homolog 3.9kF3-3 - human (fragment) {SUB 2793-2880} >pir B42175 B42175 tenascin homolog 3.9kF	gil1841546	2	1531	99	99	HUFBX52	Lung, Breast/Ovarian
290	830511	carcinoembryonic antigen [Homo sapiens] >gil178677 carcinoembryonic antigen precursor [Homo sapiens] >pirA36319 A36319 carcinoembryonic antigen precursor - human >spIP0673 JCCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E	gil180223	3	1292	99	99	HWLGV67	Pancreas, Colon
291	830512	carcinoembryonic antigen [Homo sapiens] >gil178677 carcinoembryonic antigen precursor [Homo sapiens] >pirA36319 A36319 carcinoembryonic antigen precursor - human >spIP0673 JCCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E	gil180223	3	2213	87	89	HUFC129	Lung, Pancreas

292	830513		3	215		IIPRTG72	Lung, Colon, Breast/Ovarian
293	830540	protein kinase MUK2 [Rattus norvegicus] >gi2772514 serine/threonine protein kinase [Rattus norvegicus] >sp P35465 PAK1_RAT SERINE/THREONINE-PROTEIN KINASE PAK- ALPHA (EC 2.7.1.1) (P68-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2). Length	2	733	100	HTLHR67	Lung, Pancreas, Colon
294	830550	guanine nucleotide-binding regulatory protein-beta-2 subunit [Homo sapiens] >gi339935 transducin beta-2 subunit [Homo sapiens] >gi3135310 (AF053356) GNB2 [Homo sapiens] >pirB26617RGHUB2 GTP-binding regulatory protein beta-2 chain - human >sp P11016 GB	3	500	100	HTWJC08	Lung, Breast/Ovarian
295	830567		141	377		HTTBH33	Lung, Pancreas
296	830586	(2'-5')oligoadenylate synthetase [Homo sapiens] Length = 364	2	1192	98	HKACP86	Pancreas, Prostate, Breast/Ovarian
297	830632	P2 gene for c subunit of mitochondrial ATP synthase gene product [Homo sapiens] >gnl PID d1002921 ATP synthase subunit c precursor [Homo sapiens] >pir S34067 S34067 H+- transporting ATP synthase (EC 3.6.1.34) lipid- binding protein P2 precursor, mitochondri	264	803	85	HTPCV95	Lung, Breast/Ovarian

298	830645	propionyl CoA carboxylase beta subunit, beta PCC {EC 6.4.1.3} [human, liver, placenta, HL 1008. Peptide, 539 aa] [Homo sapiens] >pirJA53020 A53020 propionyl-CoA carboxylase (EC 6.4.1.3) beta chain precursor - human >gil3036995 propionyl-CoA carboxylase B	bbs 140816	54	1505	99	99	HTEDS58	Lung, Pancreas, Colon
299	830652	strong homology to human RING3 sequence [Homo sapiens] >sp O60885 O60885 HUNK1 MRNA. Length = 722	gnl PID e1290115	1	177	64	64	HUKFL74	Lung, Colon
300	830659	CDC42 GTP-binding protein [Canis familiaris] >gil183490 GTP-binding protein G25K [Homo sapiens] >gil293321 CDC42Mm [Mus musculus] >gil1049309 CDC42 protein [Mus musculus] >pirJA39265 A39265 GTP-binding protein G25K, placental - human >pirJS57563 S57563 CD	gil887408	118	714	100	100	HKAOE74	Lung, Pancreas, Breast/Ovarian
301	830696			2	514			HSTBJ95	Lung, Breast/Ovarian
302	830706			2457	2909			HELFC05	Pancreas, Breast/Ovarian
303	830743	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL (EC 3.6.1.34). Length = 50	sp P56381 ATPE_HUMAN	53	262	100	100	HCBBAS1	Lung, Colon
304	830770	p21-activated protein kinase [Homo sapiens] >pirJS58682 S58682 protein kinase, p21-activated (EC 2.7.1.-) - human Length = 525	gil780808	1	498	99	99	HEMCG27	Lung, Colon, Breast/Ovarian
305	830830	(AF002822) cyclin B2 [Homo sapiens] >sp G4101270 G4101270 CYCLIN B2. Length = 398	gil4101270	99	1358	99	99	HROC157	Lung, Pancreas, Colon

306	830838		1	747		HS2AF59	Lung, Pancreas, Colon, Breast/Ovarian
307	830851		2	718		HTX1J25	Pancreas, Colon
308	830853		2	1183		IIRDS42	Pancreas, Colon
309	830856		542	874		HSAX81	Colon, Breast/Ovarian
310	830862	ribosomal protein [Homo sapiens] >gi453281 ribosomal protein S23 [Rattus norvegicus] >pirS41955[S41955 ribosomal protein S23, cytosolic - rat >pirS42105[S42105 ribosomal protein S23, cytosolic - human >pirI52292[I52292 ribosomal protein S23 - rat >gnl	3	518	100	III.L.CC05	Lung, Prostate, Breast/Ovarian
311	830879	(AJ002120) Zfx [Monodelphis domestica] >spO19019[O19019 ZFX TYPE GENE (FRAGMENT). Length = 180	2	592	39	HVAAB82	Pancreas, Colon
312	830919		69	536		HOUHK65	Pancreas, Breast/Ovarian
313	830969	(AF005046) serine/threonine kinase [Homo sapiens] >gnlPIDe1371371 (AJ011855) PAK4 protein [Homo sapiens] >spG4101587[G4101587 SERINE/THREONINE KINASE. Length = 591	140	514	96	HOGAU20	Pancreas, Breast/Ovarian
314	830991	insulin-like growth factor-binding protein [Homo sapiens] >gi1386791 growth factor-binding protein- 3 [Homo sapiens] >gi1398164 insulin-like growth factor binding protein 3 [Homo sapiens] >pirA36578[OHU3 insulin-like growth factor- binding protein 3 precu	2	607	86	HDLAE73	Pancreas, Breast/Ovarian

315	831002	cyclin [Homo sapiens] >gi1387005 proliferating cell nuclear antigen (PCNA) [Homo sapiens] >pirA27445 WMHUET proliferating cell nuclear antigen - human >sp P12004 PCNA_HUMAN PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN). Length = 261	gi181272	168	974	100	100	HOEMJ36	Colon, Breast/Ovarian
316	831003	T-plastin - human >sp P13797 PLST_HUMAN T-PLASTIN. (SUB 4-630) >gil190028 T-plastin polypeptide [Homo sapiens] (SUB 61-630) >gi1339848 T-plastin [Homo sapiens] (SUB 1-143) >gi1292832 T-plastin [Homo sapiens] (SUB 588-630) Length = 630	pirA34789 A34789	91	2007	94	95	HAIBD64	Lung, Pancreas
317	831021			474	662			HE8BN45	Pancreas, Colon, Breast/Ovarian
318	831036	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens] >sp E1363774 E1363774 DTDP-D-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46). Length = 350	gn PID e1363774	1	621	100	100	HNTSQ61	Pancreas, Colon
319	831071	lrp gene product [Homo sapiens] >pirSS7723 SS7723 lrp protein - human >sp Q14764 MVP_HUMAN MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN). Length = 896	gi1895840	67	2610	94	94	HWLEG93	Lung, Pancreas
320	831094			755	928			HNFE067	Colon, Breast/Ovarian

321	831099	fibronectin receptor beta subunit precursor (AA -20 to 778) [Homo sapiens] >pir B27079 B27079 fibronectin receptor beta chain precursor - human >sp P05556 TBI_HUMAN FIBRONECTIN RECEPTOR BETA SUBUNIT PRECURSOR (INTEGRIN BETA-1) (CD29) (INTEGRIN VLA-4 BETA	gi 31442	3	1697	99	100	HA5AB03	Lung, Pancreas, Colon, Breast/Ovarian
322	831113	4E-binding protein 1 [Homo sapiens] >pir S50866 S50866 4E-BP1 protein - human >pir JC5899 JC5899 initiation factor 4E-binding protein 1 - human >sp Q13541 Q13541 4E- BINDING PROTEIN 1. Length = 118	gi 561630	1	414	100	100	HMWHP74	Lung, Pancreas, Colon, Breast/Ovarian
323	831120			1	1221			HWLHY12	Pancreas, Colon
324	831172	Similarity to Human hnRNP F protein (PIR Acc. No. S43484): (AF042501) cytochrome b [Homo sapiens] >sp O78829 O78829 CYTOCHROME B (FRAGMENT). Length = 380	gn P1D1e 349655	2	721	52	66	III.WBE22	Pancreas, Breast/Ovarian
325	831178		gi 3372365	512	829	69	70	HDLAC61	Lung, Colon
326	831184			770	1399			HWLGP91	Lung, Pancreas, Colon
327	831203			3	545			HMICQ42	Pancreas, Colon, Breast/Ovarian
328	831210	TGF-beta masking protein large subunit [Rattus norvegicus] >pir A38261 A38261 masking protein precursor - rat Length = 1712	gi 207286	1	498	86	91	HMEIJ62	Pancreas, Colon
329	831228			104	214			HMEAM30	Lung, Pancreas, Breast/Ovarian

330	831256	MLN 64 [Homo sapiens] >dbj D38255.1 CABI [Homo sapiens] >pir I38027 I38027 MLN 64 protein - human >sp Q14849 Q14849 MLN64 MRNA. Length = 445	gi 951279	658	1164	94	94	HMTBL29	Lung, Pancreas
331	831257	MLN 64 [Homo sapiens] >dbj D38255.1 CABI [Homo sapiens] >pir I38027 I38027 MLN 64 protein - human >sp Q14849 Q14849 MLN64 MRNA. Length = 445	gi 951279	323	862	91	91	HLWDQ05	Pancreas, Colon
332	831277			3	1310			HUTHD56	Lung, Pancreas, Colon
333	831317	inter-alpha-trypsin inhibitor light chain [Homo sapiens] >gi 32047 HC polypeptide [Homo sapiens] >gi 24479 precursor polypeptide [Homo sapiens] >gi 825614 alpha I-microglobulin [Homo sapiens] >pir S13433 HCHU alpha-I-microglobulin/inter- alpha-trypsin inhib	gi 186600	193	1290	100	100	HLQAC21	Pancreas, Breast/Ovarian
334	831339	(AB012276) ATFX [Mus musculus] >sp O7019 O70191 ATFX (FRAGMENT). >sp G246896 G246896 ATFX=ATF4 RELATED PROTEIN. (SUB 1-37) >sp G246899 G246899 ATFX=ATF-4-RELATED PROTEIN. (SUB 38- 76; Length = 84	gnl PID d1026241	631	1029	90	93	HLJCC93	Lung, Colon, Breast/Ovarian
335	831363	acyl coenzyme A:cholesterol acyltransferase, carboxylesterase, ACAT (EC 2.3.1.26) [human, liver, Peptide, 568 aa] [Homo sapiens] >sp G415564 G415564 CARBOXYLESTERASE (EC 3.1.1.1). (SUB 20-568) >gi 179930 carboxylesterase [Homo sapiens] (SUB 62-568) Length	bbs 156481	123	1871	98	98	HLDNR55	Lung, Colon

336	831367	D-dopachrome tautomerase [Homo sapiens] >gi 1864028 D-dopachrome tautomerase [Homo sapiens] >gi 3047378 (AF058293) D-dopachrome tautomerase [Homo sapiens] >gi P1D1e311354 phenylpyruvate tautomerase II [Homo sapiens] >gi 2352915 (AF012434) D-dopachrome ta	gi 1805303	325	618	100	100	III.DDR74	Lung, Colon
337	831379	cDNA from hypercalcemic tumour [Rattus norvegicus] >pir S28223 S28223 parathyroid hormone-like protein - rat >sp Q05310 L10K_RAT LEYDIG CELL TUMOR 10 KD PROTEIN. Length = 93	gi 57064	3	383	90	95	HKQAC03	Lung, Pancreas, Colon, Breast/Ovarian
338	831385			96	377			HKIMC75	Lung, Pancreas, Colon, Breast/Ovarian
339	831390	aldehyde reductase (EC 1.1.1.2) [Homo sapiens] >gi 2707824 (AF036683) aldehyde reductase [Homo sapiens] >pir A33851 A33851 alcohol dehydrogenase (NADP+) (EC 1.1.1.2) - human >sp G2707824 G2707824 ALDEHYDE REDUCTASE. >sp P14550 ALDX_HUMAN ALCOHOL DEHYDROGE	gi 178481	254	1312	94	94	HKGDF04	Lung, Pancreas

340	831391	islet regenerating protein [Homo sapiens] >pir A35197 RGHUIA regenerating islet lectin I- alpha precursor - human >sp P05451 LITA_HUMAN LITHOSTATHINE I ALPHA PRECURSOR (PANCREATIC STONE PROTEIN) (PSP) (PANCREATIC THREAD PROTEIN) (PTP) (ISLET OF LANGERHANS PROTEIN)	gil190979	71	592	100	100	HLDBE06	Pancreas, Colon
341	831405	factor H homologue [Homo sapiens] >pir I56100 I56100 factor H homologue - human >sp Q03591 CFH1_HUMAN COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36). Length = 330	gil183763	53	1078	94	94	HLDOB31	Lung, Pancreas, Colon, Breast/Ovarian
342	831442	PDGF associated protein [Homo sapiens] >sp Q13442 HP28_HUMAN 28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF ASSOCIATED PROTEIN). Length = 181	gil1136584	2	595	60	60	HKAEB15	Lung, Pancreas, Colon, Breast/Ovarian
343	831476	dermatopontin [Homo sapiens] >pir A47220 A47220 dermatopontin precursor - human >sp Q07507 DERM_HUMAN DERMATOPONTIN PRECURSOR. >pir S34838 S34838 tyrosine-rich acidic matrix protein - pig [SUB 101-144] Length = 201	gil311614	1	630	91	91	HJMBK21	Lung, Pancreas, Colon
344	831488	similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gil1401053 SUPT4H [Homo sapiens] >gil1401055 SUPT4H [Homo sapiens] >gil1401066 Supt4h [Mus musculus] >gil3779194 chromatin structural protein homolog [M	gil1209779	158	580	100	100	HJBCG39	Colon, Breast/Ovarian

345	831518		240	467		HATCV09	Pancreas, Colon, Breast/Ovarian
346	831519	(AF062536) cullin 1 [Homo sapiens] >sp O60719 O60719 CULLIN 1. >gi 4153866 (AC005229) cullin 1 [Homo sapiens] (SUB 1-263) Length = 776	165	1712	100	H01EC149	Pancreas, Breast/Ovarian
347	831521		3	863		HIBCE91	Colon, Breast/Ovarian
348	831550	met-13a protein - mouse Length = 132	158	457	70	HCHNH46	Lung, Pancreas, Breast/Ovarian
349	831560		1474	1818		HCR0A68	Pancreas, Breast/Ovarian
350	831562	fibromodulin [Homo sapiens] >sp O06828 FMOD_HUMAN FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN). Length = 376	28	1272	90	HIEGAD80	Pancreas, Breast/Ovarian
351	831570	(AF042822) epithin [Mus musculus] >sp G4104970 G4104970 EPTTHIN. Length = 902	2	1861	77	HLWCC68	Lung, Pancreas, Colon
352	831593		726	878		HHBFW28	Lung, Pancreas
353	831596	32 kd accessory protein [Bos taurus] >gi 190376 proton A TPase accessory subunit [Homo sapiens] {SUB 264-351} Length = 351	2	808	100	HHEDJ61	Colon, Breast/Ovarian
354	831627		1	903		HBJHI46	Lung, Pancreas
355	831649		1	738		HIPTDD09	Lung, Colon
356	831664	transformation upregulated nuclear protein - human Length = 464	180	1574	94	HIIPCU40	Lung, Colon

357	831674	complement protein C8 beta subunit precursor [Homo sapiens] >pir A4307 C8HUB complement C8 beta chain precursor - human >sp P07358 C8B_HUMAN COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR. Length = 591	gi 179720	1	1338	96	96	HLDOX36	Pancreas, Colon
358	831684	(AF033630) monocyte/neutrophil elastase inhibitor [Homo sapiens] >pir S27383 S27383 elastase inhibitor - human >sp P30740 ILEU_HUMAN LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI). >sp G2997692 G2997692 MONOCYTE/NEUTROPHI	gi 2997692	1	1311	96	96	HFOXEX22	Pancreas, Colon
359	831687	Mpv17 [Mus musculus] >pir S29031 S29031 mpv17 protein - mouse >sp P19258 MPV1_MOUSE MPV17 PROTEIN. >gi 3252875 (AF038632) Mpv17 protein [Mus musculus] (SUB 155-176) Length = 176	gi 199790	60	305	89	93	HPK1D75	Pancreas, Colon
360	831726	rat ribosomal protein L36 [Rattus norvegicus] >pir N0483 N0483 ribosomal protein L36 - rat Length = 105	gi 312345	77	454	98	98	HAGDQ96	Lung, Breast/Ovarian
361	831736			95	484			HLWEQ18	Colon, Breast/Ovarian
362	831762			37	720			HEQB179	Pancreas, Colon
363	831801	ear-2 gene product [Homo sapiens] >pir S02709 S02709 ear-2 protein - human >sp P10588 EAR2_HUMAN V-ERBA RELATED PROTEIN EAR-2. Length = 403	gi 31065	3	812	76	77	HKAHB85	Lung, Pancreas, Breast/Ovarian

364	831848		2018	2284		HE8AF82	Lung, Colon, Breast/Ovarian
365	831861	(AF076786) serum amyloid A-activating factor SAF-8 [Oryctolagus cuniculus] >sp G3986442 G3986442 SERIUM AMYL(III) A- ACTIVATING FACTOR SAF-8 (FRAGMENT). Length = 214	341	775	77	HJPCX51	Lung, Pancreas, Breast/Ovarian
366	831866	(AF054174) histone macroH2A1.2 [Homo sapiens] >sp G3341992 G3341992 HISTONE MACROH2A1.2. Length = 371	53	1186	100	HE6FG90	Lung, Colon
367	831878		2	661		HDTLN67	Colon, Breast/Ovarian
368	831899		1	693		HDTBQ51	Colon, Breast/Ovarian
369	831913	nuclear antigen H731 [Homo sapiens] >pir JC5193 JC5193 nuclear protein H731 - human >sp Q99834 Q99834 NUCLEAR ANTIGEN H731. Length = 458	95	1132	96	HL YG1A31	Lung, Colon
370	831972	p619 [Homo sapiens] >pir S71752 S71752 giant protein p619 - human >sp Q15751 Q15751 P619. Length = 4861	331	855	33	HDPKK57	Lung, Pancreas, Breast/Ovarian
371	831985		425	805		HDPPP36	Lung, Pancreas, Colon, Breast/Ovarian
372	831986		30	467		HCIC1168	Pancreas, Colon, Breast/Ovarian
373	832010	(AL021918) b3418.1 (Kruppel related Zinc Finger protein 184) [Homo sapiens] >sp O60792 O60792 B3418.1 (KRUPPEL RELATED ZINC FINGER PROTEIN 184). Length = 751	1	348	57	HIDF1B44	Lung, Pancreas, Colon

374	832016	C protein (AA 1-159) [Homo sapiens] >pir S01387 S01387.U1 snRNP protein C - human Length = 159	gi 37543	2	604	100	100	HT1DG34	Lung, Breast/Ovarian
375	832041	metalloelastase HME (EC 3.4.24.-) - human >sp P39900 COGM_HUMAN MACROPHAGE METALLOELASTASE PRECURSOR (EC 3.4.24.65) (HME) (MATRIX METALLOPROTEINASE-12) (MMP-12). Length = 470	pir A49499 A49499	54	1472	100	100	HDPGC33	Lung, Pancreas, Colon
376	832044	5-aminimidazole-4-carboxamide-1-beta-D- ribofuranose transferase [Homo sapiens] >gnl PID d102226 7 5-aminimidazole-4- carboxamide ribonucleotide transferase [Homo sapiens] >pir JC4642 JC4642 purH bifunctional enzyme - human >sp Q13856	gnl PID d1012226	1	1794	99	99	HGCOL40	Lung, Pancreas, Colon, Breast/Ovarian
377	832049	proteasome subunit HsC10-11 [Homo sapiens] >pir S55041 S55041 multicatalytic endopeptidase complex (EC 3.4.99.46) beta chain C10-II - human >sp P49720 PRCT_HUMAN PROTEASOME THIETA CHAIN (EC 3.4.99.46) (MACROPAIN THIETA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE C	gnl PID d1006190	84	710	99	100	HCFAU68	Lung, Pancreas, Breast/Ovarian
378	832122			427	846			HCUDT18	Lung, Pancreas, Colon, Breast/Ovarian
379	832148			246	380			HFHN81	Colon, Breast/Ovarian
380	832197			433	642			HICQA151	Pancreas, Breast/Ovarian
381	832237			290	553			HOCTE23	Lung, Colon
382	832246			66	959			HCMSD61	Lung, Pancreas

383	832256	ligand for eph-related receptor tyrosine kinases [Homo sapiens] >gil1809292 putative EPH-related PTK receptor ligand LERK-8 [Homo sapiens] >sp Q15768 IEFB3_HUMAN EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECE	gil1469782	1	81	100	100	HBXAC19	Pancreas, Colon, Breast/Ovarian
384	832280	(AF071747) topoisomerase II alpha [Homo sapiens] >sp G3869316 G3869316 TOPOISOMERASE II ALPHA. Length = 1531	gil3869316	2	1141	79	79	INTSQ37	Lung, Colon, Breast/Ovarian
385	832285			1550	1783			HLTBQ30	Lung, Prostate
386	832294			1	666			HBMC80	Lung, Colon
387	832326			472	1131			HJPAT43	Lung, Colon, Breast/Ovarian
388	832333	CENP-B protein [Ovis aries] >sp P49451 CENB_SHEEP MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) (FRAGMENT). Length = 239	gil1016292	3	551	96	96	HCHMS55	Pancreas, Breast/Ovarian
389	832346			295	471			HBAGU45	Colon, Breast/Ovarian
390	832370	HER2 receptor [Homo sapiens] >gil553282 c-erb-2 protein [Homo sapiens] (SUB 737-1031) >gil553332 HER-2/neu [Homo sapiens] (SUB 1- 191) >gil183989 HER2 receptor (AA at 3) [Homo sapiens] (SUB 740-910) >gil182169 c-erb B2/neu protein [Homo sapiens] (SUB 1081-	gil306840	2	406	83	83	HFIEC83	Lung, Breast/Ovarian
391	832381			138	539			HATAA19	Pancreas, Breast/Ovarian

392	832394	platelet-endothelial tetraspan antigen 3 [Homo sapiens] >sp P48509 C151_HUMAN PLATELET- ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN). Length = 253	gij541613	2	847	85	85	HF1T1D21	Lung, Pancreas
393	832454	precursor polypeptide [Homo sapiens] >pir A25971 C2HU complement C2 precursor - human >gij187765 MHC complement component C2 [Homo sapiens] {SUB 21-46} Length = 752	gij34628	160	357	100	100	HLQBT44	Prostate, Breast/Ovarian
394	832465	X box binding protein-1 [Homo sapiens]		1	324			HAIJBC51	Lung, Pancreas
395	832475	>pir A36299 A36299 transcription factor hXBP-1 - human Length = 260	gij306893	470	817	100	100	HTJMJ52	Pancreas, Breast/Ovarian
396	832495	EB1 [Homo sapiens] >pir 52726 52726 EB1 - human >sp Q15691 Q15691 EB1. Length = 268	gij998357	1	933	100	100	HAIDB85	Lung, Pancreas
397	832498	pyrroline-5-carboxylate synthase [Homo sapiens] >sp G4097816 G4097816 PYRROLINE-5- CARBOXYLATE SYNTHASE. Length = 793	gij4097816	2	1036	95	95	HLTGQ24	Lung, Pancreas
398	832501	protein synthesis factor [Homo sapiens] >sp P47813 P47813 HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF- 1A) (EIF-4C). {SUB 2-144} Length = 144		736	996			HAGF157	Lung, Pancreas, Colon
399	832505	protein synthesis factor [Homo sapiens] >sp P47813 P47813 HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF- 1A) (EIF-4C). {SUB 2-144} Length = 144	gij306725	61	648	100	100	HRABV57	Lung, Pancreas, Prostate
400	832539	protein synthesis initiation factor 4A [Mus musculus] Length = 408	gij673433	472	1125	93	93	HRABO69	Lung, Breast/Ovarian
401	832554	hISGCN1 [Homo sapiens] >sp Q99736 Q99736 hISGCN1 (FRAGMENT). Length = 1928	gij2282576	409	927	99	99	HC1C0X71	Pancreas, Breast/Ovarian

402	832569	(AL023777) rna binding protein	gnl P1D e1295805	2	667		HFCAE43	Lung, Colon
403	832578	[Schizosaccharomyces pombe] >sp O74978 O74978 RNA BINDING PROTEIN. Length = 276		123	956	64	HBBD67	Pancreas, Colon, Breast/Ovarian
404	832615			630	992		H2CBK94	Lung, Colon
405	832620			190	297		H2CBG53	Colon, Breast/Ovarian
406	832632	(AC002388) 60S ribosomal protein L30 isolog [Arabidopsis thaliana] >sp Q22165 Q22165 60S RIBOSOMAL PROTEIN L30 ISOLOG. Length = 159	gij2344898	41	592	69	I12CBD94	Lung, Colon, Breast/Ovarian
407	832633	putative phospho-beta-glucosidase [Bacillus stearothermophilus] >pir D49898 D49898 cellobiose phosphorylase system celC - Bacillus stearothermophilus >sp Q45401 Q45401 PUTATIVE PHOSPHO-BETA-GLUCOSIDASE. Length = 245	gij466475	3	566	64	HWACF51	Pancreas, Breast/Ovarian
408	833483			2	604		HCTCK33	Lung, Breast/Ovarian
409	834574	similar to S. cerevisiae longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans] >sp Q17870 Q17870 SIMILAR TO S. CEREVISIAE LONGEVITY-ASSURANCE PROTEIN 1. Length = 362	gij1123105	634	1431	59	HHBH126	Lung, Pancreas, Colon, Breast/Ovarian
410	834859	acidic calponin [human, kidney, Peptide, 329 aa] [Homo sapiens] >pir JC4501 JC4501 acidic calponin - human >sp Q15417 Q15417 ACIDIC CALPONIN. Length = 329	hbsj174416	53	541	100	HSTA170	Lung, Pancreas, Colon, Breast/Ovarian

411	834861	factor activating exoenzyme S [Bos taurus] >gi189953 phospholipase A2 [Homo sapiens] >gi1899459 14-3-3 protein [Homo sapiens] >pirA38246/PSHUAM 14-3-3 protein zeta - human >pirA47389/A47389 14-3-3 protein zeta - bovine >sp P29312 I43Z_HUMAN 14-3-3 PROT	gil163042	74	967	99	99	HBXFL41	Lung, Pancreas, Prostate, Breast/Ovarian
412	834890	TRANSCRIPTION FACTOR BTTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3). Length = 204	sp Q64152 BTTF3_MOUSE	70	588	90	91	112C1112	Lung, Pancreas, Prostate, Breast/Ovarian
413	835079			151	348			HOELH62	Lung, Pancreas, Breast/Ovarian
414	835554	homologue to sec61 [Rattus rattus] Length = 476	gi206886	121	1287	98	98	HOHBH04	Lung, Pancreas
415	835560			2	574			HE9NK60	Lung, Pancreas
416	835723	immunoglobulin M heavy chain [Homo sapiens] >gi38408 immunoglobulin M heavy chain [Homo sapiens] >pirS37768/S37768 Ig mu chain C region - human Length = 453	gi38406	48	1421	100	100	HLVYF90	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
417	835791	(A1005890) JM1 [Homo sapiens] >sp O60826 O60826 JM1 PROTEIN, COMPLETE CDS (CLONE LLNLC110M0111Q7 (RZPD BERLIN)/AND LI.NLC110K2140Q7 (RZPD BERLIN)). Length = 627	gn P1D1e1289743	437	1177	87	87	HTXJH25	Pancreas, Breast/Ovarian
418	835817			1369	1554			HAJAZ17	Lung, Breast/Ovarian
419	835840			2	730			HHEQJ47	Lung, Pancreas
420	836048			2052	2276			IIDQDV21	Lung, Prostate

421	836898	human P5 [Homo sapiens] >pir JC4369 JC4369 P5 protein - human >sp Q15084 ERP5 HUMAN PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1). Length = 440	gnl P D d 1009061	3	1427	90	90	HW11PA75	Lung, Pancreas, Colon, Breast/Ovarian
422	836927	(AF027299) protein 4.1-G [Homo sapiens] >sp O43491 O43491 PROTEIN 4.1-G. Length = 1005	gi 2739096	3	1196	84	84	IIDTKY58	Lung, Pancreas
423	837344	SIR [Cowpox virus] >sp O72763 O72763 SIR PROTEIN. Length = 210	gnl P D d 1289272	38	658	48	58	HLDAG32	Lung, Prostate
424	837789	bikunin [Homo sapiens] >sp O00271 O00271 BIKUNIN. Length = 252	gi 2065529	365	1231	91	91	IIDABR73	Colon, Breast/Ovarian
425	838549	(AL023828) Y17G7B.14 [Caenorhabditis elegans] >sp E1323274 E1323274 Y17G7B.14 PROTEIN. Length = 364	gnl P D d 1323274	2	853	42	55	HDQDW56	Lung, Breast/Ovarian
426	838754			437	1198			HTEQK83	Lung, Pancreas, Breast/Ovarian
427	838768			570	770			IIVBCW80	Lung, Pancreas, Breast/Ovarian
428	839486	fibronectin precursor [Homo sapiens] >gi 4096846 fibronectin [Homo sapiens] {SUB 76-434} >gi 4096848 fibronectin [Homo sapiens] {SUB 1892-2103} >gi 182706 fibronectin [Homo sapiens] {SUB 1921-2040} >gi 182684 fibronectin [Homo sapiens] {SUB 2233-2328} Len	gi 31397	2	493	98	98	HSLGC71	Lung, Breast/Ovarian
429	839561	p34 protein [Rattus sp.] >pir S36779 S36779 ribosome-binding protein p34 - rat >sp Q63742 Q63742 P34 PROTEIN. Length = 307	gnl P D d 1003291	45	1133	86	88	HUVFB27	Lung, Pancreas, Prostate

430	839816	similar to plasmodium merozoite surface antigen precursor (SP:P04933) [Caenorhabditis elegans] >sp Q22585 Q22585 SIMILAR TO PLASMODIUM MEROZITE SURFACE ANTIGEN PRECURSOR. Length = 634	gil1293808	1	432	46	61	HWADY11	Lung, Breast/Ovarian
431	840068	UMP-CMP kinase [Sus scrofa] >pir JC418 JC4181 cytidylate kinase (EC 2.7.4.14) - pig >sp Q29561 KCY_PIG UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE). Length = 196	gnl P D d1006692	2	757	97	99	HE8EH64	Lung, Pancreas, Breast/Ovarian
432	840279	(AF062328) p120 catenin isoform 1AB [Homo sapiens] >sp O60715 O60715 P120 CATENIN ISOFORMS 1AB, 2AB, 3AB AND 4AB. >gil3152823 (AF062322) p120 catenin isoform 2AB [Homo sapiens] [SUB 55-962] >gil3152855 (AF062338) p120 catenin isoform 3AB [Homo sapiens] [S	gil3152835	219	1493	93	93	HSRB181	Lung, Pancreas
433	840489	connective tissue growth factor [Homo sapiens] >gil474934 connective tissue growth factor [Homo sapiens] >pir A40551 A40551 connective tissue growth factor - human >sp P29279 CTGF_HUMAN CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR. >gil984956 connective tiss	gil180924	1038	1370	100	100	HOEMS29	Lung, Pancreas

434	840538	glycy1 tRNA synthetase [Homo sapiens] >pirA55314 A55314 glycine--tRNA ligase (EC 6.1.1.14) precursor - human >gil600727 glycy1- tRNA synthetase [Homo sapiens] [SUB 55-739] >gil3845409 (AC004976) glycy1 tRNA synthetase/ [Homo sapiens] [SUB 348-739] Length =	gnl P D d 006904	1	2298	100	100	100	HYAAN81	Lung, Pancreas, Prostate, Breast/Ovarian
435	840545			145	1302				HMCCK75	Lung, Pancreas, Colon, Breast/Ovarian
436	840549			1	492				HWHGB33	Lung, Prostate
437	840551	IgG Fc binding protein [Homo sapiens] Length = 5405	gnl P D d 020288	3	1409	93	93		HWLKM77	Lung, Prostate, Colon
438	840557			346	1014				H6EDS19	Prostate, Colon
439	840561	putative [Mus musculus] >pirJ515785 S15785 heat- stable antigen-related hypothetical protein HSA-C - mouse >sp Q61692 Q61692 HSA-C GENE CODING FOR HEAT STABLE ANTIGEN. Length = 141	gil51442	385	495	48	72		HLIBZ07	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
440	840562	(AB008549) type I procollagen C-proteinase enhancer protein [Homo sapiens] >gil313316 (AF053356) PCOLCE [Homo sapiens] >sp Q14550 Q14550 TYPE I PROCOLLAGEN C- PROTEINASE ENHANCER PROTEIN. Length = 449	gil2589011	103	1476	96	96		LISSD165	Lung, Pancreas, Prostate, Colon
441	840564	PQ-rich protein [Homo sapiens] >pirJ58222 S58222 PQ-rich protein - human >sp Q15184 Q15184 PQ-RICH PROTEIN. Length = 400	gil292660	2	688	67	68		HPJDB01	Lung, Pancreas

442	840572	putative [Homo sapiens] >pir 54339 54339 prot-oncogene - human >sp P35226 BMII_HUMAN DNA-BINDING PROTEIN BMI-1. Length = 326	gi 291873	3	1172	95	95	HTGAZ34	Prostate, Colon
443	840600			3	119			HYAB130	Prostate, Breast/Ovarian
444	840604	Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE):	gnl P1D1e1344589	1	1359	82	87	HWLHN58	Lung, Pancreas, Prostate, Breast/Ovarian
445	840608	olfactomedin [Rana catesbeiana] >pir A47442 A47442 olfactomedin precursor - bullfrog >sp Q07081 OLFM_RANCA OLFACTOMEDIN PRECURSOR (OLFACTORY MUCUS PROTEIN). Length = 464	gi 294502	200	1349	55	75	HWLFY46	Pancreas, Colon
446	840620			776	1267			HTXGB37	Lung, Prostate
447	840625			138	257			HTXDT74	Lung, Prostate
448	840626	nicotinamide N-methyltransferase [Homo sapiens] >gi 1063610 nicotinamide N-methyltransferase [Homo sapiens] >pir A54060 A54060 nicotinamide N-methyltransferase (EC 2.1.1.1) - human >sp P40261 NNMT_HUMAN NICOTINAMIDE N-METHYLTRANSFERASE (EC 2.1.1.1). Length = 196	gi 494989	485	1282	100	100	HULAS90	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
449	840638			16	351			HTTDV02	Prostate, Breast/Ovarian
450	840649	BL34=B cell activation gene [human, Peptidc, 196 aa] [Homo sapiens] >pir 56165 56165 B cell activation protein BL34 - human Length = 196	bbs 129951	1	651	100	100	HTWCY84	Lung, Prostate
451	840651			2	706			HTTAD76	Pancreas, Prostate

452	840666	siah binding protein 1 [Homo sapiens] >sp Q99628 Q99628 SIAH BINDING PROTEIN 1 (FRAGMENT). Length = 541	2	826	99	HTOAF86	Lung, Prostate
453	840681			2187		HTAER63	Lung, Prostate
454	840682			1734		HE9PW64	Lung, Breast/Ovarian
455	840684	t-complex-type molecular chaperone TCP1 - human >gi 339211 t-complex 1 protein [Homo sapiens] {SUB 308-365} Length = 556	3	539	97	HTGBT14	Pancreas, Prostate, Breast/Ovarian
456	840697			560		HTECA52	Lung, Prostate
457	840698			1853		HDABW50	Pancreas, Prostate
458	840708	(AF053304) mitotic checkpoint component Bub3 [Homo sapiens] >gi 2921873 (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] >gi 3639060 (AF081496) kinetochore protein BUB3 [Homo sapiens] >sp O43684 O43684 SPLEEN MITOTIC CHECKPOINT BUB3. Length = 328	1200	1487	100	HTEAF73	Lung, Prostate
459	840714			1170		HTEGU90	Lung, Pancreas, Prostate, Breast/Ovarian
460	840716			1860		HSYA164	Lung, Prostate, Colon, Breast/Ovarian
461	840721	(AC005326) asparagine synthetase [Homo sapiens] >sp G3341715 G3341715 ASPARAGINE SYNTHETASE. >gi 703119 asparagine synthetase [Homo sapiens] {SUB 1-83} Length = 561	166	1324	2	HSUSE92	Lung, Pancreas, Prostate, Colon

462	840735	(AC002425) Gene product with similarity to Rat P8 [Homo sapiens] >gi 3202004 (AF069073) P8 protein [Homo sapiens] >gi 3202006 (AF069074) P8 protein [Homo sapiens] >sp O60356 O60356 GENE: PRODUCT WITH SIMILARITY TO RAT P8. Length = 82	gi 2947054	111	392	64	64	64	HSRDN44	Lung, Pancreas, Prostate, Breast/Ovarian
463	840738			985	1230				IITQJ11	Prostate, Colon
464	840745	52-kD SS-A/Ro autoantigen [Homo sapiens] Length = 475	gi 338490	2	694	46	63		HSSGC06	Lung, Prostate, Colon
465	840747	(AC004522) Zn-alpha2-glycoprotein [Homo sapiens] >sp O60386 O60386 ZN-ALPHA2-GLYCOPROTEIN. Length = 334	gi 3006228	368	877	95	95		HLDDL02	Lung, Pancreas, Breast/Ovarian
466	840756	(AB005624) rig-analog DNA-binding protein [Sus scrofa] >gi 306898 rig-analog protein (putative); putative [Homo sapiens] >gi 337416 human homologue of rat insulinoma gene (rig); putative [Homo sapiens] >gi 305361 Rig DNA-binding protein (putative); putati	gi P1D1022359	148	480	97	97		HCHBQ33	Lung, Pancreas, Colon, Breast/Ovarian
467	840776	Notch3 [Homo sapiens] >sp G2668592 G2668592 NOTCH3. Length = 2321	gi 2668592	2	364	82	82		HSKJZ22	Lung, Breast/Ovarian
468	840784	aldehyde dehydrogenase 6 [Homo sapiens] >pir A55684 A55684 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 6 precursor, salivary - human >sp P47895 DHA6_HUMAN ALDEHYDE DEHYDROGENASE 6 (EC 1.2.1.5). Length = 512	gi 544482	1	618	94	95		HSKAC75	Lung, Prostate, Colon, Breast/Ovarian

469	840788	P1 gene for c subunit of human mitochondrial ATP synthase gene product [Homo sapiens] >gnl PID 1002920 ATP synthase subunit c precursor [Homo sapiens] >pir S34066 S34066 H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P1 precursor, mitoc	gi 38430	59	484	85	85	HHFUM32	Lung, Prostate, Colon, Breast/Ovarian
470	840794			162	1646			HOIIBT28	Lung, Pancreas, Prostate, Colon
471	840797	OSF-2p1 [Homo sapiens] >pir S36111 S36111 osteoblast-specific factor 2 - human >sp Q15064 Q15064 OSF-2P1. Length = 779	gnl PID 1003341	2	2371	93	93	HDTIM52	Pancreas, Breast/Ovarian
472	840799			292	510			HWBCI48	Lung, Pancreas, Colon, Breast/Ovarian
473	840818	translational initiation factor eIF-2, alpha subunit [Homo sapiens] >sp P05198 P2A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA), {SUB 2-315} Length = 315	gi 181995	3	806	100	100	HIIBHM68	Lung, Prostate
474	840822	fatty acid synthase [Homo sapiens] >pir G01880 G01880 fatty-acid synthase (EC 2.3.1.85) - human >sp Q16702 Q16702 FATTY ACID SYNTHASE (EC 2.3.1.85) (FATTY-ACID SYNTHASE). Length = 2509	gi 915392	1423	2367	93	93	IKIHX28	Lung, Prostate, Colon, Breast/Ovarian
475	840830	diubiquitin [Homo sapiens] >sp O15205 O15205 DIUBIQUITIN. Length = 165	gnl PID e321293	1	573	99	99	HFHP85	Pancreas, Prostate

476	840846	glutathione S-transferase Ha subunit 1 (EC 2.5.1.18) [Homo sapiens] >gi306815 glutathione S-transferase (GST, EC 2.5.1.18) [Homo sapiens] >gi306809 glutathione S-transferase [Homo sapiens] >bbsj76373 glutathione S-transferase Ha subunit [EC 2.5.1.18] {	gi306810	144	833	95	95	HFVHP57	Prostate, Breast/Ovarian
477	840848	prohibitin [human, Peptide: 272 aa] [Homo sapiens] >pirI52690/prohibitin - human >spjP35232/PHB_HUMAN PROHIBITIN. Length = 272	bbsj85658	81	917	93	93	IIIIIIIM75	Lung, Pancreas, Prostate, Breast/Ovarian
478	840860	NAP [Homo sapiens] >pirS40510/S40510 nucleosome assembly protein 1-like 1 - human >spjP55209/NPL1_HUMAN NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1 (NAP-1 RELATED PROTEIN). Length = 391	gi189067	92	1309	80	80	HDTLJ39	Lung, Pancreas, Colon, Breast/Ovarian
479	840861	(AL021546) Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1) [Homo sapiens] >spjO43714/O43714 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3))	gnjPIDje1248288	2	520	100	100	HFPBO29	Lung, Prostate, Breast/Ovarian
480	840871	DNA polymerase delta small subunit [Homo sapiens] >pirI38950/I38950 DNA-directed DNA polymerase (EC 2.7.7.7) delta regulatory chain - human >spjP49005/DPD2_HUMAN DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7). Length = 469	gi1008458	2	628	99	99	HSDJX61	Pancreas, Colon, Breast/Ovarian

481	840874	secreted cyclophilin-like protein [Homo sapiens] >gil181335 cyclophilin B [Homo sapiens] (SUB 9-216) >gil181250 cyclophilin [Homo sapiens] (SUB 10-216) Length = 216	gil337999	1	873	94	94	11FTDK64	Lung, Prostate
482	840878	unknown [Homo sapiens] >sp P41271 DAN_HUMAN ZINC FINGER PROTEIN DAN (N03). Length = 180	gnl PID d1006216	227	676	99	100	H2MBT19	Lung, Pancreas, Colon, Breast/Ovarian
483	840880			153	320			HFXK16	Prostate, Colon, Breast/Ovarian
484	840884	mutY homolog [Homo sapiens] >sp Q15830 Q15830 MUTY HOMOLOG. Length = 535	gil1458228	108	1565	99	99	IIIBCH18	Lung, Prostate
485	840907			103	366			HETAD58	Pancreas, Prostate
486	840926			76	1347			HEONT66	Lung, Pancreas, Prostate
487	840932	ATP synthase beta subunit precursor [Homo sapiens] >pir A33370 A33370 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor. mitochondrial - human >sp P06576 ATPB_HUMAN ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34). >gil28931 bc	gil179281	2	1675	93	93	11FIBB89	Lung, Prostate
488	840940	carbonyl reductase [Sus scrofa] >pir JN0703 JN0703 carbonyl reductase (NADPH) (EC 1.1.1.184) - pig >sp Q29529 CBR2_PIG LUNG CARBONYL REDUCTASE [NADPH] (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL REDUCTASE) (LCR). Length = 244	gnl PID d1004479	277	678	61	76	HCHNJ32	Pancreas, Breast/Ovarian

489	840947		2	565		HEG4N45	Lung, Pancreas, Prostate, Breast/Ovarian
490	840959	signal peptidase complex 25 kDa subunit [Canis familiaris] >pir A55012 A55012 signal peptidase 25k chain - dog Length = 226	2	712	99	HEDAD53	Lung, Pancreas, Prostate, Breast/Ovarian
491	840964		177	344		HE8UK92	Prostate, Colon
492	840979	transcription factor-like protein 4 - human Length = 298	11	631	99	HE9HD45	Lung, Pancreas, Prostate, Colon
493	840984	p167 [Homo sapiens] >gnl PID d1010130 The KIAA0139 gene product is related to mouse centrosomin B. [Homo sapiens] >gi 2501783 translation initiation factor 3 large subunit [Homo sapiens] >sp Q14152 Q14152 KIAA0139 PROTEIN. >gi 1399801 p167 [Homo sapiens]	3	3017	91	HE8OC40	Lung, Pancreas, Prostate, Breast/Ovarian
494	840986		1	693		HE8TB60	Pancreas, Prostate, Colon
495	840988		1	465		HE8QQ04	Pancreas, Prostate, Breast/Ovarian
496	840990	(AB010415) dTDP-4-keto-L-rhamnose reductase [Actinobacillus actinomycetemcomitans] >sp O66251 O66251 DTDP-4-KETO-L-RHAMNOSE REDUCTASE. Length = 294	157	1140	32	HE8AM92	Pancreas, Prostate
497	840992	nidogen gene product [Homo sapiens] Length = 1246	3	194	96	HE8BX38	Lung, Prostate, Colon, Breast/Ovarian
498	841009	sin3 associated polypeptide p18 [Homo sapiens] >sp O00422 O00422 SIN3 ASSOCIATED POLYPEPTIDE P18. Length = 153	59	523	92	HDTGJ88	Lung, Pancreas, Prostate, Colon, Breast/Ovarian

499	841012	ribosomal protein L39 [Homo sapiens] >gnl PI D d1012131 ribosomal protein L39 [Homo sapiens] >gi 575382 ribosomal protein L39 [Rattus norvegicus] >pir JC4229 R6RT39 ribosomal protein L39 - rat >pir G02654 G02654 ribosomal protein L39 - human Length = 51	gi 1373419	2	217	100	100	HSKXP01	Lung, Pancreas, Breast/Ovarian
500	841016	connexin 43 [Homo sapiens] >gi 29917 gap junction protein (AA 1-382) [Homo sapiens] >pir A35853 A35853 gap junction protein Cx43, cardiac - human >sp P17302 CX41 HUMAN GAP JUNCTION ALPHA-1 PROTEIN (CONNEXIN 43) (CX43) (GAP JUNCTION 43 KD HEART PROTEIN). {	gi 181209	1	810	94	94	IIDTID113	Lung, Pancreas, Prostate, Colon
501	841017			402	683			HE2AY01	Lung, Prostate
502	841021			983	1357			HNAAE75	Lung, Pancreas, Colon, Breast/Ovarian
503	841032	(AB000910) ribosomal protein [Sus scrofa] >gi 1684917 L44-like ribosomal protein [Homo sapiens] >gi 1666702 ribosomal protein [Mus musculus] >gi 206732 ribosomal protein L36a [Rattus norvegicus] >pir A29820 R6RT36 ribosomal protein L36a - rat Length = 106	gnl PI D d1019960	3	395	100	100	HDQAD36	Lung, Colon
504	841051			656	880			HDpDC65	Lung, Pancreas
505	841064	small subunit ribonucleotide reductase [Homo sapiens] >pir S25854 S25854 ribonucleoside-diphosphate reductase (EC 1.17.4.1) small chain - human Length = 389	gi 36155	6	1244	96	96	HDPMF32	Prostate, Colon, Breast/Ovarian

506	841069		81	809		HDPMJ48	Prostate, Breast/Ovarian
507	841072	regulatory protein [Mus musculus] >gi452276 npdcf-1 [Mus musculus] >pir148691 [148691] regulatory protein - mouse >spQ64322[NPD1_MOUSE NPDC-1 PROTEIN PRECURSOR. Length = 332	162	1139	91	HDPICF81	Lung, Prostate, Colon, Breast/Ovarian
508	841078		521	706		HDPKD92	Pancreas, Prostate
509	841080	HCNGP gene product [Mus musculus] >pirS26660[S26660 HCNGP protein - mouse >spQ02614[HCNGP_MOUSE TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP. Length = 308	1	936	88	HDPJR07	Prostate, Breast/Ovarian
510	841088	quinone oxidoreductase [Homo sapiens] >gi516534 quinone oxidoreductase2 [Homo sapiens] >pirA32667[A32667 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) 2 - human Length = 231	320	1096	100	HDPFX64	Lung, Pancreas, Prostate, Breast/Ovarian
511	841092		1187	1402		HJMBH15	Lung, Colon
512	841095	L protein (AA 1-558) [Homo sapiens] >pirA33616[A33616 heterogeneous ribonuclear particle protein L - human Length = 558	2	904	84	H2LAT51	Lung, Pancreas, Colon, Breast/Ovarian
513	841096	(AB013357) 49 kDa zinc finger protein [Mus musculus] Length = 460	510	1907	80	HCFLJ15	Lung, Pancreas, Breast/Ovarian
514	841102		2	256		HDLAVI2	Lung, Pancreas, Prostate, Breast/Ovarian
515	841104	zinc finger protein [Homo sapiens] >pirS35305[S35305 finger protein ZNF91 - human Length = 1191	712	2451	54	HDLAB16	Pancreas, Prostate, Breast/Ovarian
516	841108	factor XIII a subunit [Homo sapiens] Length = 732	3	1838	99	HDPFE82	Lung, Pancreas, Colon

517	841118			320	487		IIDLAE34	Lung, Pancreas, Prostate
518	841119	C11 protein [Homo sapiens] >gil1890300 eukaryotic release factor 1 [Homo sapiens] >gnlPIDle118068 C11 protein [Mesocricetus auratus] >pirIS50853[S50853 translation releasing factor eRF-1 - human >spP46055]ERF1_HUMAN EUKARYOTIC PEPTIDE CHAIN RELEASE FACT	gnlPIDle118910	123	1367	100	HDPAE95	Lung, Pancreas, Prostate
519	841124	similar to deoxyribose-phosphate aldolase [Caenorhabditis elegans] >spQ19264]DEOC_CAEEL PUTATIVE DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4) (PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE). Length = 303	gil1019952	2	358	62	HDAAB17	Prostate, Colon
520	841137	(AF096285) serine-threonine kinase receptor- associated protein [Mus musculus] >sp[G4063383]G4063383 SERINE-THREONINE KINASE RECEPTOR-ASSOCIATED PROTEIN. Length = 351	gil4063383	3	848	98	IIDAAAP84	Lung, Pancreas, Prostate, Breast/Ovarian
521	841143	fibrillarin [Homo sapiens] >pirA38712/A38712 fibrillarin - human >gil3399667 (AC005393) FBRL_HUMAN; 34 KD NUCLEOLAR SCLERODERMA ANTIGEN [Homo sapiens] {SUB 4-321} Length = 321	gil31395	39	1040	100	HCRMJ87	Pancreas, Prostate, Breast/Ovarian
522	841148			2	1807		HCRNF38	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
523	841149			324	797		HCRBS04	Prostate, Breast/Ovarian

524	841151	keratin [Carassius auratus] Length = 455	gi 212995	2	1399	45	64	HCRNY54	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
525	841155			103	561			HC110F85	Prostate, Breast/Ovarian
526	841161	(AB014458) ubiquitin specific protease [Homo sapiens] >sp D1035685 D1035685 UBIQUITIN SPECIFIC PROTEASE. Length = 785	gn P1D1035685	3	1199	95	95	HC11CA56	Lung, Prostate
527	841162	set [Homo sapiens] >pir A57984 A45018 template activating factor-1, splice form beta - human Length = 277	gi 338039	284	1063	99	100	HCWFR92	Prostate, Colon
528	841163	histone H2A [Mus musculus domesticus] >pir S45110 S45110 histone H2A - mouse >sp Q64426 Q64426 HISTONE H2A (FRAGMENT). Length = 137	gi 817939	201	665	100	100	HBMBF44	Pancreas, Breast/Ovarian
529	841169			21	440			HCFOF83	Lung, Prostate, Colon, Breast/Ovarian
530	841172	CLN3 protein [Homo sapiens] >gn P1D1c283670 CLN3 protein [Homo sapiens] >gi 2947055 (AC002425) CLN3 [Homo sapiens] >gi 3337387 (AC002544) CLN [Homo sapiens] >gi 4102729 (AF015593) CLN3 protein [Homo sapiens] >pir A57219 A57219 Batten disease-related prot	gi 1039423	291	740	100	100	HC11AC93	Prostate, Breast/Ovarian
531	841174	zinc finger protein 7 (ZFP7) [Homo sapiens] >pir A34612 A34612 zinc finger protein ZNF7 - human Length = 686	gi 340446	3	386	98	98	HCHAW34	Prostate, Breast/Ovarian

532	841179	(AF069517) RNA binding protein DEF-3 [Homo sapiens] >sp O75524 O75524 RNA BINDING PROTEIN DEF-3. Length = 1123	gi 3212101	549	1742	85	85	HCHBU86	Lung, Pancreas, Prostate
533	841183	keratin 18 [Homo sapiens] >gi 307081 keratin 18 precursor [Homo sapiens] >gi 34037 cyokeratin 18 [Homo sapiens] >pir S05481 S05481 keratin 18, type I, cytoskeletal - human >sp P05783 K1CR_HUMAN KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 1	gi 386844	1	501	80	92	HC11C120	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
534	841186	(AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus] >sp O88719 O88719 CMP-N-ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP-SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE). Length = 432	gn P1D1e1314953	78	1421	95	97	HCFCC126	Lung, Prostate
535	841204	similar to beta-mannosyltransferase [Caenorhabditis elegans] >sp Q22797 Q22797 SIMILAR TO BETA-MANNOSYLTRANSFERASE. Length = 487	gi 470340	1	1407	51	72	HCEPZ02	Lung, Pancreas, Prostate, Colon
536	841206	(AF062484) SDP8 [Mus musculus]		251	1192			HCEEM52	Lung, Prostate
537	841207	>sp O70493 O70493 SDP8. Length = 165	gi 3126981	193	585	41	63	HMTAK23	Prostate, Colon
538	841211	(AC004908) zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens] Length = 430	gi 4159888	110	766	47	62	HCEDM42	Prostate, Breast/Ovarian

539	841225	membrane protein [Homo sapiens] >gil1048989 CD9 antigen [Homo sapiens] >gil34769 MRP-1 (motility related protein) [Homo sapiens] >hbsj131345 CD9 antigen [human, leukocytes, Peptide, 228 aa] [Homo sapiens] >pirA46123/A40402 CD9 antigen - human >spP21926	gil508496	41	865	88	88	HCRBB01	Lung, Pancreas, Prostate, Colon
540	841229	P1cd47 [Homo sapiens] >pirS70583/S70583 CDC47 homolog - human >spP33993/MCM7_HUMAN DNA REPLICATION LICENSING FACTOR MCM7 (CDC47 HOMOLOG) (P1.1-MCM3). >gnlPIDj1006386 hMCM2 [Homo sapiens] {SUB 177-719} Length = 719	gnlPIDj1010177	1	2298	98	98	HCE1D58	Lung, Pancreas, Prostate, Breast/Ovarian
541	841237	NAD(P)H:menadione oxidoreductase [Homo sapiens] >gil189292 NAD(P)H:quinone oxidoreductase [Homo sapiens] >pirA41135/A30879 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) 1 - human >spP15559/DHQU_HUMAN NAD(P)H DEHYDROGENASE (QUINONE) 1 (EC 1.6.99.2) (QUINON	gil189246	141	1028	95	95	HBM7A19	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
542	841241	Thy-1 [Homo sapiens] >pirA02106/TDTHU Thy-1 membrane glycoprotein precursor - human Length = 161	gil339683	128	622	86	87	HDXFG67	Lung, Pancreas, Prostate, Breast/Ovarian
543	841259	(AD001528) spermidine aminopropyltransferase [Homo sapiens] >spO00544/O00544 SPERMIDINE AMINOPROPYLTRANSFERASE. Length = 366	gil2198557	3	1199	93	93	HCEIC53	Lung, Pancreas, Prostate, Breast/Ovarian

544	841260	FKBP51 [Homo sapiens] >pirJCS422JCS422 FK506-binding protein, FKBP51 - human >sp Q13451 FKB5_HUMAN 51 KD FK506- BINDING PROTEIN (FKBP51) (PEPTIDYL- PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PIPAE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNO	gil1916641	3	863	88	91	IIBODM14	Lung, Prostate
545	841264			1	618			HBJHU33	Lung, Pancreas, Prostate
546	841275	Lutheran blood group glycoprotein [Homo sapiens] >pir I38000 I38000 Lutheran blood group glycoprotein precursor - human >sp P50895 LU_HUMAN LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B- CAM CELL SURFACE GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN	gil603560	2	1183	89	89	IIBGMO35	Prostate, Breast/Ovarian
547	841311	(AF019661) zeta proteasome chain; PSMA5 [Mus musculus] >sp G3805976 G3805976 ZETA PROTEASOME CHAIN. Length = 241	gil3805976	45	836	100	100	HCFMY64	Lung, Pancreas, Prostate, Breast/Ovarian
548	841313	neuronal protein 15.6 [unidentified] >sp O09111 O09111 NEURONAL PROTEIN 15.6. Length = 133	gnl PID c274746	11	544	75	82	HBCNM82	Lung, Prostate, Colon, Breast/Ovarian
549	841317	unnamed protein product [unidentified] >gil496609 basic transcription factor 2, 44 kD subunit [Homo sapiens] >sp Q13888 Q13888 BASIC TRANSCRIPTION FACTOR 2, 44 KD SUBUNIT		1155	1553			HAI5G63	Lung, Prostate
550	841322	(BASIC TRANSCRIPTION FACTOR 2 P44) (FRAGMENT). >gil1737212 basic transcription factor	gnl PID c306259	200	1402	95	95	HAMGE23	Pancreas, Prostate

551	841331			2	955		HHFJL19	Lung, Breast/Ovarian
552	841332	alpha-2-macroglobulin precursor [Homo sapiens] >pir A94033 MAHU alpha-2-macroglobulin precursor - human >sp P01023 A2MG1 HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M). >gi 825615 alpha2-macroglobulin [Homo sapiens] (SUB 672-746) Length = 1474	gij177870	2	3856	98	HAPQO79	Lung, Prostate
553	841338			1139	1363		HAIJU58	Pancreas, Prostate
554	841345	yeast methionyl-tRNA synthetase homolog [Homo sapiens] >pir JC5224 JC5224 methionine--tRNA ligase (EC 6.1.1.10) - human >gi 804996 mitoxanthone-resistance associated gene [Homo sapiens] (SUB 423-900) Length = 900	gnl PID e218477	2	2761	94	HAIJAQ46	Lung, Pancreas, Prostate, Breast/Ovarian
555	841349			151	1578		IIMWFM73	Lung, Pancreas, Prostate, Breast/Ovarian
556	841355	glucose regulated protein 94 (400 AA) [Mesocricetus auratus] >pir A26258 A26258 endoplasmic - hamster (fragment) >sp P08712 ENPL_MESAU ENDOPLASMIN (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (FRAGMENT). Length = 400	gij49628	2	562	96	HAIJAA78	Prostate, Breast/Ovarian
557	841417	arginine-rich nuclear protein [Homo sapiens] >pir A40988 A40988 54K arginine-rich nuclear protein - human >sp Q05519 Q05519 ARGININE- RICH 54 KD NUCLEAR PROTEIN. Length = 484	gij178997	708	1835	73	HNTCL10	Lung, Pancreas, Colon, Breast/Ovarian

558	841548		278	613		HBXDN79	Lung, Breast/Ovarian
559	841632	(AF073298) 4F5rel [Homo sapiens] >gil3641536 (AF073297) 4F5rel [Mus musculus] >sp O75918 O75918.4F5REL. >sp O88891 O88891.4F5REL. Length = 39	49	255	100	HTLGV25	Lung, Breast/Ovarian
560	841662	HYA22 protein - human Length = 338	2	532	78	HLQCP61	Prostate, Colon
561	841771		901	1146		HSYDN46	Lung, Pancreas
562	841827	RTP1 [Homo sapiens] >gil3046386 (AF004162) nickel-specific induction protein [Homo sapiens] >sp Q92597 Q92597 RTP, COMPLETE CDS. Length = 394	358	1110	97	HHFD126	Pancreas, Prostate
563	841835		1232	1612		HWLJT54	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
564	842259		2	691		HHFGF52	Lung, Pancreas, Prostate, Colon
565	842463		600	836		HETVY08	Lung, Pancreas
566	842595	Erp28 [Homo sapiens] >sp P30040 ERP29_HUMAN'ENDOPLASMIC RETICULUM PROTEIN ERP29 PRECURSOR (ERP31) (ERP28). >sp E1314951 E1314951 ERP28 PRECURSOR. Length = 261	50	916	92	HUFAB73	Lung, Breast/Ovarian
567	842722		2	1465		HYABD24	Lung, Pancreas, Prostate, Breast/Ovarian
568	842815		780	971	79	HPMSG47	Pancreas, Colon
569	842818	(AF038954) vacuolar H(+)-ATPase subunit [Homo sapiens] >sp O75348 O75348 VACUOLAR H(+)- ATPASE SUBUNIT. Length = 118	91	477	79	HSKJR03	Lung, Pancreas, Prostate, Breast/Ovarian

570	843251	(AF057297) ornithine decarboxylase antizyme 2 [Homo sapiens] >gi3766170 (AF057297) ornithine decarboxylase antizyme 2 [Homo sapiens] >sp G3766170 G3766170 ORNITHINE DECARBOXYLASE ANTIZYME 2. >gn P D d1020346 product is unknown; seizure-related gene [Mus]	gi3766170	215	745	92	92	HTLIF83	Lung, Breast/Ovarian
571	843422			563	898			HISCW60	Lung, Pancreas, Colon, Breast/Ovarian
572	843784			1307	1864			HCECS78	Lung, Pancreas
573	844017			243	566			HKABG31	Lung, Colon
574	844138	Epithelin 1 & 2 [Homo sapiens] >gi3005730 (AF055008) epithelin 1 and 2 [Homo sapiens] >pir JC1284 GYHU granulatin precursor - human >sp G3005730 G3005730 EPTHELIN 1 AND 2. Length = 593	gi31193	104	1966	100	100	HDPWW59	Lung, Breast/Ovarian
575	844166	(AF039689) antigen NY-CO-7 [Homo sapiens] >sp O60526 O60526 ANTIGEN NY-CO-7. Length = 303	gi3170178	1	1020	94	94	HABAE22	Lung, Pancreas, Prostate, Breast/Ovarian
576	844194			3	707			HE8PB56	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
577	844394			378	635			HHIEUP26	Lung, Pancreas, Breast/Ovarian
578	844450	weak similarity to rat TEGT protein (GI:456207) [Caenorhabditis elegans] >sp P91373 P91373 SIMILARITY TO RAT TEGT PROTEIN. Length = 342	gi1825601	113	1165	61	78	HTXOX92	Lung, Pancreas
579	844534			2	244			HCE3165	Lung, Pancreas, Breast/Ovarian

580	844535	isocitrate dehydrogenase (NADP+) [Homo sapiens] >pir S57499 S57499 isocitrate dehydrogenase (NADP+) (EC 1.1.1.42) precursor, mitochondrial - human >sp P48735 IDHP_HUMAN ISOCITRATE DEHYDROGENASE [NADP]. MITOCHONDRIAL PRECURSOR (EC 1.1.1.42) (OXALOSUCCINATE	gi 872121	3	1454	96	96	HCWGLE38	Lung, Breast/Ovarian
581	844644	(AJ002308) synaptogyrin 2 [Homo sapiens] >sp O43760 O43760 SYNAPTOGYRIN 2. Length = 224	gn P D e 1254905	1	720	91	91	HDPBQ51	Lung, Breast/Ovarian
582	844653	immunoglobulin lambda light chain gene product [Homo sapiens] >pir S25745 S25745 Ig lambda chain - human (fragment) Length = 226	gi 33718	1	732	89	91	HCKQC91	Lung, Pancreas, Colon
583	844659	cathepsin D [Homo sapiens] >gi 29678 precursor polypeptide (AA -20 to 392) [Homo sapiens] >gi 181180 precathpsin D [Homo sapiens] >pir A2577 K1IHU cathepsin D (EC 3.4.23.5) precursor - human >sp P07339 CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5).	gi 179948	21	539	94	94	HLDDQ71	Lung, Breast/Ovarian
584	844796			2	1054			HE6BS09	Colon, Breast/Ovarian
585	844812	(AF040642) contains similarity to transacylases [Caenorhabditis elegans] >sp O44793 O44793 CS0D2.7 PROTEIN. Length = 895	gi 2746788	13	1542	33	59	HDPFV13	Lung, Pancreas
586	844894	E25B protein [Mus musculus] >sp O89051 O89051 E25B PROTEIN. Length = 266	gi 3746127	66	1013	96	99	HCLBO47	Lung, Pancreas, Colon

587	845361	phosphoglycerate kinase (EC 2.7.2.3) [Homo sapiens] >gi387021 phosphoglycerate kinase [Homo sapiens] >gi35435 coding sequence [Homo sapiens] >pir159050(KIHUG phosphoglycerate kinase (EC 2.7.2.3) - human length = 417	gi387020	39	1232	100	100	HHEUJ91	Pancreas, Colon
588	845620			508	1254			IHWIGQ46	Lung, Pancreas, Prostate, Breast/Ovarian
589	845639	leukocyte antigen F [Homo sapiens] >gi3273731 (AF055066) MHC class I HLA-F [Homo sapiens] >pir/A60384/A60384 MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human >sp1P30511 HLAF_HUMAN HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F A	gi312407	2	814	90	90	HCFNA68	Lung, Pancreas, Colon, Breast/Ovarian
590	845660	Cyr61 [Homo sapiens] >gnlPIDe311857 Gig1 protein [Homo sapiens] >gi2196782 (AF003594) growth-factor inducible immediate early gene product CYR61 [Homo sapiens] >gnlPIDe1249319 hCYR61 protein [Homo sapiens] >sp Q00622 CYR6_HUMAN CYR61 PROTEIN PRECURSOR	gi2130527	1	1365	91	91	HKAJW79	Lung, Pancreas, Prostate, Breast/Ovarian
591	845720			1	261			HKDAF83	Lung, Breast/Ovarian
592	845785			180	509			HSODT09	Pancreas, Colon, Breast/Ovarian
593	845897			1369	1677			HAIDAB09	Pancreas, Breast/Ovarian

594	845922	beta actin [Ovis aries] >gi2661136 (AF035774) beta actin [Equus caballus] >gi3320892 (AF076190) beta-actin [Trichosturus vulpecula] >gi177968 cytoplasmic beta actin [Homo sapiens] >gnlPID d1021082 (AB004047) beta-actin [Homo sapiens] >gi28252 beta-act	gi2182269	1	1239	100	100	100	HWLQQ65	Lung, Pancreas, Colon
595	846016	(AB005894) ecalactin [Homo sapiens] >sp O75028 O75028 ECALECTIN. Length = 323	gnlPID d1032501	47	337	97	97	97	HDPIT90	Lung, Pancreas
596	846040	0-44 protein [Rattus sp.] >pir 57612 57612 Rat brain 0-44 mRNA, segment 2 - rat >sp P38718 P044_RAT 0-44 PROTEIN. Length = 127	gi203072	127	585	84	88	88	HLICQ57	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
597	846073	protein p68 (AA 1-614) [Homo sapiens] >gi35220 p68 protein (AA 1-614) [Homo sapiens] >gi2599360 (AF015812) RNA helicase p68 [Homo sapiens] >pir C1087 C1087 RNA helicase, ATP-dependent - human >sp P1784 DDX5_HUMAN PROBABLE RNA-DEPENDENT HELICASE P68	gi38318	23	1051	91	92	92	HCWDW01	Lung, Pancreas
598	846257			286	651				HPWDE09	Lung, Prostate
599	HITXPN06R			65	286				HITXPN06	Lung, Breast/Ovarian
600	I12LAQ12R	(AB000911) ribosomal protein [Sus scrofa] >gnlPID e1339008 (AL031228) d1033B10.4 (40S ribosomal protein S18 (RPS18, KE-3)) [Homo sapiens] >gi198580 ribosomal protein [Mus musculus] >gi1433447 ribosomal protein S18 [Rattus rattus] >gi3811382 (AF100956)		3	311	71	79	79	I12LAQ12	Pancreas, Colon
601	HWAFU16R		gnlPID d1019961	3	320	86	86	86	HWAFU16	Lung, Pancreas, Colon, Breast/Ovarian

602	HAEAM91R	(AB005218) L subunit of photosynthetic reaction center complex [Acidiphilium rubrum] >gnlPID d1026488 (AB005219) L subunit of photosynthetic reaction center complex [Acidiphilium angustum] >sp O70105 O70105 L SUBUNIT OF PHOTOSYNTHETIC REACTION CENTER COM	gnlPID d1026481	174	215	66	66	66	HAEAM91	Pancreas, Colon, Breast/Ovarian
603	HOEMT44R	(AB010959) natural killer cell enhancing factor [Cyprinus carpio] Length = 199	gnlPID d1033048	54	431	84	93		HOEMT44	Lung, Colon, Breast/Ovarian
604	HEZOW04R	(AF001631) glucose-regulated protein GRP94 [Oryctolagus cuniculus] >sp O18750 ENPL_RABIT ENDOPLASMIN (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (FRAGMENT). Length = 716	gi 2581793	7	297	87	89		HEZOW04	Lung, Colon
605	HPFCR25R	(AF012422) ribosomal protein 46 [Drosophila melanogaster] Length = 51	gi 2307014	3	143	65	87		HPFCR25	Lung, Colon, Breast/Ovarian
606	HAPQP94R	(AF018432) dUTPase [Homo sapiens] >gi 144332 deoxyuridine nucleotidohydrolase [Homo sapiens] >gi 1421818 deoxyuridine triphosphatase [Homo sapiens] >pir G02777 G02777 dUTP pyrophosphatase (EC 3.6.1.23) - human >gi 292877 dUTP nucleotidohydrolase [Homo sa	gi 2443581	3	320	97	97		HAPQP94	Lung, Pancreas, Colon
607	H2CBI37R	(AF042107) ribosomal protein S3a [Eimeria tenella] >gi 2792508 (AF042107) ribosomal protein S3a [Eimeria tenella] Length = 264	gi 2792508	3	182	64	64		H2CBI37	Colon, Breast/Ovarian
608	HEOPQ13R	(AF042505) cytochrome b [Homo sapiens] >sp G337237 G337237 CYTOCHROME B (FRAGMENT). Length = 380	gi 3372377	82	216	80	82		HEOPQ13	Lung, Colon

609	HCRNC25R	(AF051894) 15 kDa selenoprotein [Homo sapiens] Length = 161	gi 3095111	61	162	100	100	100	HCRNC25	Lung, Pancreas, Colon
610	HTTF28R	(AF056218) superficial zone protein [Bos taurus] >sp 077765 O77765 SUPERFICIAL_ZONE PROTEIN (FRAGMENT). Length = 401	gi 3676501	3	185	73	80		HTTF28	Pancreas, Colon
611	H2LAY26R			24	155				H2LAY26	Pancreas, Colon
612	HAPQA06R	40-kDa keratin protein [Homo sapiens] >pir A31370 KRRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi 386803	2	355	62	62		HAPQA06	Lung, Pancreas, Colon, Breast/Ovarian
613	HAQBM72R	40-kDa keratin protein [Homo sapiens] >pir A31370 KRRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi 386803	2	145	81	81		HAQBM72	Pancreas, Colon
614	HBGOK18R	40-kDa keratin protein [Homo sapiens] >pir A31370 KRRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi 386803	1	429	91	92		HBGOK18	Lung, Pancreas, Colon, Breast/Ovarian
615	H2MAC07R	acidic ribosomal phosphoprotein (P1) [Homo sapiens] >pir B27125 RGHUP1 acidic ribosomal protein P1 - human Length = 114	gi 190234	111	458	100	100		H2MAC07	Lung, Colon, Breast/Ovarian
616	HTWKTF26R	acidic ribosomal phosphoprotein (P2) [Homo sapiens] >pir C27125 RGHUP2 acidic ribosomal protein P2 - human Length = 115	gi 190236	1	345	95	96		HTWKTF26	Lung, Pancreas, Breast/Ovarian
617	HTAHR89R	ADP-ATP carrier protein T2 - human >sp P12236 ADT3_HUMAN ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3). Length = 298	pir S03894 S03894	13	408	96	96		HTAHR89	Lung, Pancreas

618	HOACE24R	alcohol dehydrogenase [Homo sapiens] >pir A33371 DEHUE1 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) I, cytosolic - human >sp P00352 DHAC_HUMAN ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS I) (ALHD1) (ALDH-E1). (SUB 2-501) Length = 501	gil178372	3	374	91	92	HOACE24	Pancreas, Colon
619	HOELC27R	aldolase A (EC 4.1.3.13) [Homo sapiens] >gil28597 aldolase A (AA 1-364) [Homo sapiens] >pir S14084 ADHUA fructose-bisphosphate aldolase (EC 4.1.2.13) A - human >sp P04075 ALFA_HUMAN FRUCTOSE- BISPHOSPHATE ALDOLASE A (EC 4.1.2.13) (MUSCLE-TYPE ALDOLASE). {S	gil178351	68	604	100	100	HOELC27	Lung, Pancreas, Breast/Ovarian
620	HWLBS25R	aldolase A [Gallus gallus] >gil409193 aldolase A [Gallus gallus] >bbs 167536 aldolase C=fructose- 1,6-bisphosphate aldolase (EC 4.1.2.13) [chickens, brain, Peptide Partial, 42 aa] [Gallus gallus] >pir I5129 I51291 aldolase C - chicken (fragment) Length = 4	gil409191	3	95	90	93	HWLBS25	Lung, Pancreas, Colon, Breast/Ovarian
621	HWLVW62R	alpha-I type III collagen [Homo sapiens] Length = 345	gil180414	1	213	97	97	HWLVW62	Lung, Colon, Breast/Ovarian
622	HALSE08R	ALPHA-1-ANTICHYMYOTRYPSIN PRECURSOR sp P01011 AACT_H UMAN (ACT). >gil4165890 (AF089747) alpha-1- antichymotrypsin precursor [Homo sapiens] {SUB 17-423} >gil177933 alpha-1-antichymotrypsin precursor [Homo sapiens] {SUB 22-423} >gil28332 alpha 1 antichymotrypsin [Homo sapiens] {SU	sp P01011 AACT_H UMAN	3	233	95	97	HALSE08	Lung, Pancreas

623	HFKHD94R	alpha-2 chain precursor (AA -25 to 1018) (3416 is 2nd base in codon) [Homo sapiens] Length = 1043	gi 30076	2	316	97	97	HFKHD94	Pancreas, Breast/Ovarian
624	HCE2M86R	alpha-adaptin (A) (AA 1-977) [Mus musculus] >pirA30111 A30111.alpha-adaptin A - mouse >sp P17426 ADAA_MOUSE ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPT	gi 49878	58	165	75	80	HCE2M86	Lung, Colon, Breast/Ovarian
625	IIQFOA89R	annexin IV (placental anticoagulant protein II) [Homo sapiens] >gnl P1D1d I011889 annexin IV (carbohydrate-binding protein p33/41) [Homo sapiens] >pirA42077 A42077 annexin.IV - human >sp P09525 ANX4_HUMAN ANNEXIN IV (LIPOCORTIN IV) (ENDONEXIN I) (CHROMOB	gi 178699	154	399	94	94	IIQFOA89	Pancreas, Colon, Breast/Ovarian
626	HBWCN69R	beta-1,2-N-acetylglucosaminyltransferase II [Homo sapiens] >pir S66256 S66256 alpha-1,6-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase (EC 2.4.1.143) - human >sp Q10469 GNT2_HUMAN ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAM	gi 902745	60	308	88	90	HBWCN69	Pancreas, Colon
627	HLQGB43R	beta-2-microglobulin [Homo sapiens] Length = 119	gi 179318	1	78	100	100	HLQGB43	Lung, Pancreas, Colon
628	HCROL58R			3	506			HCROL58	Pancreas, Colon
629	HS2IF12R			83	475			HS2IF12	Pancreas, Colon
630	HWLWA01R			2	538			HWLWA01	Pancreas, Colon

631	HCHMV24R	12	185			HCHMV24	Pancreas, Colon, Breast/Ovarian Colon
632	HCHPT49R	94	303			HCHPT49	Breast/Ovarian Colon
633	HCRMGI2R	2	187			HCRMGI2	Pancreas, Colon
634	HWLWE68R	2	241			HWLWE68	Pancreas, Colon
635	HCHPF59R	24	179			HCHPF59	Pancreas, Breast/Ovarian
636	HS2IA81R	90	551			HS2IA81	Pancreas, Colon
637	HCRCNC17R	11	400			HCRCNC17	Pancreas, Colon
638	HISDJ39R	14	406			HISDJ39	Pancreas, Colon
639	HWLEL43R	2	337			HWLEL43	Pancreas, Colon
640	HASCG71R	91	249			HASCG71	Lung, Colon, Breast/Ovarian
641	HOEMO43R	2	184			HOEMO43	Lung, Pancreas, Colon
642	HKDF1Y9S	151	231	76	82	HKDF1Y9S	Breast/Ovarian Pancreas, Colon
643	HAGEP27R	3	137	86	86	HAGEP27	Lung, Pancreas, Colon, Breast/Ovarian

c-erb-B-2 precursor [Homo sapiens]
 >pir|A24571|A24571 protein-tyrosine kinase (EC
 2.7.1.112) erbB2 precursor - human
 >sp|P04626|ERB2_HUMAN ERBB-2 RECEPTOR
 PROTEIN-TYROSINE KINASE PRECURSOR
 (EC 2.7.1.112) (P185ERBB2) (NEU PROTO-
 ONCOGENE) (C-ERBB-2). Length
 C10 protein [Bos taurus] >pir|A38464|A38464 33K
 laminin receptor homolog - bovine Length = 295

644	HSYDGI18R	calmodulin [Homo sapiens] >sp Q13942 Q13942 CALMODULIN. >pir A56785 A56785 calmodulin - pig (fragment) {SUB 80-130} >gi 3243222 (A7069912) calmodulin [Xiphias gladius] {SUB 80-114} >pir E44101 E44101 calmodulin, vasoactive intestinal peptide-binding prote	gi 823635	3	422	100	100	HSYDGI18	Lung, Pancreas, Colon
645	HLJDZ15R	cathepsin C [Homo sapiens] >gi 1947071 prepro dipeptidyl peptidase 1 [Homo sapiens] >pir S66504 S66504 dipeptidyl-peptidase 1 (EC 3.4.14.1) precursor - human >sp P33634 CATC_HUMAN DIPEPTIDYL-PEPTIDASE 1 PRECURSOR (EC 3.4.14.1) (DPP-I) (CATHEPSIN C) (CATHE	gi 1006657	3	110	71	77	HLJDZ15	Lung, Colon
646	HAHDQ34R	cathepsin D [Homo sapiens] >gi 29678 precursor polypeptide (AA -20 to 392) [Homo sapiens] >gi 181180 preprocathepsin D [Homo sapiens] >pir A2577 KHHUD cathepsin D (EC 3.4.23.5) precursor - human >sp P07339 CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5).	gi 179948	2	103	100	100	HAHDQ34	Lung, Pancreas
647	HTLHI118R	collagen alpha 2(VI) chain precursor, long splice form - human >gi 179711 alpha-2 collagen type VI-a' [Homo sapiens] {SUB 590-1018} >gi 291918 alpha-2 type VI collagen [Homo sapiens] {SUB 315-358} Length = 1018	pir S05378 CGHU2A	2	481	89	89	HTLHI118	Lung, Pancreas

648	HACAC47R	complement component C3 [Homo sapiens] >pirA94065 C3HU complement C3 precursor - human >sp P01024 CO3_HUMAN COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN]. >gil181130 complement component C3 [Homo sapiens] {SUB 1-24} Length = 1663	gil179665	1	315	79	80	HACAC47	Lung, Pancreas, Breast/Ovarian
649	III.QFY41R	complement component C3 [Homo sapiens] >pirA94065 C3HU complement C3 precursor - human >sp P01024 CO3_HUMAN COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN]. >gil181130 complement component C3 [Homo sapiens] {SUB 1-24} Length = 1663	gil179665	3	377	96	98	III.QFY41	Lung, Pancreas, Colon, Breast/Ovarian
650	HOFMO83R	cyclin G [Homo sapiens] >gil123623 cyclin G1 [Homo sapiens] >gil123691 cyclin G1 [Homo sapiens] >pirG02401 G02401 cyclin G1 - human >sp P51959 CG2G_HUMAN G2/MITOTIC- SPECIFIC CYCLIN G1. >gnl PID d1013694 cyclin G [Homo sapiens] {SUB 1-279} >gil1486361 c	gnl PID d1012016	2	205	87	93	HOFMO83	Pancreas, Breast/Ovarian
651	HFTDR22R	cytochrome b5, hepatic - brown howler monkey (fragment) Length = 87	pir S07959 S07959	136	357	100	100	HFTDR22	Pancreas, Colon, Breast/Ovarian
652	HPJCZ01R	cytochrome c oxidase II [Macaca fascicularis] >pirA27420 A27420 cytochrome-c oxidase (EC 1.9.3.1) chain II - crab-eating macaque mitochondrion (SGC1) >sp P11948 COX2_MACACA CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1). Length = 227	gil342255	2	163	44	50	HPJCZ01	Lung, Pancreas, Colon

653	HOEKC39R	cytochrome oxidase I [Homo sapiens] >gil506829 cytochrome oxidase subunit I [Homo sapiens] >pir(A00463)ODHU1 cytochrome-c oxidase (EC 1.9.3.1) chain I - human mitochondrion (SGC1) >sp(P00395)COX1_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1). Leng	gil5006	54	167	91	95	HOEKC39	Lung, Pancreas, Colon
654	HOELI24R	cytochrome oxidase subunit 3 [Homo sapiens] Length = 260	gil2052365	29	166	97	97	HOELI24	Lung, Pancreas, Colon
655	HODEI18R	cytochrome oxidase subunit II [Homo sapiens] >gil530071 cytochrome oxidase subunit II [Homo sapiens] >gil530073 cytochrome oxidase subunit II [Homo sapiens] >gil530077 cytochrome oxidase subunit II [Homo sapiens] >gil337187 cytochrome oxidase subunit II [gil530069	1	180	69	72	HODEI18	Lung, Pancreas, Colon
656	HOSNR06R	cytochrome oxidase subunit II [Homo sapiens] >gil530071 cytochrome oxidase subunit II [Homo sapiens] >gil530073 cytochrome oxidase subunit II [Homo sapiens] >gil530077 cytochrome oxidase subunit II [Homo sapiens] >gil337187 cytochrome oxidase subunit II [gil530069	269	403	93	95	HOSNR06	Lung, Pancreas
657	HCQDL20R	cytochrome P450 PCN3 [Homo sapiens] >pir(A34101)A34101 cytochrome P450 3A5 - human >sp(P20815)CF35_HUMAN CYTOCHROME P450 3A5 (EC 1.14.14.1) (CYP3A5) (P450-PCN3). >gil950342 cytochrome P450 [Homo sapiens] [SUB 1-24] Length = 502	gil181346	39	245	98	98	HCQDL20	Pancreas, Colon

658	HTOHI64R	cyokeratin 15 (AA 1 - 456) [Homo sapiens] >pir S01069 KRHHUS keratin 15, type I, cytoskeletal - human >sp P19012 K1CO_HUMAN KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15) (CK 15). Length = 456	gij134071	149	253	89	89	HTOHI64	Prostate, Breast/Ovarian
659	HCHBR11R	cyokeratin 8 [Homo sapiens] Length = 483	gij181400	3	380	55	57	HCHBR11	Lung, Pancreas, Colon, Breast/Ovarian
660	HADBE77R	cytoplasmic chaperonin hTRiC5 [Homo sapiens] Length = 201	gij609308	43	294	80	84	HADBE77	Lung, Pancreas, Colon, Breast/Ovarian
661	HFKHD49R	D-beta-hydroxybutyrate dehydrogenase [Rattus norvegicus] Length = 93	gij930260	1	210	100	100	HFKHD49	Lung, Colon, Breast/Ovarian
662	HOEMJ59R	decorin [Homo sapiens] >gij609452 decorin [Homo sapiens] (SUB 1-70) Length = 347	gij181519	3	128	72	75	HOEMJ59	Lung, Colon
663	HTYNC43R	elongation factor 1-alpha 1 [Homo sapiens] >gij927067 elongation factor 1-alpha 1 [Homo sapiens] >pir I59399 I59399 oncogene PTI-1 - human >sp Q16577 Q16577 ONCOGENE. Length = 398	gij927065	2	217	92	94	HTYNC43	Lung, Pancreas, Colon
664	H6EAQ15R	elongation factor 2 [Homo sapiens] >gij31108 human elongation factor 2 [Homo sapiens] >pir S18294 EFHU2 translation elongation factor eEF-2 - human >sp P13639 EF2_HUMAN ELONGATION FACTOR 2 (EF-2). >gij181969 elongation factor 2 [Homo sapiens] (SUB 501-858	gij31106	2	70	100	100	H6EAQ15	Lung, Pancreas, Breast/Ovarian

665	HCFLM34R	elongation factor Tu [Mus musculus] >sp Q6151 IQ6151 EUKARYOTIC TRANSLATION ELONGATION FACTOR I ALPHA 1 (EEF-TU GENE ENCODING ELONGATION FACTOR TU, 5' END) (FRAGMENT). Length = 108	gi 553907	48	308	94	95	HCFLM34	Lung, Breast/Ovarian
666	HTTID16R	ENA-78 prepeptide [Homo sapiens] >gi 607031 neutrophil-activating peptide 78 [Homo sapiens] >gi 471243 ENA-78 gene product [Homo sapiens] >pir JC2433 A55010 neutrophil-activating peptide ENA-78 - human >sp P42830 EN78_HUMAN NEUTROPHIL ACTIVATING PROTEIN E	gi 684922	2	331	85	85	HTTID16	Pancreas, Colon
667	HDPA145R	endoglin [Homo sapiens] >pir S37628 S37628 endoglin - human Length = 625	gi 402207	2	181	65	65	HDPA145	Pancreas, Colon
668	HKIXL19R	epoxide hydrolase [Homo sapiens] >gi 340390 epoxide hydrolase [Homo sapiens] >gi 34543 epoxide hydrolase (AA 1-455) [Homo sapiens] >gi 458701 epoxide hydrolase [Homo sapiens] >pir A29939 A29939 epoxide hydrolase (EC 3.3.2.3) 1, microsomal - human >sp P070	gi 450271	1	348	100	100	HKIXL19	Lung, Pancreas, Colon
669	H2LAY52R	EWS gene product [Mus musculus] >pir A55726 A55726 RNA-binding protein Ews - mouse >sp Q61545 EWS_MOUSE RNA-BINDING PROTEIN EWS. Length = 655	gi 488513	27	494	100	100	H2LAY52	Lung, Pancreas, Colon, Breast/Ovarian
670	HAJRB09R	FAST kinase [Homo sapiens] >pir J37386 J37386 FAST kinase - human >sp Q14296 Q14296 FAST KINASE. Length = 549	gi 1006659	19	324	77	77	HAJRB09	Pancreas, Colon

671	HAPNI86R	G9a [Homo sapiens] >pir[S30385]S30385 G9a protein - human >sp Q14349 Q14349 G9A PROTEIN CONTAINING ANKYRIN-LIKE REPEATS. Length = 1001	gi 287865	3	419	97	97	HAPNI86	Lung, Colon
672	HCEVB92R	glutamate dehydrogenase [Homo sapiens] >sp Q14400 Q14400 GLUTAMATE DEHYDROGENASE (FRAGMENT). Length = 258	gi 183056	2	217	78	81	HCEVB92	Pancreas, Colon
673	HAPRJ22R	glutamate--ammonia ligase [Homo sapiens] >pir S18455 AJHUQ glutamate--ammonia ligase (EC 6.3.1.2) - human Length = 373	gi 31831	168	431	100	100	HAPRJ22	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
674	HCRMZ32R	glutamine:fructose-6-phosphate amidotransferase [Homo sapiens] >pir A45055 A45055 glutamine--fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - human >sp Q06210 GFAT_HUMAN GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2	gi 183082	2	316	91	91	HCRMZ32	Pancreas, Colon, Breast/Ovarian
675	HBMVM42R	guanine nucleotide regulatory protein [Homo sapiens] >gi 3041860 (AC004534) guanine nucleotide regulatory protein [Homo sapiens] >pir J38402 J38402 guanine nucleotide regulatory protein - human >sp Q12774 Q12774 GUANINE NUCLEOTIDE REGULATORY PROTEIN. Leng	gi 484102	1	363	84	87	I1BMVM42	Colon, Breast/Ovarian

676	HADG1:45R	guanine nucleotide-binding protein G-s-alpha-4 [Homo sapiens] >gi 31913 alpha-S1 (AA 1-380) [Homo sapiens] >pir C31927 RGHUA1 GTP-binding regulatory protein Gs alpha chain (adenylate cyclase-stimulating), splice form 4 - human Length = 380	gi 386746	2	439	96	96	IIADG1:45	Lung, Pancreas, Colon
677	HTXPN11R	heat shock-induced protein [Homo sapiens] >pir B45871 B45871 dnaK-type molecular chaperone HSP70-Hom - human >sp P3493 HHS7H_HUMAN HEAT SHOCK 70 KD PROTEIN 1-HOM (HSP70-HOM). Length = 641	gi 188492	3	413	94	98	HTXPN11	Lung, Pancreas, Colon
678	HCDBN37R	heterogeneous nuclear ribonucleoprotein C-like protein - human Length = 328	pir A44192 A44192	1	300	96	96	HCDBN37	Colon, Breast/Ovarian
679	HABGC02R	HLA-DR-beta-B [Homo sapiens] Length = 266	gi 490048	3	389	89	94	HABGC02	Lung, Colon
680	HNTSA70R	HsMcm6 [Homo sapiens] >sp Q14566 MCM6_HUMAN DNA REPLICATION LICENSING FACTOR MCM6 (P105MCM). Length = 821	gnl P1D1d1013380	3	341	69	72	HNTSA70	Lung, Colon
681	HDTKP24R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir JC1348 JC1348	397	492	64	67	HDTKP24	Lung, Pancreas, Colon
682	HODE114R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir JC1348 JC1348	164	247	62	68	HODE114	Lung, Pancreas, Colon
683	HOELC42R	IGF-BP 4 [Homo sapiens] >gnl P1D1e1227579 insulin-like growth factor binding protein 4 [Homo sapiens] >pir B37252 B37252 insulin-like growth factor-binding protein 4 precursor - human >sp P22692 BP4_HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 PREC	gi 184816	13	288	83	83	HOELC42	Pancreas, Colon

684	HWAF44R	immunoglobulin heavy chain [Homo sapiens] >pi D36005 D36005 Ig heavy chain V region (M43) - human (SUB 38-156) Length = 156	2	463	83	90	HWAF44	Lung, Colon
685	HABGF46R	immunoglobulin light chain variable region [Homo sapiens] >gi 2970534 (AF049692) immunoglobulin kappa light chain [Homo sapiens] (SUB 3-106) Length = 143	42	446	71	85	HA13GF46	Lung, Pancreas, Colon, Breast/Ovarian
686	HOELC15R	insulin-like growth factor-binding protein [Homo sapiens] >gi 386791 growth factor-binding protein-3 [Homo sapiens] >gi 398164 insulin-like growth factor binding protein 3 [Homo sapiens] >pi A36578 OHU3 insulin-like growth factor-binding protein 3 precu	8	424	96	96	HOELC15	Pancreas, Colon, Breast/Ovarian
687	H2LAR26R	keratin 18 [Homo sapiens] >gi 307081 keratin 18 precursor [Homo sapiens] >gi 34037 cyokeratin 18 [Homo sapiens] >pi S05481 S05481 keratin 18, type I, cytoskeletal - human >sp P05783 K1CR_HUMAN KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK I	72	476	97	98	H2LAR26	Colon, Breast/Ovarian
688	H2LAV85R	Ku (p70/p80) subunit [Homo sapiens] >gi 307093 Ku antigen [Homo sapiens] >pi A35051 A32626 Ku antigen 80K chain - human >sp P13010 KU86_HUMAN A.TP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P86) (86 KD SUBUNIT OF KU ANTIGEN) (T	67	462	97	98	H2LAV85	Lung, Pancreas
689	HSDC92R	l-caldesmon II [Homo sapiens] Length = 532	56	337	64	76	HSDC92	Lung, Breast/Ovarian

690	HUTHN01R	L6 [Homo sapiens] >pir(A42926/A42926 L6 surface protein - human Length = 202	gj186804	87	545	91	91	HUTHN01	Lung, Pancreas, Colon, Breast/Ovarian
691	H2LAW03R	lactate dehydrogenase B [Homo sapiens] >gj34329 lactate dehydrogenase B (AA 1 - 334) [Homo sapiens] >pir(S02795)DEHULH L-lactate dehydrogenase (EC 1.1.1.27) chain H - human >sp(P07195)LDH_HUMAN L-LACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.27) (LDH-B). {SUB	gnlPID c223241	111	536	99	100	H2LAW03	Lung, Pancreas
692	HOEMO60R	lactate dehydrogenase-A [Homo sapiens] >gj34313 lactate dehydrogenase-A [Homo sapiens] >pir(A00347)DEHULM L-lactate dehydrogenase (EC 1.1.1.27) chain M - human >sp(P00338)LDHM_HUMAN L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A). {SUB 2-332} Length	gj780261	1	201	59	59	HOEMO60	Pancreas, Breast/Ovarian
693	HKAHJ14R	latent transforming growth factor-beta-binding protein - human Length = 1820	pir(A55494/A55494	1	216			HKAHJ14	Pancreas, Colon
694	HOEA39R	lumican [Homo sapiens] Length = 338	gj699577	1	240	85	86	HOEA39	Pancreas, Breast/Ovarian
695	HOELF72R	M130 antigen [Homo sapiens] >pir(J38003)S36077	gj312142	58	468	97	97	HOELF72	Pancreas, Colon
696	HAPNX59R	M130 antigen - human >sp(Q07898)Q07898 M130 ANTIGEN PRECURSOR. Length = 1116		1	432	85	88	HAPNX59	Lung, Colon
697	HBJJS17R	methionine aminopeptidase [Homo sapiens] >gj687243 cIF-2-associated p67 homolog [Homo sapiens] >pir(S52112)DPHUM2 methionyl aminopeptidase (EC 3.4.11.18) 2 - human >sp(P50379)AMP2_HUMAN METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2) (PEPTIDASE M 2)	gj903982	1	255	100	100	HBJJS17	Lung, Pancreas

698	HA1YDU61R	midkine [Homo sapiens] >gil188571 retinoic acid inducible factor [Homo sapiens] >gil35087 neurite outgrowth-promoting protein [Homo sapiens] >gilPID1d1001932 midkine [Homo sapiens] >pirJ110385J110385 midkine precursor - human >spiP21741MK_HUMAN MIDKINE	gil182651	1	108	67	67	HA1YDU61	Pancreas, Colon
699	HCWHT65R	mitochondrial intermediate peptidase precursor [Homo sapiens] >spiQ99797/Q99797 MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (EC 3.4.24.59). Length = 713	gil1763642	1	432	74	77	HCWHT65	Prostate, Colon
700	H2CBN02R	mitochondrial matrix protein [Homo sapiens] >pirA32800/A32800 chaperonin GroEL precursor - human >spiP10809/P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (gil190127	1	435	99	99	H2CBN02	Pancreas, Colon
701	H2CBV68R	mitochondrial matrix protein [Homo sapiens] >pirA32800/A32800 chaperonin GroEL precursor - human >spiP10809/P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (gil190127	2	406	100	100	H2CBV68	Colon, Breast/Ovarian

702	H6EDK07R	Mr 110,000 antigen [Homo sapiens] >pir I52703 I52703.42K membrane glycoprotein - human >sp Q16186 G100_HUMAN 110 KD CELL MEMBRANE GLYCOPROTEIN. Length = 407	gnl PID d1011683	1	252	90	90	H6EDK07	Lung, Breast/Ovarian
703	HACAH10R	NADH dehydrogenase subunit 2, ND2 [human, brain, Peptide Mitochondrial Partial Mutant, 67 aa] [Homo sapiens] >sp Q36734 Q36734 NADH DEHYDROGENASE SUBUNIT 2 (FRAGMENT). Length = 67	bbs 75898	1	66	89	96	HACAH10	Lung, Pancreas, Colon
704	HCCMC56R	NADH-UBIQUINONE OXIDOREDUCTASE B18 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B18) (CI-B18) (CELL ADHESION PROTEIN SQM1). Length = 134	sp P17568 NB8M_HUMAN	16	351	83	83	HCCMC56	Lung, Colon, Breast/Ovarian
705	H2CBN54R	NADH-ubiquinone oxidoreductase B22 subunit (C-terminal) [human, placenta, Peptide Mitochondrial Partial, 179 aa] [Homo sapiens] Length = 179	bbs 178894	2	427	99	99	H2CBN54	Pancreas, Colon
706	HMCGL12R	NMB gene product [Homo sapiens] >pir 38065 38065 gene NMB protein - human >sp Q14956 NMB_HUMAN PUTATIVE TRANSMEMBRANE PROTEIN NMB PRECURSOR. Length = 560	gi 666043	96	389	76	80	HMCGL12	Lung, Pancreas
707	HWHPX50R	nucleolar protein [Mus musculus] >pir 52858 52858 nucleolar protein - mouse >sp Q61937 NPM_MOUSE NUCLEOPHOSMIN (NPM) (NUCLEOLAR PHOSPHOPROTEIN B23) (NUMATRIN) (NUCLEOLAR PROTEIN NO38). Length = 292	gi 200011	1	414	87	87	HWHPX50	Lung, Pancreas, Colon, Breast/Ovarian

708	HAPQD84R		115	267		HAPQD84	Lung, Pancreas, Colon, Breast/Ovarian
709	HLIBN66R		1	219		HLIBN66	Lung, Pancreas
710	HE2BD84R	OSF-2p1 [Homo sapiens] >pirS3611 S3611 osteoblast-specific factor 2 - human >sp Q15064 Q15064 OSF-2P1. Length = 779	2	394	77	HE2BD84	Pancreas, Colon, Breast/Ovarian
711	HLQFY45R	pancreatitis-associated protein [Homo sapiens] >gi 312807 preprotein [Homo sapiens] >bbs 121222 PAP-H=pancreatitis-associated protein [human, pancreas, Peptide, 175 aa] [Homo sapiens] >gn P D d1003233 PAP homologous protein [Homo sapiens] >pir A49616 A49	57	374	60	HLQFY45	Pancreas, Colon
712	HAMQ78R	phosphate carrier isoform A (alternatively spliced, exon IIIA) - human >sp Q00325 MPCP_HUMAN MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR. Length = 362	2	352	82	HAMQ78	Lung, Colon
713	HODEV64R	poly(A)-binding protein [Homo sapiens] >gi 1562511 poly(A)-binding protein [Homo sapiens] >sp P11940 PAB1_HUMAN POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1). Length = 636	1	492	97	HODEV64	Lung, Pancreas

714	H2CBD48R	precursor polypeptide (AA -21 to 782) [Homo sapiens] >pirA35954/A35954 endoplasmin precursor - human >sp P14625 ENPL_HUMAN ENDOPLASMIN PRECURSOR (94 Kd GLUCOSE-REGULATED PROTEIN) (GRP94) (GP96 HOMOLOG) (TUMOR REJECTION ANTIGEN 1). Length = 803	gi 37261	2	499	95	97	H2CBD48	Pancreas, Colon
715	HCCMA82R	procarboxypeptidase B [Homo sapiens] >pirA42332/A42332 carboxypeptidase B (EC 3.4.17.2) precursor, pancreatic - human Length = 416	gi 189625	3	383	94	94	HCCMA82	Pancreas, Colon
716	HOI:MK78R	prostacyclin-stimulating factor, PG12-stimulating factor, PSF [human, cultured diploid fibroblast cells, Peptide, 282 aa] [Homo sapiens] >pirS50031/S50031 prostacyclin-stimulating factor - human >sp Q16270 Q16270 PROSTACYCLIN-STIMULATING FACTOR. Length =	bbs 161346	3	329	95	95	HOI:MK78	Lung, Pancreas
717	H2CBD13R	proteasome subunit C9 [Homo sapiens] >pirS15972 SNHUC9 multicatalytic endopeptidase complex (EC 3.4.99.46) chain C9 - human >sp P25789 PRC9_HUMAN PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT	gn P D d1001118	156	461	100	100	H2CBD13	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
718	HCFMU61R	protein-tyrosine kinase (EC 2.7.1.112) ZAP-70 - human Length = 619	pir A44266 A44266	1	477	98	98	HCFMU61	Pancreas, Colon

719	IIOSNE94R	proteoglycan core protein [Homo sapiens] >pirA45016 NBHUC8 decorin precursor - human >sp p07585 PGS2_HUMAN BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40). >gil1161226 decorin [Rattus norvegicus] (SUB 204-299) Length = 359	2	466	85	85	IIOSNE94	Lung, Pancreas
720	HCROZ08R	putative precursor (AA 1-304) [Homo sapiens] >gilPIDe224276 uracil-DNA-glycosylase, UNGI [Homo sapiens] >pir S05964 A60472 uracil-DNA glycosylase (EC 3.-.-.-) precursor - human >gilPIDe1296296 MITOCHONDRIAL LOCALIZATION PEPTIDE [unidentified] (SUB 1-3	3	218	100	100	HCROZ08	Lung, Pancreas, Colon
721	HIIBEF47R	pyruvate dehydrogenase E1-alpha precursor [Homo sapiens] >pir A60225 A60225 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain - bovine (fragment) (SUB 54-74) Length = 414	1	330	88	88	HIIBEF47	Colon, Breast/Ovarian
722	HTXPI31R	pyruvate kinase M2 [Sus scrofa] >sp Q29582 Q29582 PYRUVATE KINASE M2 (EC 2.7.1.40) (PHOSPHOENOLPYRUVATE KINASE) (PHOSPHOENOL TRANSPHOSPHORYLASE) (FRAGMENT). Length = 108	2	286	84	85	HTXPI31	Pancreas, Breast/Ovarian
723	HOEKC30R	rhoC coding region (AA 1-193) [Homo sapiens] >gil407699 GTPase [Homo sapiens] >pir S01029 TVHURC GTP-binding protein rhoC - human Length = 193	2	151	94	94	HOEKC30	Lung, Pancreas, Breast/Ovarian
724	HOSNR67R	ribosomal protein small subunit [Homo sapiens] Length = 264	1	483	97	98	HOSNR67	Lung, Pancreas

725	H2LAV92R	ribosomal protein L38 [Homo sapiens] >gi57078 ribosomal protein L38 [Rattus rattus] >pirS15658 RSRT38 ribosomal protein L38 - rat >pirS38385 S38385 ribosomal protein L38 - human >gnl P1 d1026783 (A1007185) ribosomal protein L38 [Homo sapiens] (SUB 34-70)	gi407423	13	351	72	72	H2LAV92	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
726	H2LAO74R	ribosomal protein L10 [Homo sapiens] >sp D102677 D1026771 RIBOSOMAL PROTEIN L15 (FRAGMENT). (SUB 16-57) Length = 205	gi414587	359	502	83	83	H2LAO74	Lung, Pancreas, Colon, Breast/Ovarian
727	HKMMF85R	ribosomal protein L18a [Homo sapiens] >gi3702270 (AC005796) ribosomal protein L18a [Homo sapiens] >gnl P1D d1029536 (AB007175) ribosomal protein L18a [Homo sapiens] (SUB 111- 176) Length = 176	gi401845	1	360	96	96	HKMMF85	Lung, Breast/Ovarian
728	HCLBZ27R	ribosomal protein L19 [Homo sapiens] >bbs127872 ribosomal protein L19 [human, breast cancer cell line, MCF-7, Peptide, 196 aa] [Homo sapiens] >gi206726 ribosomal protein L19 [Rattus norvegicus] >gnl P1D c218038 ribosomal protein L19 [Rattus norvegicus]	gi36128	19	273	93	98	HCLBZ27	Lung, Pancreas, Colon
729	H2LAV11R	ribosomal protein L21 [Homo sapiens] >gi984143 ribosomal protein L21 [Homo sapiens] >pirS5591 S55913 ribosomal protein L21, cytosolic - human >sp D1026774 D1026774 RIBOSOMAL PROTEIN L21 (FRAGMENT). (SUB 124-154) Length = 160	gi550015	126	530	99	99	H2LAV11	Lung, Pancreas, Colon

730	HBAGP60R	ribosomal protein L27 [Homo sapiens] >gi 3115335 ribosomal protein L27 [Homo sapiens] >gi 57694 ribosomal protein L27 (AA 1 - 136) [Rattus norvegicus] >gi 62981 ribosomal protein L27 [Gallus gallus] >pir S00401 R3R.T27 ribosomal protein L27, cytosolic - ra	gi 388769	161	373	66	70	HBAGP60	Pancreas, Colon
731	HOEMJ56R	ribosomal protein L28 [Homo sapiens] >pir SS5915 SS5915 ribosomal protein L28 - human Length = 137	gi 550019	3	206	94	94	HOEMJ56	Lung, Colon, Breast/Ovarian
732	HASAF77R	ribosomal protein L31 [Sus scrofa] >gi 36130 ribosomal protein L31 (AA 1-125) [Homo sapiens] >gi 57115 ribosomal protein L31 (AA 1-125) [Rattus norvegicus] >pir S05576 R5HU31 ribosomal protein L31 - human >pir A26417 RSRT31 ribosomal protein L31 - rat >gn	gn PID c276436	1	381	82	82	HASAF77	Lung, Prostate, Colon, Breast/Ovarian
733	H2MAC95R	ribosomal protein L37 [Homo sapiens] >bbs 172744 ribosomal protein L37 (C2-C2 zinc-finger-like) [human, HeLa cells, Peptide, 97 aa] [Homo sapiens] >gn PID d1005426 ribosomal protein L37 [Homo sapiens] >gi 57121 ribosomal protein L37 [Rattus norvegicus] >	gi 292441	67	411	79	79	H2MAC95	Lung, Colon, Breast/Ovarian
734	HDPLP40R	ribosomal protein L37 [Homo sapiens] >bbs 172744 ribosomal protein L37 (C2-C2 zinc-finger-like) [human, HeLa cells, Peptide, 97 aa] [Homo sapiens] >gn PID d1005426 ribosomal protein L37 [Homo sapiens] >gi 57121 ribosomal protein L37 [Rattus norvegicus] >	gi 292441	1	363	100	100	HDPLP40	Lung, Pancreas, Breast/Ovarian

735	HOEMK92R	ribosomal protein L37a [Homo sapiens] >gi36134 ribosomal protein L37a [Homo sapiens] >gi57123 ribosomal protein L37a (AA 1 - 92) [Rattus rattus] >gi312414 ribosomal protein L37a [Mus musculus] >pirS05014 RSRT37 ribosomal protein L37a - rat >pirS42109	gi292439	3	185	96	96	HOEMK92	Lung, Pancreas, Breast/Ovarian
736	HABAD57R	ribosomal protein L4 [Homo sapiens] >pirS39803 S39803 ribosomal protein L4 - human Length = 425	gi307385	210	431	80	90	HABAD57	Lung, Pancreas
737	HLXNA52R	ribosomal protein L4 [Rattus norvegicus] Length = 421	gnlPIDe121603	3	296	86	86	HLXNA52	Lung, Pancreas
738	I1WAFK82R	ribosomal protein L9 [Homo sapiens] >gnlPIDd1003911 human homologue of rat ribosomal protein L9 [Homo sapiens] Length = 192	gi710366	139	354	77	78	I1WAFK82	Lung, Colon, Breast/Ovarian
739	H2CBL68R	ribosomal protein S13 [Homo sapiens] >gi488417 ribosomal protein S13 [Homo sapiens] >gnlPIDd1014222 ribosomal protein S13 [Homo sapiens] >gi57730 ribosomal protein S13 [Rattus rattus] >pirS34109 S34109 ribosomal protein S13, cytosolic - human >pirA3	gi307391	3	461	100	100	H2CBL68	Lung, Pancreas
740	HNTNE17R	ribosomal protein S17 [Homo sapiens] >gi337503 S17 ribosomal protein [Homo sapiens] >pirJT0405 R4HU17 ribosomal protein S17, cytosolic - human Length = 135	gi337501	1	387	100	100	HNTNE17	Lung, Pancreas, Breast/Ovarian
741	HBJLR37R	ribosomal protein S26 [Homo sapiens] Length = 115	gi296452	2	328	98	100	HBJLR37	Pancreas, Colon, Breast/Ovarian

742	HOSNG20R	ribosomal protein S4X isoform [Homo sapiens] >gi 2791861 (AF041428) ribosomal protein s4 X isoform [Homo sapiens] >gi 200864 ribosomal protein S4 [Mus musculus] >gi 57135 ribosomal protein S4 (AA 1 - 263) [Rattus rattus] >gnl PI D 1002335 ribosomal protei	gi 337510	1	357	97	98	HOSNG20	Lung, Pancreas, Colon, Breast/Ovarian
743	HCLBZ30R	ribosomal protein S5 [Mus musculus] Length = 204	gi 1685071	2	244	89	89	HCLBZ30	Lung, Pancreas, Colon, Breast/Ovarian
744	HBGNY11R	ribosomal protein S8 [Homo sapiens] >gi 57139 ribosomal protein S8 (AA 1-208) [Rattus norvegicus] >gi 313298 ribosomal protein S8 [Mus musculus] >pir S01609 R3RT8 ribosomal protein S8 - rat >pir S42110 S42110 ribosomal protein S8 - mouse >pir S25022 S2502	gi 36150	2	334	100	100	HBGNY11	Lung, Pancreas, Breast/Ovarian
745	HOEKC80R	S19 ribosomal protein [Homo sapiens] >pir 52692 52692 ribosomal protein S19, cytosolic - human Length = 145	gi 337733	2	376	98	98	HOEKC80	Lung, Pancreas, Colon, Breast/Ovarian
746	HCHBM70R	secretory protein [Homo sapiens] >gi 940946 intestinal trefoil factor [Homo sapiens] >pir A48284 A48284 intestinal trefoil factor 3 precursor - human >sp Q07654 ITF_HUMAN INTESTINAL TREFOIL FACTOR PRECURSOR (HP1.B). Length = 80	gi 402483	1	114	57	57	HCHBM70	Lung, Pancreas, Colon, Breast/Ovarian
747	HIFCES53R	semaphorin C [Mus musculus] >pir 48746 48746 semaphorin C - mouse (fragment) >sp Q62179 Q62179 SEMAPHORIN C (SEM C) (FRAGMENT). Length = 782	gi 854328	1	165	80	86	HIFCES53	Colon, Breast/Ovarian

748	HCRQC92R	spermidine/spermine N1-acetyltransferase [Homo sapiens] >gi 338336 spermidine/spermine N1-acetyltransferase [Homo sapiens] >sp P21673 A_TDA_HUMAN DIAMINE ACETYLTRANSFERASE (EC 2.3.1.57) (SPERMIDINE/SPERMINE N1-ACETYLTRANSFERASE) (SSAT) (PUTRESCINE ACETYL-T	gi 338392	3	278	98	98	HCRQC92	Lung, Colon, Breast/Ovarian
749	HAOAG75R	TARBP-b gene product [Homo sapiens] Length = 277	gi 347964	2	418	100	100	HAOAG75	Lung, Colon
750	HWAFAE36R	TEGT gene product [Homo sapiens] >pir 38334 38334 TEGT (testis enhanced gene transcript) - human Length = 237	gi 458545	2	127	100	100	HWAFAE36	Pancreas, Colon
751	HBGOU57R	TIMP gene product [Homo sapiens] >gi 182483 prefibroblast collagenase inhibitor [Homo sapiens] >gi 189382 collagenase inhibitor [Homo sapiens] >gi 37183 precursor [Homo sapiens] >pir A93372 ZYHUEP metalloproteinase tissue inhibitor 1 precursor - human >gi	gi 490094	60	314	75	75	HBGOU57	Lung, Pancreas, Breast/Ovarian
752	HTXPF20R	TIMP gene product [Homo sapiens] >gi 182483 prefibroblast collagenase inhibitor [Homo sapiens] >gi 189382 collagenase inhibitor [Homo sapiens] >gi 37183 precursor [Homo sapiens] >pir A93372 ZYHUEP metalloproteinase tissue inhibitor 1 precursor - human >gi	gi 490094	1	549	84	84	HTXPF20	Lung, Pancreas, Colon, Breast/Ovarian
753	HCRMD09R	transforming growth factor-beta 1 binding protein precursor [Homo sapiens] >pir A35626 A35626 transforming growth factor beta-1-binding protein - human Length = 1394	gi 339548	2	460	86	87	HCRMD09	Lung, Pancreas, Colon

754	HAJRB47R	triose-phosphate isomerase [Pan troglodytes] >gi 37247 triosephosphate isomerase [Homo sapiens] >gi 1200507 triosephosphate isomerase [Homo sapiens] >gi 339841 triosephosphate isomerase (EC 5.3.1.1) [Homo sapiens] >pir S29743 SHUT triose-phosphate isomer	gi 176960	2	334	100	100	HAIJB47	Lung, Pancreas, Breast/Ovarian
755	HAIJB36R			6	251			HAIJB36	Lung, Breast/Ovarian
756	HADBF86R			3	158			HADBF86	Lung, Colon
757	HADDP09R			2	97			HADDP09	Lung, Pancreas, Colon, Breast/Ovarian
758	HAGCY06R			2	58			HAGCY06	Pancreas, Breast/Ovarian
759	HAGDI75R			1	66			HAGDI75	Colon, Breast/Ovarian
760	HAHBD47R			118	429			HAHBD47	Lung, Pancreas
761	HAHCR61R			165	422			HAHCR61	Pancreas, Colon
762	HAJAU22R			101	202			HAJAU22	Pancreas, Colon
763	HAMGB62R			212	370			HAMGB62	Lung, Pancreas, Colon, Breast/Ovarian
764	HANGC52R			3	98			HANGC52	Lung, Pancreas, Colon
765	HAI'CF30R			2	94			HAI'CF30	Lung, Colon
766	HAPPV45R			216	536			HAPPV45	Lung, Pancreas
767	HAPQK19R			200	415			HAPQK19	Lung, Pancreas
768	HAPRL82R			3	233			HAPRL82	Lung, Pancreas
769	HAQBT45R			40	255			HAQBT45	Lung, Colon
770	HAUAL56R			127	315			HAUAL56	Pancreas, Breast/Ovarian

771	HAUBR22R	2	67	HAUBR22	Pancreas, Colon, Breast/Ovarian
772	HBAFN19R	3	257	HBAFN19	Lung, Colon, Breast/Ovarian
773	HBGOK25R	274	528	HBGOK25	Pancreas, Colon
774	HBGRA76R	2	88	HBGRA76	Pancreas, Colon
775	HBGRB47R	1	111	HBGRB47	Lung, Pancreas, Colon, Breast/Ovarian
776	HBJAS24R	1	66	HBJAS24	Colon, Breast/Ovarian
777	HBJKI05R	207	362	HBJKI05	Pancreas, Colon
778	HBKEC86R	254	409	HBKEC86	Pancreas, Colon
779	HBLGD42R	3	341	HBLGD42	Lung, Pancreas, Colon, Breast/Ovarian
780	HBPAP10R	3	65	HBPAP10	Lung, Pancreas
781	HCDBU02R	65	184	HCDBU02	Pancreas, Colon
782	HCDBU04R	64	348	HCDBU04	Lung, Pancreas, Colon
783	HCDDT61R	2	121	HCDDT61	Pancreas, Colon
784	HCEGY65R	2	79	HCEGY65	Pancreas, Colon
785	HCHAK80R	1	513	HCHAK80	Colon, Breast/Ovarian
786	HCHMW79R	73	432	HCHMW79	Pancreas, Breast/Ovarian
787	HCHOB92R	93	350	HCHOB92	Colon, Breast/Ovarian
788	HCLBO01R	45	149	HCLBO01	Lung, Colon
789	HCQAN60R	3	122	HCQAN60	Pancreas, Colon
790	HCHAK70R	3	293	HCHAK70	Colon, Breast/Ovarian
791	HCRPC63R	1	129	HCRPC63	Pancreas, Colon
792	HCUDC51R	2	265	HCUDC51	Lung, Colon

793	HDPFI40R	139	453	HDPFI40	Lung, Pancreas, Breast/Ovarian
794	HDPLP23R	1	141	HDPLP23	Pancreas, Colon, Breast/Ovarian
795	IIDPRZ54R	1	165	IIDPRZ54	Colon, Breast/Ovarian
796	HE9DP46R	2	166	HE9DP46	Lung, Pancreas, Colon
797	HEGAR19R	361	534	HEGAR19	Lung, Colon
798	HFAUO64R	27	137	HFAUO64	Colon, Breast/Ovarian
799	HFIAL90R	186	308	HFIAL90	Lung, Colon
800	HHBEQ12R	218	514	HHBEQ12	Lung, Pancreas
801	HHEUL94R	2	127	HHEUL94	Lung, Pancreas, Colon
802	HISCF76R	16	153	HISCF76	Pancreas, Colon
803	HJMAU64R	1	207	IJMAU64	Lung, Colon
804	IJPC125R	275	508	IJPC125	Lung, Pancreas, Colon
805	HKBAC48R	369	542	HKBAC48	Lung, Pancreas, Colon, Breast/Ovarian
806	HKBAD57R	165	341	HKBAD57	Lung, Pancreas
807	HKDBA91R	3	332	HKDBA91	Pancreas, Colon
808	HKGDB80R	3	224	HKGDB80	Lung, Colon
809	HLDNC95R	289	537	HLDNC95	Lung, Pancreas, Prostate, Colon
810	HMSNI52R	2	271	HMSNI52	Lung, Pancreas
811	HODAY16R	134	298	HODAY16	Colon, Breast/Ovarian
812	HODEA57R	289	471	IODEA57	Lung, Pancreas
813	HOEMO27R	1	60	HOEMO27	Colon, Breast/Ovarian

814	HOEMO62R	2	73	HOEMO62	Pancreas, Breast/Ovarian
815	HOEMS18R	1	102	HOEMS18	Lung, Pancreas, Colon, Breast/Ovarian
816	HOENU53R	115	267	HOENU53	Lung, Colon
817	HOGAP33R	1	498	HOGAP33	Pancreas, Prostate, Breast/Ovarian
818	HOSMV34R	124	327	HOSMV34	Lung, Pancreas, Breast/Ovarian
819	HOSNF25R	405	587	HOSNF25	Pancreas, Colon
820	HOUHO32R	230	391	HOUHO32	Lung, Colon
821	HPIAC23R	2	286	HPIAC23	Lung, Breast/Ovarian
822	HRAAD31R	115	414	HRAAD31	Lung, Colon
823	HRACR12R	2	100	HRACR12	Pancreas, Colon
824	HRADJ57R	2	142	HRADJ57	Lung, Colon
825	HROAX48R	184	285	HROAX48	Pancreas, Colon
826	HTAHR87R	369	491	HTAHR87	Lung, Pancreas
827	HTTIO45R	1	288	HTTIO45	Colon, Breast/Ovarian
828	HTWDH05R	1	420	HTWDH05	Lung, Pancreas, Colon, Breast/Ovarian
829	HUFDS13R	51	152	HUFDS13	Pancreas, Colon
830	HUSZE86R	2	340	HUSZE86	Pancreas, Colon
831	HUTHF75R	161	418	HUTHF75	Lung, Pancreas, Breast/Ovarian
832	HWAFFW07R	3	170	HWAFFW07	Lung, Pancreas, Colon
833	HWLIB82R	209	403	HWLIB82	Pancreas, Colon
834	HWLLX91R	147	302	HWLLX91	Lung, Colon
835	HWLMZ54R	1	120	HWLMZ54	Pancreas, Colon

836	HMIAI78R		173	319		HMIAI78	Pancreas, Colon, Breast/Ovarian
837	HBGFJ39R	unknown product specific to adipose tissue [Homo sapiens] >sp Q15847 Q15847 HYPOTHETICAL 7.9 KD PROTEIN. Length = 76	1	153	100	HBGFJ39	Pancreas, Colon
838	HAMHH32R		1	123		HAMHH32	Lung, Colon
839	HAQBQ95R		104	205		HAQBQ95	Colon, Breast/Ovarian
840	HAGHY58R	URF 1 (NADH dehydrogenase subunit) [Homo sapiens] >gi 337189 protein 1 [Homo sapiens] >pir A00407 DNHUN1 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - human mitochondrion (SGC1) >sp P03886 NUIM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6	157	411	95	HAGHY58	Lung, Colon
841	HOSNE37R	URF 2 (NADH dehydrogenase subunit) [Homo sapiens] >gi 2052363 protein 2 [Homo sapiens] >gi 2582057 AF014882) NADH dehydrogenase subunit 2 [Homo sapiens] >gi 2582061 AF014884) NADH dehydrogenase subunit 2 [Homo sapiens] >gi 2582063 AF014885) NADH dehydr	73	231	59	HOSNE37	Lung, Pancreas, Colon
842	HWAFE41R	VDUP1=1,25-dihydroxyvitamin D-3 up-regulated [human, HL-60 promyelocytic leukemia cells, P-plate, 391 aa] [Homo sapiens] Length = 391	2	508	84	HWAFE41	Pancreas, Colon

The first column of Table 1 shows the "SEQ ID NO:" for each of the 842 cancer antigen polynucleotide sequences of the invention.

The second column in Table 1, provides a unique "Sequence/Contig ID" identification for each cancer associated sequence. The third column in Table 1, "Gene Name," provides a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database, such as GenBank (NCBI). The great majority of the cDNA sequences reported in Table 1 are unrelated to any sequences previously described in the literature. The fourth column, in Table 1, "Overlap," provides the database accession no. for the database sequence having similarity. The fifth and sixth columns in Table 1 provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by the nucleotide position nos. "Start" and "End". Also provided are polynucleotides encoding such proteins and the complementary strand thereto. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity) observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence.

The ninth column of Table 1 provides a unique "Clone ID" for a clone related to each contig sequence. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

The tenth column of Table 1, "Tissue," provides the tissue source where each unique SEQ ID NO:X was found to be predominantly expressed.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, or more of any one or more of these public ESTs are optionally excluded from the invention.

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing as SEQ ID NO:1 through SEQ ID NO:842) and the translated SEQ ID NO:Y

(where Y may be any of the polypeptide sequences disclosed in the sequence listing as SEQ ID NO:843 through SEQ ID NO:1684) are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X has uses including, but not limited to, in designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the related cDNA clone contained in a library deposited with the ATCC. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y have uses that include, but are not limited to, generating antibodies which bind specifically to the cancer antigen polypeptides, or fragments thereof, and/or to the cancer antigen polypeptides encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing the related cDNA clone (deposited with the ATCC, as set forth in Table 1). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC on:

5 Table 2

ATCC Deposits	Deposit Date	ATCC Designation Number
LP01, LP02, LP03, LP04, LP05, LP06, LP07, LP08, LP09, LP10, LP11,	May-20-97	209059, 209060, 209061, 209062, 209063, 209064, 209065, 209066, 209067, 209068, 209069
LP12	Jan-12-98	209579
LP13	Jan-12-98	209578
LP14	Jul-16-98	203067
LP15	Jul-16-98	203068
LP16	Feb-1-99	203609
LP17	Feb-1-99	203610
LP20	Nov-17-98	203485
LP21	Jun-18-99	PTA-252
LP22	Jun-18-99	PTA-253
LP23	Dec-22-99	PTA-1081

each is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as shown in Table 5. These deposits are referred to as "the deposits" herein. The tissues from which the clones were derived are listed in Table 5, and the vector in which the cDNA is contained is also indicated in Table 5. The deposited material includes the cDNA clones which were partially sequenced and are related to the SEQ ID NO:X described in Table 1 (column 9). Thus, a clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Although the sequence listing lists only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to complete the sequence of the DNA included in a clone isolatable from the

ATCC Deposits by use of a sequence (or portion thereof) listed in Table 1 by procedures hereinafter further described, and others apparent to those skilled in the art.

Also provided in Table 5 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for
5 convenience.

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res.* 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., *Nucleic Acids Res.* 17:9494 (1989)) and pBK (Alting-
10 Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain
15 XL-1 Blue, also available from Stratagene.

Vectors pSport1, pCMVSPORT 1.0, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus*
20 15:59 (1993). Vector lacmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res.*
25 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in a deposited cDNA clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include, but are not limited to, preparing probes or primers from the
30 disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in the related cDNA clone in the deposit, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the related cDNA clone (See, e.g., columns 1 and 9 of Table 1). The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, and/or a polypeptide encoded by the the dDNA in the related cDNA clone contained in a deposited library, are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the complement of the coding strand of the related cDNA clone contained in a deposited library.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would unduly burden the disclosure of this application. Accordingly, for each "Contig Id" listed in the first column of Table 3, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described in the second column of Table 3 by the general formula of a-b, each of which are uniquely defined for the SEQ ID NO:X corresponding to that Contig Id in Table 1. Additionally, specific embodiments are directed to polynucleotide sequences excluding at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. for each Contig Id which may be

included in column 3 of Table 3. In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example.

Table 3.

Sequence/ Contig ID	General formula	Genbank Accession No.
507291	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 542 of SEQ ID NO:1, b is an integer of 15 to 556, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:1, and where b is greater than or equal to a + 14.	
508000	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2648 of SEQ ID NO:2, b is an integer of 15 to 2662, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:2, and where b is greater than or equal to a + 14.	T40333, T41194, T66286, T66339, T73997, T86453, T87207, R17614, R19835, R43336, R45934, R48920, R53521, R43336, R45934, R61813, R75928, R75937, H30115, H42959, H39114, H43825, AA028010, AA028107, AA028148, AA031964, AA032046, AA035668, AA190570, AA233781, AA461489, AA460726, AA460898
518325	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 324 of SEQ ID NO:3, b is an integer of 15 to 338, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:3, and where b is greater than or equal to a + 14.	
523111	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 799 of SEQ ID NO:4, b is an integer of 15 to 813, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:4, and where b is greater than or equal to a + 14.	
526869	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 887 of SEQ ID NO:5, b is an integer of 15 to 901, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:5, and where b is greater than or equal to a + 14.	AA459771
532211	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 717 of SEQ ID NO:6, b is an integer of 15 to 731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:6, and where b is greater than or equal to a + 14.	H30209, H92182, W95693, W95692, AA196967
532247	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R14583, R93797, H52942, H75493, H78857, W17094, W38705, W81551, W90159, N90874, AA010244,

	where a is any integer between 1 to 2760 of SEQ ID NO:7, b is an integer of 15 to 2774, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:7, and where b is greater than or equal to a + 14.	AA029093, AA126501, AA147066
537932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2599 of SEQ ID NO:8, b is an integer of 15 to 2613, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:8, and where b is greater than or equal to a + 14.	T91131, T84801, T85952, R59198, R59256, H43456, H59480, H79111, N26560, N35676, N64506, N66078, N76033, N78705, W07594, W70111, W70169, N90844, AA026910, AA026911, AA057689, AA079631, AA079805, AA131257, AA136081, AA165115, AA210764, AA211886, AA232838, AA262352
540117	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1087 of SEQ ID NO:9, b is an integer of 15 to 1101, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:9, and where b is greater than or equal to a + 14.	T49371, T49372, T49850, T61568, T64892, N39534, W57682, AA031859
547710	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1359 of SEQ ID NO:10, b is an integer of 15 to 1373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:10, and where b is greater than or equal to a + 14.	R11154, R11155, R61204, R61205, R82674, H06105, R88575, R88638, H89977, H97031, N20224, W01143, W39387, W90318, W90788, AA001027, AA045864, AA045839, AA070190, AA070357, AA070481, AA074270, AA099007, AA099084, AA100370, AA112324, AA113319, AA158425, AA161510, AA171909, AA172133, AA173087, AA181768, AA188815, AA188874, AA190370, AA226831, AA252143
551747	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3790 of SEQ ID NO:11, b is an integer of 15 to 3804, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.	
552799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2143 of SEQ ID NO:12, b is an integer of 15 to 2157, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.	
553243	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1103 of SEQ ID NO:13, b is an integer of 15 to 1117, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is	H63183, W61352, AA151059

	greater than or equal to $a + 14$.	
553368	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 871 of SEQ ID NO:14, b is an integer of 15 to 885, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where b is greater than or equal to $a + 14$.	
554349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1010 of SEQ ID NO:15, b is an integer of 15 to 1024, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to $a + 14$.	
558491	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 531 of SEQ ID NO:16, b is an integer of 15 to 545, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to $a + 14$.	
558983	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 609 of SEQ ID NO:17, b is an integer of 15 to 623, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to $a + 14$.	
572943	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 545 of SEQ ID NO:18, b is an integer of 15 to 559, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to $a + 14$.	
585892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1341 of SEQ ID NO:19, b is an integer of 15 to 1355, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to $a + 14$.	
589390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1266 of SEQ ID NO:20, b is an integer of 15 to 1280, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to $a + 14$.	T47628, T49403, T49829, T49830, T50800, T50963, T51976, T55846, T55860, T55896, T55911, T58744, T58811, T58891, T59252, T59279, T59293, T59615, T59690, T59727, T59826, T60434, T60514, T60584, T61357, T40352, T62559, T62688, T62839, T63122, T64603, T64640.

		T67682, T67756, T68181, T68439, T68506, T68606, T68718, T68783, T68839, T68849, T68976, T69049, T71223, T71347, T71509, T71853, T71858, T71938, T72197, T72264, T72414, T72471, T72923, T73204, T73259, T73283, T73446, T73607, T73621, T73645, T73713, T73744, T73772, T73796, T74114, T74545, T74599, T87829, T90307, T90394, T91481, T92437, T92617, T81767, T82080, R27059, R27060, R31693, R31735, R50548, R50646, R64321, R64322, R75660, R75768, R75866, R76038, R79765, R79766, H22209, H24391, H25902, H27236, H28585, H29860, H29954, H41994, H42226, H42298, H43069, H43893, H43934, R83465, R84983, R94905, R94988, R96360, R96403, R97059, R98674, R98900, R99186, R99187, H50701, H50801, H57754, H62182, H63649, H63650, H64755, H64756, H69075, H70056, H70057, H70855, H70856, H71581, H75758, H75893, H80974, H80975, H83141, H83142, H83271, H85046, H84668, H91780, H92207, H92350, H94891, H94943, H94966, H95486, H99418, N52264, N58261, N74184, N77638, N81021, N92261, N99137, W04350, W07850, W16893, W39467, W45038, W47174, W47433, W52853, W63782, W67635, W67759, W67868, W67881, W93706, W94183, W96351, W96352, N89587, AA012898, AA019884, AA020863, AA025865, AA025866, AA056092, AA057434, AA070445, AA192155, AA192879, AA226741, AA227477
596882	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1177 of SEQ ID NO:21, b is an integer of 15 to 1191, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.	
616289	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 839 of SEQ ID NO:22, b is an integer of 15 to 853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.	
622140	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	W39497, W52751, AA099814, AA128882, AA173072, AA226739

	sequence described by the general formula of a-b, where a is any integer between 1 to 460 of SEQ ID NO:23, b is an integer of 15 to 474, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to a + 14.	
623566	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2266 of SEQ ID NO:24, b is an integer of 15 to 2280, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.	
647714	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1047 of SEQ ID NO:25, b is an integer of 15 to 1061, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.	
647752	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1558 of SEQ ID NO:26, b is an integer of 15 to 1572, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to a + 14.	
651774	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1991 of SEQ ID NO:27, b is an integer of 15 to 2005, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a + 14.	T69901, T69949, T70775, R20554, R33030, R33917, R48406, H58331, H58720, H67041, H68124, H93586, H94430, H94513, H97468, H99219, N23459, N26334, N35428, N49203, N50256, N64246, N93349, W19550, W19996, W25330, W73940, W77984, W93791, W94028, N90424, AA025537, AA025680, AA025371, AA026317, AA026318, AA084549, AA086048, AA086130, AA098995, AA099068, AA115309, AA136486, AA151843, AA149689, AA148825, AA150406, AA150425, AA173377
651995	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1394 of SEQ ID NO:28, b is an integer of 15 to 1408, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where b is greater than or equal to a + 14.	
652156	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 903 of SEQ ID NO:29, b is an integer of 15 to 917, where both a and	T40364, R22492, R49907, R49908, R62310, R62311, R65652, R67030, R81699, R81700, H18589, H20024, H20099, H20123, H20797, H22404, H22615, H25816, H27051, H42294,

	b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to a + 14.	H44827, H49661, H51422, H51465, H56482, H56483, H70295, H86037, H93528, H93860, H96113, H96114, N22715, N31188, N33831, N54495, N70601, N70623, N76607, N78626, W04920, W05505, W07305, W15350, W39442, W60859, W60860, W72726, W76452, AA017463, AA024543, AA024544, AA026421, AA026498, AA027270, AA034429, AA046316, AA046142, AA053920, AA056230, AA063244, AA062885, AA085305, AA128171, AA126216, AA149890, AA150552, AA187825, AA188597, AA417004, AA417190
653010	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 563 of SEQ ID NO:30, b is an integer of 15 to 577, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.	
655904	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2045 of SEQ ID NO:31, b is an integer of 15 to 2059, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to a + 14.	T61561, T90265, T90707, R09280, R17627, R43348, R54854, R54658, H20872, H27229, H64571, H64673, H64571, N47495, N54722, N75461, W73679, AA010711, AA010712, AA082107, AA130516, AA132052, AA132156, AA147852, AA147908, AA148276, AA148277, AA181933, AA187549, AA187845, AA186675, AA188310, AA193212
657852	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 535 of SEQ ID NO:32, b is an integer of 15 to 549, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.	
666414	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 827 of SEQ ID NO:33, b is an integer of 15 to 841, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to a + 14.	
667847	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 849 of SEQ ID NO:34, b is an integer of 15 to 863, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.	T47009, T47010, T55133, T55301, T57663, T57702, T59664, T59797, T59800, T49370, T72020, T26631, R22343, R46325, R48879, R50151, R50204, R55208, R71485, R71535, R72144, R72362, R72553, R74062, H13587, H16167, H18121, H20172, H20361, H22514, H40774, H40775,

		H42435, H42865, H43100, H43164, H45140, H45441, H46013, H46083, H46159, R97084, R97131, H56498, H60260, H60567, H67238, H71802, H77325, H77338, H81556, H87775, H87825, H91889, H92057, H93187, H96056, H96420, H81556, H99575, N21484, N23829, N24221, N26831, N27079, N27278, N27582, N30213, N30255, N31642, N31989, N31996, N32655, N32790, N35515, N38983, N39859, N40012, N40488, N41792, N41978, N54988, N57097, N70071, N77176, N78930, N80037, N80573, N81058, N92768, N93810, W07000, W07659, W07868, W44961, W44962, W58175, W58263, W58182, AA001206, AA017579, AA026640, AA026706, AA057605, AA058758, AA082491, AA084088, AA086460, AA100968, AA112029, AA121337, AA121500, AA130704, AA130790, AA152420, AA156094, AA156123, AA181929, AA182575, AA182617, AA186931, AA195982, AA253952, AA283976, AA426098, AA425122, AA428823, AA429359
670188	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1216 of SEQ ID NO:35, b is an integer of 15 to 1230, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to a + 14.	
670279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 626 of SEQ ID NO:36, b is an integer of 15 to 640, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.	T50781, T51265, T55324, T56327
670729	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 583 of SEQ ID NO:37, b is an integer of 15 to 597, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where b is greater than or equal to a + 14.	
674123	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 610 of SEQ ID NO:38, b is an integer of 15 to 624, where both a and b correspond to the positions of nucleotide residues	

	shown in SEQ ID NO:38, and where b is greater than or equal to a + 14.	
676496	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1015 of SEQ ID NO:39, b is an integer of 15 to 1029, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.	
678162	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1093 of SEQ ID NO:40, b is an integer of 15 to 1107, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where b is greater than or equal to a + 14.	T40233, T40521, T41098, T47133, T47529, T49156, T49157, T51636, T55352, T55402, T55422, T57649, T59314, T62530, T62806, T62954, T72271, T73592, T89655, T78884, R19194, R89249, R93164, H57861, H93645, N22493, N26661, N32984, N63146, N66448, N67443, N69984, N72141, N77952, N78933, N81091, N95826, W02074, W24850, W24972, W38365, W44897, W57997, W58080, W65414, W65435, W74634, AA007562, AA009767, AA022918, AA022939, AA025169, AA029717, AA029656, AA032096, AA040581, AA046091, AA070493, AA070646, AA070707, AA071405, AA071414, AA074752, AA075706, AA075696, AA079282, AA085620, AA100126, AA126795, AA128838, AA136579, AA143069, AA143200, AA146637, AA147370, AA147705, AA156001, AA157342, AA161090, AA164798, AA179749, AA187235, AA188048, AA187029, AA188384, AA192271, AA196973, AA235468, AA243180, AA459416, AA459642
678248	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1037 of SEQ ID NO:41, b is an integer of 15 to 1051, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where b is greater than or equal to a + 14.	
683668	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2178 of SEQ ID NO:42, b is an integer of 15 to 2192, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where b is greater than or equal to a + 14.	T49549, T49550, T49700, T49912, T49937, T50912, T51558, T53285, T53375, T53376, T53721, T54314, T54840, T55217, T56413, T99069, T99669, R01522, R31653, R32820, R32921, R35743, R50997, R64077, R65723, R69349, R71009, R72798, R72824, R76854, R77142, R79240, R79511, R80194, R80295, R81155, H39823, H39824, R84909, R85592, R91193, H50793, H52341, H53594, H53916, H92997, N26572, N32090,

		N32406, N34179, N36271, N45401, N49216, N50267, N67233, N67568, N72254, N75478, N93355, N94504, W00543, W05288, W05816, W23954, W24625, W24650, W25354, W49666, W52302, AA121852, AA121851, AA128593, AA128712, AA136731, AA136688, AA167235, AA167584, AA173693, AA176648, AA176804, AA179999, AA181456, AA181457, AA256158, AA256215, AA256247, AA458729, AA458778, AA464936, AA464937
693172	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 339 of SEQ ID NO:43, b is an integer of 15 to 353, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.	T49005, T50129, T54766, T59468, T71241, T89633, R66699, R67578, H25853, H26090, H41256, H43182, H45273, N58288, N95319, AA054338, AA057604, AA084261
694303	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3476 of SEQ ID NO:44, b is an integer of 15 to 3490, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where b is greater than or equal to a + 14.	
695042	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 767 of SEQ ID NO:45, b is an integer of 15 to 781, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a + 14.	
699799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1417 of SEQ ID NO:46, b is an integer of 15 to 1431, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:46, and where b is greater than or equal to a + 14.	T50599, R25615, R31078, R68513, R70896, R75848, R76864, R76865, H01087, H26949, H63077, H75713, H75642, H95014, H98885, N24938, N33815, N47174, N47897, N51152, N53997, N59590, N62387, N63017, N67836, N69948, N78655, N79355, N94343, N98329, W01767, W03440, W15144, W19292, W25534, W37911, W42857, W42912, W48630, W72791, W76438, W81113, W80546, W80525, W80526, W84575, W84645, AA010674, AA011261, AA026981, AA031662, AA039737, AA039810, AA040524, AA040523, AA046308, AA046396, AA099365, AA101915, AA129310, AA129354, AA131951, AA186409
702216	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T64167, T64355, T68409, T68475, T73691, T73717, T97735, T97840.

	sequence described by the general formula of a-b, where a is any integer between 1 to 1899 of SEQ ID NO:47, b is an integer of 15 to 1913, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a + 14.	T98899, T99491, R00460, R01214, R01326, H45786, R93124, R96609, H61118, H61119, H61454, H62460, H64003, H64052, H91078, H91378, N58480, N64695, N65991, N74260, N78070, N79244, N91708, N95101, W03761, W04301, N90479, AA130077, AA130076, AA152275, AA150441
703015	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1747 of SEQ ID NO:48, b is an integer of 15 to 1761, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a + 14.	R72819, R73270, H43839, W47195, W52204, AA242894, AA424584, AA424629
706391	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 942 of SEQ ID NO:49, b is an integer of 15 to 956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:49, and where b is greater than or equal to a + 14.	T48974, H26922, H30342, H44743, H45233, R88178, H81778, H92363, N29006, N44860, N46515, AA079547, AA158434, AA160590, AA428285
706892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 549 of SEQ ID NO:50, b is an integer of 15 to 563, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where b is greater than or equal to a + 14.	
706924	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3201 of SEQ ID NO:51, b is an integer of 15 to 3215, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where b is greater than or equal to a + 14.	T68892, T68966, T75421, R15205, R16398, R41650, R42339, R52995, R52996, R41650, H12000, H16753, H16861, H27652, H27653, H27982, H28497, H29323, H29416, H85752, H98511, N22580, N24339, N28586, N42727, N50084, N75803, N78815, W07245, W21306, W23840, W57924, W58128, W72277, W76304, W86460, AA002243, AA002080, AA025565, AA025683, AA026606, AA026718, AA150696, AA150801
707642	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 612 of SEQ ID NO:52, b is an integer of 15 to 626, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where b is greater than or equal to a + 14.	
710369	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 906 of SEQ ID NO:53, b is an integer of 15 to 920, where both a and	T48815, T60685, T91108, T99835, AA150217, AA157340, AA157240, AA171947

	b correspond to the positions of nucleotide residues shown in SEQ ID NO:53, and where b is greater than or equal to a + 14.	
718826	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1076 of SEQ ID NO:54, b is an integer of 15 to 1090, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:54, and where b is greater than or equal to a + 14.	
719790	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1450 of SEQ ID NO:55, b is an integer of 15 to 1464, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where b is greater than or equal to a + 14.	T47380, T47538, T47539, T53445, T53446, T54910, T55077, T59959, T60032, T62504, T62649, T63049, T63297, T63382, T65688, T71591, T71742, T93094, T93187, T94131, T94222, T91210, T84959, T99044, T99045, R26119, R26148, R33224, R35866, R36526, R53923, R53924, R69596, R69684, R76209, R76210, R79249, R79521, H03427, H03507, H12529, H13501, H19016, H19310, H21587, H21652, H21653, H30119, H39693, H42698, H46635, R93371, R98210, R99855, H54120, H54786, H54837, H58991, H65355, H65566, H67613, H72632, H74102, H95312, N48235, N58029, N64226, N66907, N70763, N78303, N93848, N94316, N95432, N98433, W01816, W02218, W05772, W21419, W24044, W24297, W30823, W32382, W37228, W37317, W40321, W42528, W46445, W49731, W51944, W53011, W53012, W60051, W60129, W60154, W68332, W68216, W72730, W74593, W92813, W93310, AA010985, AA011307, AA031435, AA035708, AA037040, AA053073, AA053374, AA055567, AA069724, AA069690, AA069682, AA069900, AA069951, AA070693, AA071421, AA074606, AA075555, AA075673, AA075544, AA081017, AA081251, AA081428, AA082119, AA082022, AA082213, AA082241, AA082247, AA082400, AA082365, AA082438, AA082679, AA083225, AA083266, AA083508, AA083411, AA083637, AA084202, AA099623, AA102015, AA099659, AA100102, AA100163, AA100429, AA100430, AA100455, AA100456, AA100711, AA100764, AA100906, AA100919, AA100963, AA101118, AA102494, AA101184, AA112123, AA122359, AA122360, AA126882, AA127103, AA128195, AA128674, AA128686, AA128741,

		AA128747, AA128785, AA133488, AA133489, AA130006, AA130007, AA134211, AA130492, AA130507, AA134345, AA134346, AA134457, AA134458, AA134461, AA134462, AA130907, AA131020, AA131973, AA132141, AA132493, AA132601, AA134904, AA135121, AA135182, AA135348, AA136318, AA143066, AA143256, AA143278, AA143386, AA146650, AA146835, AA146836, AA146860, AA146861, AA146870, AA146871, AA146918, AA147716, AA147707, AA147868, AA148130, AA148090, AA148091, AA152422, AA148435, AA148867, AA148492, AA148702, AA151453, AA151452, AA151828, AA155801, AA155886, AA156025, AA156044, AA156053, AA156155, AA156222, AA157080, AA157168, AA157325, AA157423, AA157434, AA157471, AA157605, AA157631, AA157546, AA157775, AA157826, AA158157, AA158273, AA158888, AA158887, AA159153, AA159250, AA160104, AA159856, AA161278, AA161301, AA160817, AA164741, AA165616, AA165606, AA173037, AA173038, AA176229, AA176317, AA179185, AA179190, AA179200, AA181043, AA181262, AA181342, AA181834, AA181989, AA182794, AA187247, AA187342, AA187379, AA187470, AA187528, AA187740, AA187911, AA188028, AA186378, AA186424, AA186441, AA186442, AA186568, AA186653, AA186661, AA186703, AA186910, AA187081, AA187087, AA187078, AA187135, AA188313, AA188330, AA188342, AA190473, AA193219
720222	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 971 of SEQ ID NO:56, b is an integer of 15 to 985, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where b is greater than or equal to a + 14.</p>	AA056718, AA428747
724033	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1232 of SEQ ID NO:57, b is an integer of 15 to 1246, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where b is greater than or equal to a + 14.</p>	N50855, AA076233, AA076232

724767	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:58, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where b is greater than or equal to a + 14.	
727065	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1597 of SEQ ID NO:59, b is an integer of 15 to 1611, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where b is greater than or equal to a + 14.	T26554, R31862, R31869, R67140, R70861, H00137, H23051, H23350, H60670, N28391, N28646, AA081571
727246	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1835 of SEQ ID NO:60, b is an integer of 15 to 1849, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where b is greater than or equal to a + 14.	
727932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 219 of SEQ ID NO:61, b is an integer of 15 to 233, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:61, and where b is greater than or equal to a + 14.	
731167	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2319 of SEQ ID NO:62, b is an integer of 15 to 2333, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where b is greater than or equal to a + 14.	
732514	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1456 of SEQ ID NO:63, b is an integer of 15 to 1470, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is greater than or equal to a + 14.	
734080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 925 of SEQ ID NO:64, b is an integer of 15 to 939, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where b is greater than or equal to a + 14.	
734288	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2054 of SEQ ID NO:65, b is an integer of 15 to 2068, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:65, and where b is greater than or equal to a + 14.	
739448	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1377 of SEQ ID NO:66, b is an integer of 15 to 1391, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:66, and where b is greater than or equal to a + 14.	T53676, T53677, T54741, T55855, T55906, T56935, T57622, T58975, T58979, T61059, T61143, T90498, T90594, T93775, R07734, R07735, R40067, R75954, R75978, R76790, R76809, R77290, R77315, R77348, R79433, R79434, R97814, H50168, H70091, H77406, H80889, H82088, H82195, N33576, N39028, N48219, N49421, N52598, N66328, N67208, N73788, N78932, N92856, N99411, W07071, W17213, W24422, W25582, W47407, W47574, W49651, W49725, W68140, W68467, AA025829, AA025972, AA074731, AA074835, AA075316, AA081368, AA081369, AA082652, AA082810, AA101054, AA102495, AA115718, AA115719, AA127079, AA127080, AA127200, AA127199, AA128645, AA128813, AA133732, AA130465, AA130466, AA132111, AA143233, AA143289, AA146780, AA147706, AA148134, AA151491, AA157062, AA157046, AA157630, AA165124, AA165123, AA164625, AA165420, AA165583, AA173407, AA173462, AA179910, AA179911, AA180198, AA181087, AA181556, AA182450, AA182951, AA186670, AA188289, AA192925, AA193075, AA464823
739668	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 645 of SEQ ID NO:67, b is an integer of 15 to 659, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where b is greater than or equal to a + 14.	
740060	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2967 of SEQ ID NO:68, b is an integer of 15 to 2981, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where b is greater than or equal to a + 14.	
741560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 589 of SEQ ID NO:69, b is an integer of 15 to 603, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:69, and where b is greater than or equal to a + 14.	
742543	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1087 of SEQ ID NO:70, b is an integer of 15 to 1101, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where b is greater than or equal to a + 14.	
742831	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 700 of SEQ ID NO:71, b is an integer of 15 to 714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where b is greater than or equal to a + 14.	
745327	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2876 of SEQ ID NO:72, b is an integer of 15 to 2890, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:72, and where b is greater than or equal to a + 14.	
745695	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2474 of SEQ ID NO:73, b is an integer of 15 to 2488, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where b is greater than or equal to a + 14.	T56303, T58644, T58694, R48815, R48816, R68140, R74376, R78015, R81014, H00852, H01233, H17193, H17969, H25101, H27005, H30607, H41236, H42218, H42290, H42904, H42977, H45271, H45342, R83816, R98855, R98939, H53696, H62059, H82544, H83097, N40713, N92791, W19377, AA025571, AA053695, AA053675, AA069167, AA069166, AA076604, AA076603, AA079426, AA100088, AA099771, AA130265, AA158402, AA179641, AA235643, AA253454, AA250758, AA458951, AA458978, AA459194, AA419280, AA419329, AA425117, AA430664
750316	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 697 of SEQ ID NO:74, b is an integer of 15 to 711, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where b is greater than or equal to a + 14.	
750522	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 892 of SEQ ID	

	NO:75, b is an integer of 15 to 906, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where b is greater than or equal to a + 14.	
750583	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 257 of SEQ ID NO:76, b is an integer of 15 to 271, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where b is greater than or equal to a + 14.	
751020	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 659 of SEQ ID NO:77, b is an integer of 15 to 673, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where b is greater than or equal to a + 14.	N80268, N95387, W57806, W63590, AA182782, AA187759, AA199806, AA262640, AA262111, AA262106, AA460214
752196	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 353 of SEQ ID NO:78, b is an integer of 15 to 367, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where b is greater than or equal to a + 14.	R67541
753084	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1330 of SEQ ID NO:79, b is an integer of 15 to 1344, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where b is greater than or equal to a + 14.	T93791, T93840, R77826, R78199, R99272, H54274, H65600, H67128, H75533, H75532, H81433, N57836, N58786, N72699, N77475, W02480, W78743, W80625, W90276, AA007397, AA127528, AA127529, AA130419, AA147733, AA150095, AA195008, AA195060
754957	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3734 of SEQ ID NO:80, b is an integer of 15 to 3748, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where b is greater than or equal to a + 14.	
756557	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1877 of SEQ ID NO:81, b is an integer of 15 to 1891, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:81, and where b is greater than or equal to a + 14.	
756712	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1940 of SEQ ID NO:82, b is an integer of 15 to 1954, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where b is greater than or equal to a + 14.	
757414	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 922 of SEQ ID NO:83, b is an integer of 15 to 936, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:83, and where b is greater than or equal to a + 14.	T49651, T49652, T92946, T93013, H02307, H02419, N42072, AA169576
757614	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1499 of SEQ ID NO:84, b is an integer of 15 to 1513, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where b is greater than or equal to a + 14.	T93709, T96172, H00439, H00480, R85176, H51264, H51834, H53645, H57470, H57991, H73334, N33138, N42318, N94987, AA028955, AA081550, AA082013, AA113225, AA113810, AA133619, AA133522, AA132699, AA132810, AA151877, AA149662, AA157324, AA157422, AA159905, AA165014, AA165442, AA165443, AA167837, AA166621, AA166924, AA195339, AA195338, AA252790
757815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1284 of SEQ ID NO:85, b is an integer of 15 to 1298, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:85, and where b is greater than or equal to a + 14.	
759878	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1995 of SEQ ID NO:86, b is an integer of 15 to 2009, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where b is greater than or equal to a + 14.	
760227	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 520 of SEQ ID NO:87, b is an integer of 15 to 534, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where b is greater than or equal to a + 14.	
760312	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4288 of SEQ ID NO:88, b is an integer of 15 to 4302, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:88, and where b is greater than or equal to a + 14.	
766051	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T57753, T60650, R11036, R11084, R00826, R01482, H87221, N25112,

	sequence described by the general formula of a-b, where a is any integer between 1 to 2768 of SEQ ID NO:89, b is an integer of 15 to 2782, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:89, and where b is greater than or equal to a + 14.	N33451, N42424, N47338, N48186, N62628, N68902, N71490, N78399, N99533, W16943, W78948, W85915, W95743, N89568, AA039230, AA039231, AA047564, AA047582, AA047702, AA047752, AA120926, AA126453, AA135549, AA135529, AA429718
767593	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1023 of SEQ ID NO:90, b is an integer of 15 to 1037, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:90, and where b is greater than or equal to a + 14.	T51635, T57709, T61468, T63793, T63818, T92894, T92984, T94396, T75475, T75508, T87575, T79848, T85949, R25644, R27489, R70702, R78772, H44836, H44835, R84349, R86157, R89703, R99494, H48567, H48836, H57859, H83579, H86373, H86690, H88284, H97937, H98241, H99117, H99249, N24363, N24573, N26374, N27129, N31662, N36546, N40064, N45098, N45108, N53503, N59526, N63219, N64179, N64178, N66660, N70536, N72298, N98943, W02894, W19364, W60295, W60386, W72691, W77806, W93582, W93631, W92326, W92382, N90765, AA001997, AA013356, AA017023, AA017221, AA018780, AA026639, AA026705, AA029569, AA029496, AA029736, AA035387, AA035694, AA044958, AA055558, AA063564, AA100726, AA100744, AA134118, AA130301, AA151965, AA233192, AA253060, AA253117
768053	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1038 of SEQ ID NO:91, b is an integer of 15 to 1052, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where b is greater than or equal to a + 14.	
768055	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1220 of SEQ ID NO:92, b is an integer of 15 to 1234, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:92, and where b is greater than or equal to a + 14.	T68053, R09316, R09788, T84929, R24826, R66259, R68879, R80029, H00967, H89841, H96162, N39802, N44634, N68319, N70487, N71145, N72732, W01594, W52285, W73342, W85800, AA022906, AA022975, AA031962, AA032044, AA032163, AA037604, AA043694, AA043695, AA044134, AA074287, AA081041, AA081042, AA082218, AA082461, AA082475, AA083977, AA100460, AA155926, AA167365, AA171958, AA173534, AA187036, AA224429
769685	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1557 of SEQ ID	

	NO:93, b is an integer of 15 to 1571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where b is greater than or equal to $a + 14$.	
771920	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1858 of SEQ ID NO:94, b is an integer of 15 to 1872, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:94, and where b is greater than or equal to $a + 14$.	
772790	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1502 of SEQ ID NO:95, b is an integer of 15 to 1516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:95, and where b is greater than or equal to $a + 14$.	
772916	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1756 of SEQ ID NO:96, b is an integer of 15 to 1770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:96, and where b is greater than or equal to $a + 14$.	
773225	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 924 of SEQ ID NO:97, b is an integer of 15 to 938, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:97, and where b is greater than or equal to $a + 14$.	
773632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 297 of SEQ ID NO:98, b is an integer of 15 to 311, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:98, and where b is greater than or equal to $a + 14$.	
774364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 606 of SEQ ID NO:99, b is an integer of 15 to 620, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:99, and where b is greater than or equal to $a + 14$.	W01405, AA172322
775355	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2497 of SEQ ID NO:100, b is an integer of 15 to 2511, where both a	T49285, T61774, T68350, T68396, T94414, T69842, T81078, R01216, R05674, R21522, R21626, R23745, R23797, R24081, R24137, R24753, R32662, R36359, R45484, R45484,

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:100, and where b is greater than or equal to a + 14.	R63380, R63433, R70942, R70995, R73973, R78964, H08973, H09543, H16712, H16713, H20846, H20896, R99241, H82276, H82382, H84715, H85367, H85516, H89615, H95047, H96450, H97881, N20953, N21537, N22201, N25769, N29477, N30442, N37087, N42334, N42354, N66424, N66864, N67873, N71242, N73740, N94555, N99903, W45394, W46993, W46961, W46960, W46881, W73247, W90778, AA026678, AA026215, AA043908, AA044414, AA042828, AA062957, AA076063, AA121145, AA121476, AA195131, AA234043, AA234044, AA426421
775844	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2967 of SEQ ID NO:101, b is an integer of 15 to 2981, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:101, and where b is greater than or equal to a + 14.	T73286, T66741, T66742, R12147, R15080, R19321, R39271, R42973, R44589, R44589, H06197, H08725, R94752, H71652, H71653, H79764, H79765, H79770, H79762, H79761, H79771, H92246, H96184, N45199, W93244, W93245, W93258, W93257, W94615, W94654, AA001180, AA039582, AA039689, AA082198, AA157370, AA157869, AA253368
777760	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2790 of SEQ ID NO:102, b is an integer of 15 to 2804, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:102, and where b is greater than or equal to a + 14.	
779837	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 708 of SEQ ID NO:103, b is an integer of 15 to 722, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:103, and where b is greater than or equal to a + 14.	T67628, T72838, H59238, H84693, N80048, W07009, W37555, W39191, N90251, AA057629
780769	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1622 of SEQ ID NO:104, b is an integer of 15 to 1636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:104, and where b is greater than or equal to a + 14.	T66609, T66610, T83560, R15983, R15984, R35702, R49338, R49338, H11613, R94244, H87098, H87745, W60710, W60772, W94034, AA258151, AA258913, AA425943
781445	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1547 of SEQ ID NO:105, b is an integer of 15 to 1561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:105, and where b is	

	greater than or equal to $a + 14$.	
781531	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 472 of SEQ ID NO:106, b is an integer of 15 to 486, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:106, and where b is greater than or equal to $a + 14$.	
783018	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 786 of SEQ ID NO:107, b is an integer of 15 to 800, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:107, and where b is greater than or equal to $a + 14$.	R18976
783097	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1044 of SEQ ID NO:108, b is an integer of 15 to 1058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:108, and where b is greater than or equal to $a + 14$.	
784198	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1062 of SEQ ID NO:109, b is an integer of 15 to 1076, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:109, and where b is greater than or equal to $a + 14$.	
784868	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1185 of SEQ ID NO:110, b is an integer of 15 to 1199, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:110, and where b is greater than or equal to $a + 14$.	
785428	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3616 of SEQ ID NO:111, b is an integer of 15 to 3630, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:111, and where b is greater than or equal to $a + 14$.	T47751, T39348, T39359, T98137, T79193, T95760, R16653, R16654, R24052, R24245, R33230, R44846, R50794, R50912, R44846, R60930, R61049, R71116, R71620, R77888, R80860, H00109, H04333, H04688, H05041, H09555, H30257, H30320, H47931, R94218, R99062, R99260, H50702, H50803, H52629, H52628, H54000, H67115, H70269, H83460, H83572, H84911, H99358, N21482, N21632, N24626, N33762, N41609, N67949, N69593, N70188, N71452, N71818, N77888, N79031, N99501, W02150, W03072, W05781, W19647, W19972, W20125, W30896, W33043.

		W33197, W35407, W37262, W39072, W47654, W52846, W56143, W60064, W60074, W65501, W67522, W67591, W69745, W69926, W80811, W94093, W94156, N90996, AA039462, AA040857, AA043084, AA043810, AA053423, AA053042, AA064625, AA064709, AA115540, AA115051, AA120833, AA129500, AA129499, AA146736, AA148602, AA152314, AA150343, AA150620, AA150790, AA157282, AA160296, AA173937, AA173969, AA181340, AA188207, AA186354, AA188646, AA190484, AA199676, AA199677, AA243342, AA250981, AA459647, AA459773, AA460227
785845	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1512 of SEQ ID NO:112, b is an integer of 15 to 1526, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:112, and where b is greater than or equal to a + 14.	
785854	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 571 of SEQ ID NO:113, b is an integer of 15 to 585, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:113, and where b is greater than or equal to a + 14.	T85881, W45204
786705	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 487 of SEQ ID NO:114, b is an integer of 15 to 501, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:114, and where b is greater than or equal to a + 14.	R09422
787186	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1951 of SEQ ID NO:115, b is an integer of 15 to 1965, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:115, and where b is greater than or equal to a + 14.	
787279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1046 of SEQ ID NO:116, b is an integer of 15 to 1060, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:116, and where b is greater than or equal to a + 14.	T62081, T97170, R17585, R42923, R48789, R48896, R54561, R54562, R54721, R54722, R42923, R72984, R73595, H23901, H43508, H46275, H46348, H47255, H47254, R83475, R89352, R91048, R93150, R93669, R94520, R98839, H48417, H48899, H48900, H50560, H54157, H58936,

		H58983, H67630, H69455, H72554, H72955, H89822, N23388, N33070, N35168, N40256, N44641, N52556, N59706, N68387, N80806, N92514, W17007, W19578, W20217, W38835, W49822, W56061, W65416, W65285, N90575, AA002190, AA045344, AA045446, AA052950, AA053432, AA082245, AA083753, AA102071, AA099961, AA101574, AA112070, AA125782, AA125931, AA135139, AA135268, AA146635, AA151603, AA149484, AA149981, AA152120, AA171975, AA172123, AA181805, AA181821, AA188148, AA188225, AA186556, AA186917, AA460297, AA461585
789002	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 695 of SEQ ID NO:117, b is an integer of 15 to 709, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:117, and where b is greater than or equal to a + 14.	
789008	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2039 of SEQ ID NO:118, b is an integer of 15 to 2053, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:118, and where b is greater than or equal to a + 14.	T47492, T47493, T47900, T48303, T48445, T48456, T49007, T49079, T49080, T49218, T49310, T49311, T49913, T49914, T49941, T51256, T51337, T51371, T51423, T51604, T51757, T52271, T52400, T53326, T53327, T54148, T54244, T54295, T54330, T54402, T54407, T55485, T55733, T56237, T56379, T56414, T56565, T39384, T40546, T40551, T40552, T40824, T89603, T79470, T79561, R01378, R12635, R20536, R21209, R21238, R21239, R22062, R22119, R22190, R22241, R22534, R22535, R22823, R23625, R23881, R24090, R25741, R26431, R26587, R28327, R28328, R28330, R31619, R32132, R32349, R33134, R33286, R35454, R36658, R39739, R50498, R50581, R20536, R56656, R65717, R65777, R65870, R67856, R67857, R68076, R69399, R69531, R69752, R69920, R71289, R72350, R74061, R77148, R77149, R80495, R80640, R82550, H00862, H01301, H01472, H01571, H02637, H02893, H03072, H03073, H03443, H03525, H03812, H03836, H23457, H23458, H26513, H26583, H26584, R86226, R86227, R87053, R91130, R91174, R92513, R92642, R93418, R93468, R93700, R94462, R94463, R94793, R95110,

		R96330, R96329, R96675, R96943, R97000, R98195, R99857, H48277, H48366, H48451, H53119, H54247, H54246, H57144, H57217, H58791, H59276, H59324, H59614, H59654, H62873, H62997, H66302, H67109, H67468, H67594, H67634, H67646, H67685, H67891, H67935, H68007, H68476, H72996, H73208, H73882, H74057, H74076, H74196, H75522, H75366, H77704, H77705, H78593, H79262, H79373, H81287, H81343, H82036, H82218, H82313, H87010, H87011, H90552, H90551, H93198, H94403, N28269, N30773, N34862, N38975, N38989, N39317, N43935, N45164, N48122, N48136, N50666, N50756, N52570, N53559, N53589, N55006, N55026, N57654, N58258, N58340, N58627, N58738, N70218, N72552, N72649, N77216, N77511, N77635, N80637, W01074, W58701, W68231, W68232, W68700, W72561, W72580, W72399, W76223, W85725, W92304, W92318, W92144, W92354, AA004478, AA004551, AA009715, AA009825, AA024464, AA024465, AA025660, AA039523, AA039522, AA040081, AA040128, AA040033, AA040827, AA045744, AA053323, AA099152, AA099250
789555	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1810 of SEQ ID NO:119, b is an integer of 15 to 1824, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:119, and where b is greater than or equal to a + 14.</p>	T85669, H62189, H62190, H73963, H73295, N74147, W04314, W23625, W35215, AA040573, AA040671
789631	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 592 of SEQ ID NO:120, b is an integer of 15 to 606, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:120, and where b is greater than or equal to a + 14.</p>	
789779	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 824 of SEQ ID NO:121, b is an integer of 15 to 838, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:121, and where b is greater than or equal to a + 14.</p>	N69694, AA151932
790387	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide</p>	H19654, H87102, H87749, N29354, N34298, N44187, N57052, W69612,

	sequence described by the general formula of a-b, where a is any integer between 1 to 642 of SEQ ID NO:122, b is an integer of 15 to 656, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:122, and where b is greater than or equal to a + 14.	W93844, W93865, AA027893, AA029638, AA058317, AA058495, AA179870, AA232827, AA233881, AA235809
790461	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1372 of SEQ ID NO:123, b is an integer of 15 to 1386, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:123, and where b is greater than or equal to a + 14.	R66275, R76171, R82537, AA054476, AA056199, AA127010, AA143025, AA151006, AA150976
790931	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 831 of SEQ ID NO:124, b is an integer of 15 to 845, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:124, and where b is greater than or equal to a + 14.	T92052, R10686, T84927, R21818, R22331, R22332, R22401, R23139, R23140, R23369, R32153, R32154, R63527, R63575, R68799, R68901, R80768, H12779, H12836, H56522, H56704, H94832, H96055, H96058, H96422, H96418, N26715, N27088, N31910, N32532, N33383, N34596, N42693, N42748, W32121, W37432, W44577, W44627, W51792, W61294, W65390, AA026773, AA026774
791176	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1642 of SEQ ID NO:125, b is an integer of 15 to 1656, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:125, and where b is greater than or equal to a + 14.	T51708, T51919, T69384, R50942, R73632, R73706, H28125, N22822, N78772
791983	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 823 of SEQ ID NO:126, b is an integer of 15 to 837, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:126, and where b is greater than or equal to a + 14.	
792539	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1203 of SEQ ID NO:127, b is an integer of 15 to 1217, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:127, and where b is greater than or equal to a + 14.	H53623, H53662, N23079, N69293, N89689, AA034518, AA035409, AA035410, AA046490, AA046762, AA085037, AA085105, AA134976, AA135078, AA459951, AA460040
792749	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1335 of SEQ ID NO:128, b is an integer of 15 to 1349, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:128, and where b is greater than or equal to a + 14.	R13058, R13951, R40011, R51765, R51766, R40011, R67629, R67630, H01808, H29310, H29403, R99196, H52742, H52788, H61636, H71767, H71768, N20919, N27779, N36030, N41741, N47900, N55480, N76967, W21551, W44410, W44331, W46458, W46528, W46810, W46928, W51766,

		W57869, W58140, W86456, N90422, AA029174, AA029253, AA031374, AA031375, AA062913, AA082549, AA133965, AA167773, AA166872, AA176295, AA176395, AA428235
792961	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2304 of SEQ ID NO:129, b is an integer of 15 to 2318, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:129, and where b is greater than or equal to a + 14.	
793206	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2135 of SEQ ID NO:130, b is an integer of 15 to 2149, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:130, and where b is greater than or equal to a + 14.	
793249	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1006 of SEQ ID NO:131, b is an integer of 15 to 1020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:131, and where b is greater than or equal to a + 14.	T48358, T48359, T71001, T71063, T72193, T72972, T67531, T69528, T86709, T86804, T89854, T90890, T91159, T85694, T85895, T95466, T95467, R00007, R00008, R12353, R23932, R23933, R37279, R63973, R64080, R73825, R73826, R76905, R77073, R77445, R77538, R79797, R79808, R79894, R79908, H11925, H11926, H15192, H16754, H16862, H19737, H20072, H21725, H22675, H24523, H26125, H26391, H39766, H41271, H41373, H41374, H43544, H43545, H44881, H45180, H45181, R92671, R94833, H57801, H58122, H58123, H62248, H62337, H69587, H69586, H80840, H80930, H85462, H85747, H86829, H86902, H96591, H96708, H97829, H99614, N25266, N26147, N27161, N29792, N33452, N33767, N33906, N36535, N38816, N39177, N40101, N42935, N42425, N44530, N45252, N45445, N57801, N59012, N78685, N79046, N91819, N98480, W02726, W04566, W15191, W15596, W17335, W24253, W25723, W30937, W31253, W31429, W31674, W39685, W44989, W46619, W46654, W57768, W57804, W57841, W57622, W67135, W67136, W73878, W73364, W73441, W77815, W80810, W80903, W92682, W92512, W92513, W96375, W96526, AA001447, AA001482, AA021374, AA021375, AA037268, AA037489, AA037569, AA039708, AA040262, AA040417, AA057011,

		AA074646, AA074679, AA075303, AA088467, AA098947, AA100987, AA126026, AA126122, AA126778, AA128010, AA128034, AA136619, AA136750, AA143234, AA143291, AA143564, AA143565, AA146915, AA151446, AA151447, AA156218, AA157383, AA159151, AA173294, AA179768, AA180442, AA181155, AA181156, AA181722, AA186611, AA188254, AA190686, AA191758, AA191547, AA195441, AA223540, AA223587
793626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2305 of SEQ ID NO:132, b is an integer of 15 to 2319, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:132, and where b is greater than or equal to a + 14.	
794417	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1359 of SEQ ID NO:133, b is an integer of 15 to 1373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:133, and where b is greater than or equal to a + 14.	
795197	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1643 of SEQ ID NO:134, b is an integer of 15 to 1657, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:134, and where b is greater than or equal to a + 14.	
795251	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2346 of SEQ ID NO:135, b is an integer of 15 to 2360, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:135, and where b is greater than or equal to a + 14.	T89826, T74514, T89080, R24028, H03686, H97493, N54611, W94797, W94798, AA129537, AA190765, AA191357, AA256363, AA425151, AA429405
795752	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1028 of SEQ ID NO:136, b is an integer of 15 to 1042, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:136, and where b is greater than or equal to a + 14.	
796261	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1023 of SEQ ID	

	NO:137. b is an integer of 15 to 1037, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:137, and where b is greater than or equal to $a + 14$.	
796933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1476 of SEQ ID NO:138. b is an integer of 15 to 1490, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:138, and where b is greater than or equal to $a + 14$.	
799424	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1670 of SEQ ID NO:139. b is an integer of 15 to 1684, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:139, and where b is greater than or equal to $a + 14$.	
799698	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 413 of SEQ ID NO:140. b is an integer of 15 to 427, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:140, and where b is greater than or equal to $a + 14$.	
800351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 875 of SEQ ID NO:141. b is an integer of 15 to 889, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:141, and where b is greater than or equal to $a + 14$.	
800573	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1491 of SEQ ID NO:142. b is an integer of 15 to 1505, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:142, and where b is greater than or equal to $a + 14$.	
805815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1221 of SEQ ID NO:143. b is an integer of 15 to 1235, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:143, and where b is greater than or equal to $a + 14$.	
806445	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1406 of SEQ ID NO:144. b is an integer of 15 to 1420, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:144, and where b is greater than or equal to $a + 14$.	
810309	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1905 of SEQ ID NO:145, b is an integer of 15 to 1919, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:145, and where b is greater than or equal to $a + 14$.	
811022	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1365 of SEQ ID NO:146, b is an integer of 15 to 1379, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:146, and where b is greater than or equal to $a + 14$.	
811023	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 500 of SEQ ID NO:147, b is an integer of 15 to 514, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:147, and where b is greater than or equal to $a + 14$.	
811143	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2044 of SEQ ID NO:148, b is an integer of 15 to 2058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:148, and where b is greater than or equal to $a + 14$.	
811381	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1767 of SEQ ID NO:149, b is an integer of 15 to 1781, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:149, and where b is greater than or equal to $a + 14$.	
811595	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1695 of SEQ ID NO:150, b is an integer of 15 to 1709, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:150, and where b is greater than or equal to $a + 14$.	T51013, T51104, T54094, T54185, T68577, T68655, T90261, T90702, T92691, R34639, R49168, R51392, R49168, R84952, R84994, H84723, H84890, N29820, N42512, N64677, N67206, N73458, N80110, N92710, W02861, W20327, W23680, W76675, AA031294, AA062736, AA062781, AA070243, AA070244, AA084464, AA100714, AA100767, AA136726, AA136684, AA191613, AA223541, AA223589, AA252636
813000	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 908 of SEQ ID NO:151, b is an integer of 15 to 922, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:151, and where b is greater than or equal to a + 14.	
813288	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 621 of SEQ ID NO:152, b is an integer of 15 to 635, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:152, and where b is greater than or equal to a + 14.	
813431	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2314 of SEQ ID NO:153, b is an integer of 15 to 2328, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:153, and where b is greater than or equal to a + 14.	T94237, T89464, T89552, R09285, T78198, R14453, R15241, R15311, R21130, R33140, R33292, R40972, R46726, R42211, R40972, R46726, R66207, R67085, R73679, R73770, H12485, H19135, H22930, H24111, H26774, H26884, R89854, R89894, R92012, R92057, H53798, H61991, H61992, H64854, H65452, H73213, H74063, H79753, H79754, H80620, H80654, H81209, H81210, H84019, H84020, N35581, N68664, N73792, N91681, N92730, N99417, W20349, W46901, W52684, W60422, W61136, W61108, W61174, W68119, W73989, W79021, W79231, W80414, W80777, W80930, AA040315, AA045023, AA045024, AA045188, AA045352, AA181735, AA181799, AA223229, AA223428, AA464186, AA464780, AA428152, AA430305
813450	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1254 of SEQ ID NO:154, b is an integer of 15 to 1268, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:154, and where b is greater than or equal to a + 14.	T90954, T84401, T85262, R22109, R48652, R72000, R73453, H14261, H27403, H42017, H42018, H38149, H38150, H69302, H69397, N98775, AA148803, AA150212
813478	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4285 of SEQ ID NO:155, b is an integer of 15 to 4299, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:155, and where b is greater than or equal to a + 14.	
813505	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 992 of SEQ ID NO:156, b is an integer of 15 to 1006, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:156, and where b is greater than or equal to a + 14.	
815552	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1672 of SEQ ID NO:157, b is an integer of 15 to 1686, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:157, and where b is greater than or equal to a + 14.	
815606	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4133 of SEQ ID NO:158, b is an integer of 15 to 4147, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:158, and where b is greater than or equal to a + 14.	T69152, T69213, T80080, T80327, R19043, R27520, R38534, R38898, R44031, R44031, R67769, H11493, H11852, H13644, H22161, H28042, H39529, H42500, H43488, N32678, N50022, N51861, N54126, N54677, W16972, W32896, W35293, W38598, N89624, N90277, AA027830, AA027892, AA035739, AA055806, AA069223, AA078890, AA078891, AA099437, AA099478, AA101431, AA112543, AA121794, AA129629, AA136251, AA143110, AA150576, AA157125, AA158242, AA158709, AA159976, AA160357, AA159491, AA160534, AA160629, AA165150, AA165151, AA164643, AA166799, AA169647, AA169822, AA173082, AA187009, AA224150, AA224303, AA224514, AA224513, AA224488, AA226779, AA227396, AA227518, AA232104, AA232580, AA256938, AA255494, AA429442
816048	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1228 of SEQ ID NO:159, b is an integer of 15 to 1242, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:159, and where b is greater than or equal to a + 14.	T54940, T59322, R35627, R46514, R48419, R48536, R48537, R48569, R48582, R48668, R48683, R49781, R49827, R53111, R53210, R66870, R67958, R69435, R69517, R70414, R71907, R71948, R72113, R72818, R73269, R75924, R75959, R79565, R79566, R80393, H25645, H26211, H29817, H29904, H39626, H39738, H39881, H40715, H42210, H42281, H42354, H42710, H43124, R83615, R86066, R92103, R92104, R96726, R96727, H54075, H54232, H54233, H62253, H62342, H80441, H80442, H91114, H97541, H99927, N27357, N27665, N93636, W19226, W19703, W25418, W25514, W44404, W63554, W78078, N89960, AA027093, AA027132, AA045021, AA045022, AA045721, AA045720, AA046247, AA046280, AA058624, AA074786, AA074787, AA082394, AA085101, AA085282, AA100996, AA127562, AA127729, AA127784, AA128372,

		AA134954, AA143611, AA148145, AA150570, AA161257, AA182028, AA188387, AA232423, AA464270, AA464381, AA421219, AA425804, AA428372
822978	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2215 of SEQ ID NO:160, b is an integer of 15 to 2229, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:160, and where b is greater than or equal to a + 14.	R28400, R82355, R82411, H01338, H01388, N24952, N33829, AA043471, AA043472, AA125807, AA128280, AA129405, AA133871, AA129367, AA133179, AA133312, AA131385, AA428408
823616	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1906 of SEQ ID NO:161, b is an integer of 15 to 1920, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:161, and where b is greater than or equal to a + 14.	
823981	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2605 of SEQ ID NO:162, b is an integer of 15 to 2619, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:162, and where b is greater than or equal to a + 14.	
824364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1405 of SEQ ID NO:163, b is an integer of 15 to 1419, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:163, and where b is greater than or equal to a + 14.	R21933, H39733, N69879, AA027031, AA100964, AA157234, AA173338
824423	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3796 of SEQ ID NO:164, b is an integer of 15 to 3810, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:164, and where b is greater than or equal to a + 14.	
825279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 803 of SEQ ID NO:165, b is an integer of 15 to 817, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:165, and where b is greater than or equal to a + 14.	R06729, R61520, R86829, H51131, N57993, W93696, AA423827
825442	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1564 of SEQ ID	

	NO:166, b is an integer of 15 to 1578, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:166, and where b is greater than or equal to a + 14.	
825548	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:167, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:167, and where b is greater than or equal to a + 14.	
825725	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1622 of SEQ ID NO:168, b is an integer of 15 to 1636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:168, and where b is greater than or equal to a + 14.	
826639	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 653 of SEQ ID NO:169, b is an integer of 15 to 667, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:169, and where b is greater than or equal to a + 14.	
827079	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3584 of SEQ ID NO:170, b is an integer of 15 to 3598, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:170, and where b is greater than or equal to a + 14.	
827153	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 926 of SEQ ID NO:171, b is an integer of 15 to 940, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:171, and where b is greater than or equal to a + 14.	
827351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1444 of SEQ ID NO:172, b is an integer of 15 to 1458, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:172, and where b is greater than or equal to a + 14.	R14710, H92769, H92882, AA195498, AA242878, AA242884, AA252152, AA251967, AA465181, AA465542, AA481105, AA481210, AA492206, AA732326
827503	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2695 of SEQ ID NO:173, b is an integer of 15 to 2709, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:173, and where b is greater than or equal to $a + 14$.	
827563	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 999 of SEQ ID NO:174, b is an integer of 15 to 1013, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:174, and where b is greater than or equal to $a + 14$.	
827565	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1683 of SEQ ID NO:175, b is an integer of 15 to 1697, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:175, and where b is greater than or equal to $a + 14$.	
827893	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1395 of SEQ ID NO:176, b is an integer of 15 to 1409, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:176, and where b is greater than or equal to $a + 14$.	
828072	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1489 of SEQ ID NO:177, b is an integer of 15 to 1503, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:177, and where b is greater than or equal to $a + 14$.	R20502, R45322, R45322, H29062, H29165, N36388, N39601, AA043930, AA044003, AA115568, AA115087, AA232982, AA234020, AA251431, AA251432, AA459761, AA768137, AA830696, AA918618, AA977409
828228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1364 of SEQ ID NO:178, b is an integer of 15 to 1378, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:178, and where b is greater than or equal to $a + 14$.	T76992, T83862, R37649, R68086, R68125, H05325, H05379, H11520, H60866, N27826, N59149, N71661, AA004459, AA004512, AA026983, AA031653, AA045803, AA045870, AA127220, AA126199, AA129772, AA133788, AA131742, AA166788, AA216416, AA229513, AA469120, AA469189, AA503687, AA516488, AA522741, AA542827, AA614664, AA847108, AA876618, AA886579, AA887825, AA888263, AA888262, AA934459, N31217, D79619, N55800, AA026982, AA031743
828241	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2237 of SEQ ID NO:179, b is an integer of 15 to 2251, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:179, and where b is greater than or equal to $a + 14$.	R09047, H71262, N28995, W07805, W89157, AA007537, AA203119

828287	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 986 of SEQ ID NO:180, b is an integer of 15 to 1000, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:180, and where b is greater than or equal to a + 14.</p>	R00158, R34699, R34806, R55812, R55897, H02931, H04234, H38596, H38841, H38877, R84345, R84762, R85507, H51401, N22910, N31298, N36027, N64463, N70710, N80820, N94519, N99846, W15234, W15579, W15620, W23968, W24669, W30920, W31655, W37399, W37400, W39182, W45512, W44342, W45653, W44569, W44608, W47630, W47631, W52183, W52421, W57603, W58189, W58466, W60614, W73715, W78044, W90451, W90258, W92042, W91902, AA012954, AA013060, AA013459, AA013460, AA018132, AA018050, AA021226, AA021359, AA021556, AA021640, AA033802, AA040580, AA040552, AA047883, AA054092, AA055181, AA055893, AA082252, AA082502, AA099128, AA099165, AA100988, AA131285, AA136296, AA136178, AA151469, AA151470, AA156144, AA158033, AA158325, AA164422, AA164402, AA167105, AA182609, AA182541, AA187289, AA187406, AA523678, AA582094, AA570257, AA573999, AA574305, AA579097, AA661683, AA662869, AA664665, AA736798, AA770689, AA865267, AA902336, AA923648, AA933570, AA939196, AA988468, A1000226, A1089764, D79059, N84733, W73650, N86290, N88454, C04677, C06015, AA033803, R29541, AA089664, AA089996, C17096, C17255, C19033, AA093458
828364	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1415 of SEQ ID NO:181, b is an integer of 15 to 1429, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:181, and where b is greater than or equal to a + 14.</p>	R55711, R55921, R68105, R68149, R72479, R72941, N70480, W72759
828371	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2711 of SEQ ID NO:182, b is an integer of 15 to 2725, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:182, and where b is greater than or equal to a + 14.</p>	T62048, T62112, T91683, T92364, T92416, T93284, N49690, N49793, N64329, N80813, W15549, W15404, W31643, W53039, W92220, W92342, AA055521, AA055520, AA149883, AA150063, AA148836, AA150436
828403	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1737 of SEQ ID NO:183, b is an integer of 15 to 1751, where both a</p>	AA485171, AA515218, AA603721, AA612760, AA838541, AA970526, C18512

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:183, and where b is greater than or equal to $a + 14$.	
828501	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2186 of SEQ ID NO:184, b is an integer of 15 to 2200, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:184, and where b is greater than or equal to $a + 14$.	H19145, N75547, AA044653, AA128979, AA159576, AA423963, AA523306, H62675, H97872, AA610503, AA010941, AA011327, AA043344
828520	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1973 of SEQ ID NO:185, b is an integer of 15 to 1987, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:185, and where b is greater than or equal to $a + 14$.	H70392, N30525, N30537, AA010769, AA463668, AA927343, AA091744
828527	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1723 of SEQ ID NO:186, b is an integer of 15 to 1737, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:186, and where b is greater than or equal to $a + 14$.	T39306, T40514, R08857, R08964, R00734, R00735, R13824, R20172, R37684, R44959, R44959, H05503, H17017, H17018, H54295, H54372, H54503, H67654, H67974, H87993, N33311, N37017, N44843, N55182, N75469, N75534, N77241, N93004, W05278, W05327, W45465, W88760, W88865, AA010623, AA010624, AA234956, AA235130, AA424457, AA282705, AA283023, AA283109, AA481529, AA481595, AA490727, AA491218, AA554176, AA614573, AA665370, AA687964, AA736921, AA765107, AA767430, AA809487, AA865595, N88052
828538	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1118 of SEQ ID NO:187, b is an integer of 15 to 1132, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:187, and where b is greater than or equal to $a + 14$.	
828541	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:188, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:188, and where b is greater than or equal to $a + 14$.	
828549	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3773 of SEQ ID NO:189, b is an integer of 15 to 3787, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:189, and where b is greater than or equal to a + 14.	
828562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 540 of SEQ ID NO:190, b is an integer of 15 to 554, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:190, and where b is greater than or equal to a + 14.	
828576	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 860 of SEQ ID NO:191, b is an integer of 15 to 874, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:191, and where b is greater than or equal to a + 14.	
828602	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2089 of SEQ ID NO:192, b is an integer of 15 to 2103, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:192, and where b is greater than or equal to a + 14.	
828628	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1303 of SEQ ID NO:193, b is an integer of 15 to 1317, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:193, and where b is greater than or equal to a + 14.	
828667	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1238 of SEQ ID NO:194, b is an integer of 15 to 1252, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:194, and where b is greater than or equal to a + 14.	
828684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1674 of SEQ ID NO:195, b is an integer of 15 to 1688, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:195, and where b is greater than or equal to a + 14.	R11676, R12284, N68621, N71575, N99448, W02008, W58632, W74361, W76341, W78934, W85701, AA070898, AA070787, AA102636, AA102661, AA102678, AA190864, AA190957, AA197279, AA251577, AA464994, AA421724, AA470741, AA505341, AA506137, AA583780, AA579967, AA714136, AA743352, AA747903, AA814422, AA826755, AA836633, AA837944, AA936844, A1004160, C00265, AA641021
828727	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R35925, R35954, R49443, R49468, R49443, R49468, N74960, AA083678, AA086366, AA100585, AA111863,

	where a is any integer between 1 to 742 of SEQ ID NO:196. b is an integer of 15 to 756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:196, and where b is greater than or equal to a + 14.	AA156573, AA159175, AA192611, AA195925, AA195976, AA418567, AA418582
828734	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1457 of SEQ ID NO:197. b is an integer of 15 to 1471, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:197, and where b is greater than or equal to a + 14.	
828750	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 678 of SEQ ID NO:198. b is an integer of 15 to 692, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:198, and where b is greater than or equal to a + 14.	
828842	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1559 of SEQ ID NO:199. b is an integer of 15 to 1573, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:199, and where b is greater than or equal to a + 14.	R31695, R31737, R86919, R86763, H66952, N30849, N41376, N95538, W03782, W24227, N90171, AA020001, AA046039, AA046149, AA099753, AA489705, AA552582, AA580818, AA584291, AA730113, AA910268
828843	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2728 of SEQ ID NO:200. b is an integer of 15 to 2742, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:200, and where b is greater than or equal to a + 14.	T57326, T57387, T94838, T94837, T94879, T94925, T74456, R11995, R15234, R19543, R21728, R36670, R39752, R39834, R40808, R40808, R43895, R70936, R70988, R74057, R74152, R79967, R80062, H02983, H04277, H08966, H09537, H25298, H25343, H25449, H25495, H29439, H29438, H29887, H29987, R86318, H65676, H87966, H88350, H97859, N20316, N26629, N27590, N39724, N52972, W39188, W45099, W45149, N90248, AA004834, AA033776, AA039900, AA039901, AA041524, AA044928, AA082729, AA085742, AA112974, AA128343, AA133157, AA171997, AA418609, AA418664, AA421626, AA430065, AA230107, AA230108, AA513630, AA521134, AA622056, AA635868, AA639882, AA714929, AA715480, AA715556, AA729814, AA731061, AA811597, AA830222, AA873240, AA886078, AA886270, AA907208, AA932201, AA977447, AA989000, D81476, N56281, C21262, AA089709
828851	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1403 of SEQ ID NO:201, b is an integer of 15 to 1417, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:201, and where b is greater than or equal to a + 14.	
828856	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1498 of SEQ ID NO:202, b is an integer of 15 to 1512, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:202, and where b is greater than or equal to a + 14.	
828862	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 405 of SEQ ID NO:203, b is an integer of 15 to 419, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:203, and where b is greater than or equal to a + 14.	AA021223
828870	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2819 of SEQ ID NO:204, b is an integer of 15 to 2833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:204, and where b is greater than or equal to a + 14.	
828873	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 5816 of SEQ ID NO:205, b is an integer of 15 to 5830, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:205, and where b is greater than or equal to a + 14.	
828892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 741 of SEQ ID NO:206, b is an integer of 15 to 755, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:206, and where b is greater than or equal to a + 14.	R54649, W46198
828893	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1982 of SEQ ID NO:207, b is an integer of 15 to 1996, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:207, and where b is greater than or equal to a + 14.	
828897	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1654 of SEQ ID NO:208, b is an integer of 15 to 1668, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:208, and where b is greater than or equal to a + 14.	
828910	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2236 of SEQ ID NO:209, b is an integer of 15 to 2250, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:209, and where b is greater than or equal to a + 14.	T91595, T65436, T65518, T70584, T70847, T75377, R09159, R09261, R09950, T96365, T96446, R12590, R13068, R18120, R21193, R22430, R22480, R22810, R25025, R26742, R26976, R32026, R32079, R33017, R33904, R36588, R39200, R40499, R45972, R40499, R45972, R56330, R64494, R65591, R67446, R70974, R74477, R74579, R77932, R78301, R78497, R78547, R80142, R80143, H00643, H00729, H03024, H04306, H06614, H07124, H09643, H09677, H28706, H28835, H42802, H47310, R92010, H65658, H65657, H67068, H68151, H71685, H72248, H72786, H72785, H73342, H75583, H75514, H77433, H98557, N20087, N22979, N23822, N28617, N29593, N32509, N33262, N40705, N42724, N44752, N45195, N57760, N58105, N59101, N59726, N64423, N66868, N71993, N73995, N99375, W01801, W02025, W19280, W19667, W19930, W25451, W25645, W31475, W31938, W32153, W32005, W37711, W37710, W46758, W46905, W49818, W56089, W57771, W57844, W61375, W61376, W60415, W60416, W61142, W61190, W67942, W67941, W74649, W84332, W84393, W86146, W94323, AA016041, AA015933, AA022593, AA022594, AA030003, AA043309, AA069392, AA069393, AA069775, AA069812, AA102392, AA112674, AA112673, AA135337, AA135336, AA143448, AA152405, AA152459, AA149804, AA149829, AA149849, AA149856, AA156559, AA157731, AA159045, AA160734, AA173662, AA173661, AA235812, AA242974, AA243081, AA242998, AA252146, AA460003, AA460542, AA428205, AA429142, AA285041, AA283758, AA283993, AA480305, AA506566, AA524852, AA631324, AA575859, AA658502, AA766717, AA808234, AA837876, AA866075, AA877425, AA879058, AA886608, AA902179, AA904000, AA928667, AA937136, AA962263, AA995987, A1024986, W25995, W26229, W27231, W26246, W28106,

		W28807, W48809, C01974, AA640952, C14885, C15137
828927	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 824 of SEQ ID NO:210, b is an integer of 15 to 838, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:210, and where b is greater than or equal to a + 14.	
828932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1199 of SEQ ID NO:211, b is an integer of 15 to 1213, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:211, and where b is greater than or equal to a + 14.	T50679, T51209, T78077, R42605, R48768, R42605, R91277, H61157, W38635, W44738, W46899, W80700, AA017684, AA017707, AA018069, AA019662, AA040254, AA053989, AA054041, AA070137, AA070138, AA074661, AA086354, AA158859, AA223111, AA224210, AA224315, AA232155, AA471047, AA588037, AA720832, AA872503
828933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 955 of SEQ ID NO:212, b is an integer of 15 to 969, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:212, and where b is greater than or equal to a + 14.	
828941	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:213, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:213, and where b is greater than or equal to a + 14.	
828957	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1196 of SEQ ID NO:214, b is an integer of 15 to 1210, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:214, and where b is greater than or equal to a + 14.	R09987, R16645, R16734, R81727, H58067, H58066, H59815, H59816, H64860, H65458, N70923, W81647, W81187, AA052891, AA053046, AA251319, AA251723, AA262259, AA262870, AA463359, AA463865, AA417918, AA418169, AA480203, AA521273, AA836429, AA858135, AA888105, AA917914, AA937591, AA947712, AA961752, AA973797, AI085881
828963	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1762 of SEQ ID NO:215, b is an integer of 15 to 1776, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:215, and where b is greater than or equal to a + 14.	
828964	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1404 of SEQ ID NO:216, b is an integer of 15 to 1418, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:216, and where b is greater than or equal to a + 14.	
828966	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2186 of SEQ ID NO:217, b is an integer of 15 to 2200, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:217, and where b is greater than or equal to a + 14.	T57322, T57383, R07432, R07433, R24183, R37889, R64196, R64212, H10798, H16281, H96182, N24864, N31801, N31897, N51466, N53607, N71323, N71374, N71696, N78973, N91801, N99595, N99806, W17338, W38617, W44695, W52815, W93325, W95029, AA027074, AA031625, AA031706, AA034522, AA101476, AA101477, AA156927, AA157179, AA173234, AA196758, AA506558, AA541561, AA552220, AA573198, AA687807, AA732065, AA769029, AA804914, AA858375, AA931935, AA995830, AI075078, AI075079, AA641307
828967	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1839 of SEQ ID NO:218, b is an integer of 15 to 1853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:218, and where b is greater than or equal to a + 14.	T86194, T99270, R00981, R21065, R28076, R28291, R46245, R46245, R61751, R61752, H20415, H41325, H46347, H46354, W01107, W96450, W96548, AA082920, AA192528, AA494252, AA507548, AA604189, AA604361, AA614008, AA622126, AA573865, AA578191, AA568157, AA780392, AA812241, AA830010, AA836096, AA876742, C21216
828977	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1079 of SEQ ID NO:219, b is an integer of 15 to 1093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:219, and where b is greater than or equal to a + 14.	T54853, T55018, T61617, T61701, T71718, T71787, R43855, R43855, H79047, W23509, W78022, AA028959, AA028960, AA035641, AA035749, AA040562, AA042827, AA044641, AA150059, AA459301, AA459532, AA419054, AA532924, AA603462, AA573839, AA863332, AA877269, AI016670, AI083871, AI085531
828978	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2141 of SEQ ID NO:220, b is an integer of 15 to 2155, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:220, and where b is greater than or equal to a + 14.	
828979	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1250 of SEQ ID NO:221, b is an integer of 15 to 1264, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:221, and where b is greater than or equal to a + 14.	

829001	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2071 of SEQ ID NO:222, b is an integer of 15 to 2085, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:222, and where b is greater than or equal to a + 14.	
829003	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2907 of SEQ ID NO:223, b is an integer of 15 to 2921, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:223, and where b is greater than or equal to a + 14.	T56900, T56901, T57894, T57976, T58709, T83854, T83994, T83995, T85283, T85493, T85938, T98545, T98546, R23866, R51491, R51492, R70815, H06524, H06579, H21400, H22212, H26306, H26465, H40800, H42803, H44004, H45104, H45577, R84544, R85933, R95902, R98186, R98187, R99129, H51499, H62734, H62818, H67266, H67280, H67971, H72027, H72028, H86532, H86617, H97834, N22060, N22322, N22927, N23444, N23843, N27358, N27627, N31797, N53099, N55505, N55527, N62760, N76278, N76994, N81072, N99969, W07363, W15385, W30908, W32209, W32266, W37612, W39341, W45721, W44369, W60688, W60728, W74331, W79764, W79508, AA010902, AA011007, AA013382, AA013383, AA017180, AA018376, AA021435, AA128552, AA128295, AA161229, AA160487, AA236095, AA259037, AA458538, AA428449, AA491943, AA492101, AA501898, AA505736, AA551906, AA552335, AA554636, AA564579, AA588897, AA593936, AA595710, AA610733, AA612690, AA569349, AA570259, AA570263, AA573856, AA579746, AA658849, AA721609, AA743280, AA743326, AA808972, AA831035, AA836900, AA887420, AA887859, AA970292, AA994943, AA994947, AI014465, F19724, N36447, D78889, N75198, W37467, W79607, C03008, C04753
829016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4381 of SEQ ID NO:224, b is an integer of 15 to 4395, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:224, and where b is greater than or equal to a + 14.	
829027	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3021 of SEQ ID	

	NO:225, b is an integer of 15 to 3035, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:225, and where b is greater than or equal to a + 14.	
829028	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1497 of SEQ ID NO:226, b is an integer of 15 to 1511, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:226, and where b is greater than or equal to a + 14.	
829031	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2225 of SEQ ID NO:227, b is an integer of 15 to 2239, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:227, and where b is greater than or equal to a + 14.	T52373, T52446, T65540, T91789, R10959, T84998, R06717, R28502, R48288, R48390, R48442, R54616, R54879, R55311, R55316, R55413, R55418, R72602, R72669, R72946, H15595, H27333, H41543, H37781, R84976, R85050, R88513, R88514, H49052, H49116, H96219, H96754, H97979, N23664, N25056, N26150, N32997, N51857, N54122, W65281, W65277, W72409, W76488, W92510, N91031, AA045475, AA056943, AA057662, AA057806, AA126670, AA127032, AA136891, AA137001, AA158595, AA158989, AA279342, AA604130, AA604929, AA631863, C01812
829034	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2332 of SEQ ID NO:228, b is an integer of 15 to 2346, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:228, and where b is greater than or equal to a + 14.	
829036	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2232 of SEQ ID NO:229, b is an integer of 15 to 2246, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:229, and where b is greater than or equal to a + 14.	W19899, W56172, N91246, AA053015, AA258943, AA508101, AA557537, AA744258, C06034, AA053503
829049	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1988 of SEQ ID NO:230, b is an integer of 15 to 2002, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:230, and where b is greater than or equal to a + 14.	
829073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 980 of SEQ ID	N71827, W07562, W79070, W94296, AA026190, AA215725, AA279902, AA832099

	NO:231, b is an integer of 15 to 994, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:231, and where b is greater than or equal to a + 14.	
829075	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 472 of SEQ ID NO:232, b is an integer of 15 to 486, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:232, and where b is greater than or equal to a + 14.	
829076	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2067 of SEQ ID NO:233, b is an integer of 15 to 2081, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:233, and where b is greater than or equal to a + 14.	
829080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 502 of SEQ ID NO:234, b is an integer of 15 to 516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:234, and where b is greater than or equal to a + 14.	
829087	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1115 of SEQ ID NO:235, b is an integer of 15 to 1129, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:235, and where b is greater than or equal to a + 14.	
829092	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1031 of SEQ ID NO:236, b is an integer of 15 to 1045, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:236, and where b is greater than or equal to a + 14.	
829095	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 676 of SEQ ID NO:237, b is an integer of 15 to 690, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:237, and where b is greater than or equal to a + 14.	T98739, T98740, R53404, R72484, H09731, H16600, H21795, H25680, N79773, N93472, AA812105, AA826523, AA954170, AJ084914
829096	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1859 of SEQ ID NO:238, b is an integer of 15 to 1873, where both a	T40001, T40939, R53257, R62981, R62980, R63036, H15127, H15187, H24078, H24188, H81472, H88927, H88927, H99390, N32032, N47835, N66666, N98950, AA022842,

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:238, and where b is greater than or equal to a + 14.	AA022965, AA024917, AA024918, AA035721, AA062907, AA102646, AA101299, AA223395, AA419511, AA421963, AA421964, AA524699, AA532380, AA614315, AA570194, AA742712, AA865440, AA887301, AA987486, AA988144, AA091175
829118	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 891 of SEQ ID NO:239, b is an integer of 15 to 905, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:239, and where b is greater than or equal to a + 14.	
829152	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1470 of SEQ ID NO:240, b is an integer of 15 to 1484, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:240, and where b is greater than or equal to a + 14.	T72498, T73568, T74363, T86984, R10378, R10477, T85969, R05924, R06022, H58205, H65999, H66000, N68870, N92084, N92944, AA188651, AA188754, N72345
829160	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1507 of SEQ ID NO:241, b is an integer of 15 to 1521, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:241, and where b is greater than or equal to a + 14.	R19077, R24890, R70937, R70989, R75822, R75823, H13581, R88030, H97197, H97205, H97610, H97622, H97640, H99011, N22163, N22211, N25706, N31618, N31627, N34096, N35586, N57066, N57078, N57083, N63961, N71248, N71530, N79638, W23686, W25345, W80523, W80524, AA027117, AA044025, AA044347, AA056543, AA056646, AA082122, AA120870, AA120871, AA129173, AA129197, AA173547, AA173713, AA190689, AA252595, AA258865, AA259007, AA576323, AA768606, N55993, N84224
829163	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1130 of SEQ ID NO:242, b is an integer of 15 to 1144, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:242, and where b is greater than or equal to a + 14.	R27150, H50951, N39917, N41848, N41877
829176	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 920 of SEQ ID NO:243, b is an integer of 15 to 934, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:243, and where b is greater than or equal to a + 14.	T46875, T53785, T62036, T73807, R11065, R11122, T84299, T85183, R01714, R02656, R02737, R02738, H41134, H64904, H79712, H79713, N68598, N71315, N71366, N99798, W01984
829204	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R50489, R50573, R74498, R74499, AA234014, AA535362, AA554207, AA847239

	where a is any integer between 1 to 901 of SEQ ID NO:244, b is an integer of 15 to 915, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:244, and where b is greater than or equal to a + 14.	
829207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1262 of SEQ ID NO:245, b is an integer of 15 to 1276, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:245, and where b is greater than or equal to a + 14.	
829228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3352 of SEQ ID NO:246, b is an integer of 15 to 3366, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:246, and where b is greater than or equal to a + 14.	T40764, T49773, T49774, H05098, H49148, H51985, H52105, N36154, N51490, N52526, N53635, AA054314, AA074167, AA152473, AA152472, AA188950, AA278366, AA281330, AA468930, AA469004, AA482010, AA542938, AA554491, AA565215, AA579406, AA741363, AA807139, AA832066, AA836995, AA876036, AA995854
829252	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2134 of SEQ ID NO:247, b is an integer of 15 to 2148, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:247, and where b is greater than or equal to a + 14.	
829254	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2211 of SEQ ID NO:248, b is an integer of 15 to 2225, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:248, and where b is greater than or equal to a + 14.	
829269	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1190 of SEQ ID NO:249, b is an integer of 15 to 1204, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:249, and where b is greater than or equal to a + 14.	
829277	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1300 of SEQ ID NO:250, b is an integer of 15 to 1314, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:250, and where b is greater than or equal to a + 14.	
829290	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1145 of SEQ ID NO:251, b is an integer of 15 to 1159, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:251, and where b is greater than or equal to a + 14.	
829294	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2474 of SEQ ID NO:252, b is an integer of 15 to 2488, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:252, and where b is greater than or equal to a + 14.	
829299	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1540 of SEQ ID NO:253, b is an integer of 15 to 1554, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:253, and where b is greater than or equal to a + 14.	T82894, H25618, N48726, W52191, AA037331, AA223798, AA224330, AA635842, AA748884, AA826495, AA864458, AA903250, AA908466, AA931986, D81481, N56293, C02225
829308	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1492 of SEQ ID NO:254, b is an integer of 15 to 1506, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:254, and where b is greater than or equal to a + 14.	R13979, R17378, R40039, R42616, R42616, R40039, R56257, R56346, H05467, H07018, R86778, H99527, H99526, H99763, N24571, N25539, N25635, N28490, N30121, N34013, N34136, N34233, N35730, N49189, N50244, N92737, W20356, AA255602, AA262707, AA255576, AA262183, AA279758, AA570002, AA572777, AA721016, AA814424, AA864521, AA902860, AA948310, AI024777, AI056401
829349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 640 of SEQ ID NO:255, b is an integer of 15 to 654, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:255, and where b is greater than or equal to a + 14.	T39288, T47082, T50451, T50586, T59000, T59073, T59535, T59586, T63704, T63861, T69920, T69974, T71240, T72474, T72943, T90268, T90710, T83786, T95048, R31368, R33435, R34369, R34489, R73911, R80467, R80667, R94351, R97310, R97345, H57329, H57376, H62783, H64845, H65444, H82981, H83214, H93955, H93956, N29780, N42940, N45379, N57200, N80805, W06876, W15396, W47162, W47283, W52164, W52024, W52758, W73045, W73275, W73604, W73643, W86783, W87274, AA009954, AA010849, AA011288, AA022621, AA022757, AA025805, AA025929, AA025968, AA046835, AA054475, AA058513, AA063327, AA075215, AA075451, AA088739, AA088740, AA099371, AA099457, AA112397, AA113053, AA121065, AA121066, AA132025, AA132147, AA132237, AA132357, AA146935,

		AA147721, AA147756, AA147602, AA148113, AA156063, AA157120, AA157223, AA157610, AA165107, AA164710, AA173741, AA173185, AA187331, AA187332, AA187293, AA187393, AA187741, AA188097, AA187033, AA188455, AA188457, AA188467, AA216356, AA228668, AA229001, AA228993, AA229108, AA397406, AA482922, AA483319, AA483431, AA491567, AA501502, AA507889, AA508445, AA513947, AA515053, AA522563, AA523140, AA525478, AA524922, AA526106, AA534088, AA535846, AA548219, AA552477, AA555012, AA558315, AA564882, AA565458, F16817, F16991, F17527, AA582793, AA587225, AA588487, AA595626, AA602055, AA602240, AA603392, AA631634, AA638971, AA639988, AA640535, AA576051, AA576894, AA566049, AA655021, AA659001, AA661609, AA662354, AA664631, AA664721, AA664980, AA665338, AA688035, AA714993, AA715012, AA720861, AA730373, AA730633, AA742678, AA742934, AA746812, AA747153, AA747192, AA747959, AA808437, AA836880, AA837645, AA838637, AA872341, AA876822, AA922665, AA961515, AA968734, AA970649, AA978219, AA988051, AA988404, AA991418, AA994111, A1002489, A1053409, A1053609, A1053760, A1082351, A1083631, N83854, N83948, N85971, N86260, N86628, N87758, AA641679, AA642097, AA642839, C20758, AA092159, AA092465, AA094493
829354	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1978 of SEQ ID NO:256, b is an integer of 15 to 1992, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:256, and where b is greater than or equal to a + 14.</p>	
829388	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2259 of SEQ ID NO:257, b is an integer of 15 to 2273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:257, and where b is greater than or equal to a + 14.</p>	
829540	<p>Preferably excluded from the present invention are</p>	N26408, N28830, N28838, N31522,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1490 of SEQ ID NO:258, b is an integer of 15 to 1504, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:258, and where b is greater than or equal to a + 14.	W15157, W81560, W81561, AA126749, AA126756, AA126772, AA187148
829626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1778 of SEQ ID NO:259, b is an integer of 15 to 1792, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:259, and where b is greater than or equal to a + 14.	
829730	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2034 of SEQ ID NO:260, b is an integer of 15 to 2048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:260, and where b is greater than or equal to a + 14.	
829892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1268 of SEQ ID NO:261, b is an integer of 15 to 1282, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:261, and where b is greater than or equal to a + 14.	R84306, N99830, N90467, AA113938, AA192541, AA243317, L44546, AA713588
829933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 585 of SEQ ID NO:262, b is an integer of 15 to 599, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:262, and where b is greater than or equal to a + 14.	AA121059, AA429187
829938	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1247 of SEQ ID NO:263, b is an integer of 15 to 1261, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:263, and where b is greater than or equal to a + 14.	AA001837, AA142857, AA235114, AA235222, AA614412, AA687460, AA857702, AA857893, AA962131, AA962521
829969	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1006 of SEQ ID NO:264, b is an integer of 15 to 1020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:264, and where b is greater than or equal to a + 14.	R22931, R23036, H09755, H47088, N38971, N38985, N57545, AA075344, AA075597, AA136299, AA136180, AA279124, AA279243, AA279928, AA279929, AA909786, AI000293, N48117, N48131
829982	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	H40097, N80803, N93871, W07650, W15482, W40363, W42635, W45238,

	sequence described by the general formula of a-b, where a is any integer between 1 to 557 of SEQ ID NO:265, b is an integer of 15 to 571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:265, and where b is greater than or equal to a + 14.	W67482, W67483, W70331, W72456, W73235, W73290, W76515, W78220, AA040927, AA040928, AA074829, AA075095, AA083686, AA166708, AA167049, AA228843, AA468686, AA469044, AA505509, AA548788, AA564157, AA595572, AA622149, AA633298, AA576799, AA746697, AA807946, AA873193, AA903706, AA919114, AA932502, AA938506, AA974058, AA977996, A1000750, N85073, N86741, N87037, N88197, N88746, AA090569
830007	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1336 of SEQ ID NO:266, b is an integer of 15 to 1350, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:266, and where b is greater than or equal to a + 14.	
830019	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1305 of SEQ ID NO:267, b is an integer of 15 to 1319, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:267, and where b is greater than or equal to a + 14.	T61424, T53868, T61391, T63785, R23153, R23154, R23905, R64468, R65575, R69390, R69523, R79153, R79154, H14532, H14533, H47318, H47402, H53647, H61347, H93017, H94242, N29789, N42932, W57927, W58148, W67701, W68160, W74342, W81702, W81703, W94692, W95218, W95440, W95785, AA043712, AA056570, AA114073, AA133633, AA133634, AA151774, AA149729, AA149782, AA149795, AA425861, AA425990, AA428095, AA428642, AA494401, AA515475, AA523534, AA548827, AA552032, AA564916, F16977, AA593645, AA613557, AA617694, AA618542, AA576565, AA576574, AA746168, AA766359, AA833956, AA837906, AA857421, AA857877, AA903383, AA903849, AA903888, AA916517, AA922889, AA962544, AA970534, AA974964, AA975402, AA976089, AA983583, AA992448, F18477, C04429, C17306
830073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3680 of SEQ ID NO:268, b is an integer of 15 to 3694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:268, and where b is greater than or equal to a + 14.	T93694, T96159, H04182, H04181, H15428, H48586, N74976, W05676, W44928, AA085826, AA085971, AA126446, AA425304, AA425408, AA280817, AA280995, AA287270, AA287417, AA668788, AA836455, AA977754
830130	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1228 of SEQ ID	

	NO:269, b is an integer of 15 to 1242, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:269, and where b is greater than or equal to a + 14.	
830134	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2043 of SEQ ID NO:270, b is an integer of 15 to 2057, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:270, and where b is greater than or equal to a + 14.	
830135	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 946 of SEQ ID NO:271, b is an integer of 15 to 960, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:271, and where b is greater than or equal to a + 14.	
830148	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1153 of SEQ ID NO:272, b is an integer of 15 to 1167, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:272, and where b is greater than or equal to a + 14.	R15244, R31943, R31992, H06853, H06894, H13355, H30882, R84410, R84411, R94120, H53381, H97695, H99925, N46996, N69023, N77897, W00690, W19694, W38937, W74721, W74795, N89822, N89950, AA009490, AA009904, AA031349, AA031350, AA035629, AA035719, AA046140, AA062845, AA062905, AA079564, AA079636, AA116062, AA116046, AA126968, AA148568, AA159591, AA160429, AA161272, AA161273, AA160576, AA179774, AA180491, AA179635, AA182631, AA182727, AA179634, AA192371, AA192282, AA199831, AA251312, AA256883, AA255477, AA430121, AA533720, AA551694, AA552307, AA552661, AA582138, AA586611, AA587906, AA594387, AA602977, AA605299, AA633388, AA573941, AA574038, AA579715, AA687647, AA741352, AA838339, AA857603, AA858082, AA866081, AA865003, AA875861, AA910672, AA927563, A1076918, W21962
830149	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2757 of SEQ ID NO:273, b is an integer of 15 to 2771, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:273, and where b is greater than or equal to a + 14.	R60249, R60762, R63751, R67526, H95029, H95095, N59347, N77158, W19778, AA047615, AA047555, AA047687, AA047738, AA056453, AA070880, AA112293, AA113105, AA112550, AA112614, AA158015, AA158228, AA160995, AA160996, AA190555, AA191131, AA224574, AA227422, AA255563, AA255586, AA418477, AA424689, AA470392, AA515485, AA515507, AA583475,

		AA588210, AA602533, AA573902, AA568354, AA746111, AA766146, AA804893, N83302
830154	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1875 of SEQ ID NO:274, b is an integer of 15 to 1889, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:274, and where b is greater than or equal to a + 14.	
830183	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 590 of SEQ ID NO:275, b is an integer of 15 to 604, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:275, and where b is greater than or equal to a + 14.	
830194	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1367 of SEQ ID NO:276, b is an integer of 15 to 1381, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:276, and where b is greater than or equal to a + 14.	T51023, T51115, T52795, T53595, T56300, T56767, T59691, T59827, T59904, T63354, T72200, T72269, T92900, T92990, R07165, R07217, R44334, R49609, R44334, R49609, H11106, H20800, H22618, H42472, H43453, H50320, H50321, H69947, N20118, N21306, N26128, N63140, N67225, N67232, W45407, W56419, W56420, W72419, W76279, W94626, W94710, AA029459, AA029524, AA034511, AA035053, AA035563, AA039819, AA041465, AA053002, AA055974, AA056002, AA070356, AA070320, AA074029, AA074039, AA074189, AA074336, AA075645, AA075646, AA076380, AA084435, AA084465, AA084453, AA085290, AA086454, AA099172, AA101922, AA101959, AA099618, AA102011, AA112794, AA126226, AA126304, AA128510, AA129955, AA133875, AA128443, AA133328, AA133403, AA134003, AA130990, AA131028, AA132940, AA135158, AA135628, AA143273, AA146730, AA151853, AA155641, AA155696, AA155726, AA157967, AA158903, AA158902, AA158943, AA158944, AA159293, AA159526, AA161206, AA160558, AA160739, AA160740, AA165357, AA167787, AA169218, AA169512, AA169691, AA176365, AA179272, AA179388, AA180903, AA181001, AA181325, AA181508, AA182781, AA173899, AA187757, AA188120, AA186725, AA187070, AA187152, AA190896, AA199819, AA223210,

		AA223254, AA227038, AA232399, AA233288, AA243192, AA252285, AA492525, AA420611, AA420688, AA492171, AA492254, AA503950, AA507398, AA513704, AA513757, AA515944, AA525799, AA558212, AA563863, AA565107, F17110, AA582829, AA586678, AA603895, AA604163, AA568617, AA617883, AA622814, AA635987, AA569079, AA570078, AA570258, AA570419, AA573205, AA573965, AA574048, AA566065, AA748781, AA834135, AA837022, AA838454, AA838636, AA838049, AA838058, AA856831, AA909853, AA910298, AA927706, AA932101, AA937900, AA953604, AA969555, AA973234, AA978074, AA985430, AA985432, AA988742, AA994207, A1002611, A1014411, N84537, N85082, W22113, W22114, W22431, W22639, W23207, W23271, W29046, N88675, AA640915, AA092777
830207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1135 of SEQ ID NO:277, b is an integer of 15 to 1149, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:277, and where b is greater than or equal to a + 14.	R51744, R88177, W05323, AA746479, AA761644, AA826038, W27619, AA642452
830242	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 797 of SEQ ID NO:278, b is an integer of 15 to 811, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:278, and where b is greater than or equal to a + 14.	
830328	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1246 of SEQ ID NO:279, b is an integer of 15 to 1260, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:279, and where b is greater than or equal to a + 14.	
830340	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1654 of SEQ ID NO:280, b is an integer of 15 to 1668, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:280, and where b is greater than or equal to a + 14.	
830341	Preferably excluded from the present invention are	T62985, T63236, T71911, T66677,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2314 of SEQ ID NO:281, b is an integer of 15 to 2328, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:281, and where b is greater than or equal to a + 14.	T66678, T80777, T81178, R16218, R16219, R67281, H15642, H15643, R96139, R96356, H61487, H61952, H62021, H62022, H62510, H62577, H62887, H63016, H65659, H65660, H72388, H72834, H80906, H97768, N30162, N35776, N52509, N66853, W44421, AA004323, AA004410, AA025214, AA026003, AA040205, AA040849, AA079158, AA079159, AA137066, AA137080, AA137137, AA136971, AA193479, AA532656, AA602312, AA828635, AA872751, AA934418, D80729, C15337
830351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 942 of SEQ ID NO:282, b is an integer of 15 to 956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:282, and where b is greater than or equal to a + 14.	
830358	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1388 of SEQ ID NO:283, b is an integer of 15 to 1402, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:283, and where b is greater than or equal to a + 14.	
830390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 661 of SEQ ID NO:284, b is an integer of 15 to 675, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:284, and where b is greater than or equal to a + 14.	
830400	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1325 of SEQ ID NO:285, b is an integer of 15 to 1339, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:285, and where b is greater than or equal to a + 14.	T40239, T41103, T60782, T61153, T92326, T95403, R16530, R16587, R46049, R49231, R49231, R46049, H26122, H26387, H67872, H67872, H97917, N23194, N29748, N57652, N64158, N67587, N77509, N80178, W03502, W23838, W57929, W72584, AA011087, AA011088, AA070667, AA074878, AA075068, AA075019, AA076166, AA079857, AA082235, AA099016, AA099093, AA100754, AA113152, AA126886, AA128207, AA126932, AA128546, AA130882, AA136302, AA136408, AA143052, AA143693, AA148079, AA149931, AA151001, AA151091, AA155761, AA157290, AA160781, AA165535, AA173281, AA179903, AA180211, AA181162, AA181673, AA181986,

		AA187551, AA191657, AA192202, AA196746, AA196944, AA223166, AA224485, AA242866, AA397377, AA468734, AA514807, AA523669, AA534165, AA534195, AA565551, AA565552, H67199, AA581627, AA588734, AA588752, AA593857, AA595407, AA595555, AA603965, AA610486, AA614617, AA631563, AA635960, AA636057, AA576256, AA577470, AA580124, AA580480, AA714208, AA728790, AA729276, AA729361, AA744895, AA745002, AA746940, AA746948, AA747346, AA804602, AA810873, AA833970, AA836938, AA838563, AA858405, AA872330, AA922975, AA946823, AA954185, AA962678, AA978008, AA985504, AA987717, AI004904, AI017374, AI075264, F19611, AI089951, N83301, AA082282, AA091465, AA093298, AA094459
830437	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1384 of SEQ ID NO:286, b is an integer of 15 to 1398, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:286, and where b is greater than or equal to a + 14.	
830458	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 912 of SEQ ID NO:287, b is an integer of 15 to 926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:287, and where b is greater than or equal to a + 14.	T47583, T47584, T49761, T50148, T50203, T47161, R11382, R14878, H18220, H18258, R92715, N78687, W20222, W58210, W58319, W72115, W77801, W79332, W79431, W79487, W79631, W94437, N90582, AA043441, AA043442, AA148009, AA147947, AA150837, AA224863, AA225964, AA226110, AA259194, AA259193, AA420769, AA420829, AA470787, AA493672, AA501962, AA502082, AA506908, AA528607, AA588435, AA603500, AA603814, AA627229, AA627233, AA627240, AA632058, AA632689, AA639239, AA579023, AA580698, AA662633, AA661967, AA665215, AA729443, AA730546, AA737851, AA745424, AA745526, AA747036, AA878568, AA879157, AA886627, AA902180, AA922294, AA933050, AA962580, AA977360, AA985679, AA996058, AA996145, AI053546, AI085892, N83274, W15194, N88934, C04128, AA640839, AA091328, AA093116, AA094048, AA094287
830466	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3080 of SEQ ID NO:288, b is an integer of 15 to 3094, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:288, and where b is greater than or equal to a + 14.	
830497	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1969 of SEQ ID NO:289, b is an integer of 15 to 1983, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:289, and where b is greater than or equal to a + 14.	T47088, T47089, T58430, T58462, R00971, H42144, N77388, W51953, W52502, AA036671, AA114976, AA593693, AA575857, C01052
830511	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1284 of SEQ ID NO:290, b is an integer of 15 to 1298, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:290, and where b is greater than or equal to a + 14.	
830512	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2445 of SEQ ID NO:291, b is an integer of 15 to 2459, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:291, and where b is greater than or equal to a + 14.	
830513	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 556 of SEQ ID NO:292, b is an integer of 15 to 570, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:292, and where b is greater than or equal to a + 14.	
830540	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2454 of SEQ ID NO:293, b is an integer of 15 to 2468, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:293, and where b is greater than or equal to a + 14.	T66458, T98908, R15832, R21916, R22565, H12306, R99043, H57499, H82961, AA046203, AA046283, AA055081, AA055141, AA173411, AA173467, AA173996, AA176693
830550	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1066 of SEQ ID NO:294, b is an integer of 15 to 1080, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:294, and where b is greater than or equal to a + 14.	R50040, R60172, R71512, H09125, H09475, H21789, R84538, R85928, R94762, R96633, R96680, R97580, H53135, H53241, H82960, H83191, N68166, N68684, N77903, N80174, N80625, N92442, N93242, N93314, N98261, W03498, W05839, W20000, W25100, W31279, W37087, W60751, W67554, W67583, W73877, W77814, W80412, W95868, W95954, N91343,

		AA026891, AA026892, AA033547, AA034170, AA069175, AA088435, AA151307, AA161037, AA237097, AA251326, AA251729, AA428848, AA429940, AA287366, AA287504, AA470593, AA470594, AA514493, AA564438, H67293, AA582501, AA583172, AA587111, AA602517, AA603483, AA569955, AA732412, AA737913, AA810504, AA832193, AA857743, AA915872, AA915896, AA915992, AA948498, AA983538, AA991546, AI052409, AI053921
830567	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2681 of SEQ ID NO:295, b is an integer of 15 to 2695, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:295, and where b is greater than or equal to a + 14.	R69708, R75813, R75814, N22294, N47088, N50300, N50983, N81194, N93236, AA074258, AA083867, AA083973, AA195801, AA196063, AA252500, AA252415, AA258014, AA287593, AA291332, AA492017, AA522597, AA617684, AA713960, AA740158, AA749386, AA808100, AA808680, AA814350, AA826203, AA831453, AA887306, AA918645, AA972761, N88184
830586	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1380 of SEQ ID NO:296, b is an integer of 15 to 1394, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:296, and where b is greater than or equal to a + 14.	R99131, H81094, W01508, AA045861, AA085947, AA102188, AA146772, AA148854, AA233843, AA424679, AA491204, AA514459, AA532818, AA809984, AA838521, AA954880, AI089939
830632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 984 of SEQ ID NO:297, b is an integer of 15 to 998, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:297, and where b is greater than or equal to a + 14.	T47818, R21519, R21621, R22056, R22112, R31393, R32890, R48823, R48824, R66656, R67377, R71682, H25037, H25038, H25842, H26215, H26515, H26994, H28312, H28313, H29756, H30178, H41920, H41966, H42490, H43473, R83733, R85464, R88798, R89058, R93321, H52733, H59363, H60020, H73314, H73513, H80831, H80832, H82603, H86794, H86795, H86853, H86852, H92710, H96832, H98741, N23451, N23463, N26478, N26861, N31350, N31593, N35529, N39970, N42652, N62104, N74283, N76446, N78334, N92771, W04383, W19424, W20392, W24569, W35168, W60060, W60111, W84373, W84420, AA025658, AA029558, AA062705, AA062707, AA063390, AA062771, AA081934, AA126557, AA136019, AA151638, AA192245, AA194655, AA470430, AA493634, AA552261, AA552348, AA565278, AA565462, AA583788, AA593646, AA594277, AA604853, AA613755.

		AA632449, AA632505, AA657974, AA730677, AA730804, AA748100, AA765824, AA857805, AA954102, AA961763, AA962500, AA974525, AA983564, AA987422, AA987934, AA989423, A1000235, F19140, N84058, N84994, C03222, AA091370, AA091545
830645	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1652 of SEQ ID NO:298, b is an integer of 15 to 1666, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:298, and where b is greater than or equal to a + 14.	
830652	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2430 of SEQ ID NO:299, b is an integer of 15 to 2444, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:299, and where b is greater than or equal to a + 14.	
830659	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1012 of SEQ ID NO:300, b is an integer of 15 to 1026, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:300, and where b is greater than or equal to a + 14.	T65101, T66494, T66636, T84051, T86086, R05580, R13805, R15868, R16050, H05221, H05222, H13512, H16069, H18275, H21247, H44169, R83705, R92365, H48479, H48643, H54436, H54526, H73472, H73726, H97495, N29822, N30479, N31551, N32563, N39176, N39961, N45251, N68667, N91684, W07693, W32510, W32607, W38017, W74179, W79849, AA018138, AA028191, AA033572, AA033571, AA042915, AA043002, AA053878, AA054501, AA058344, AA099556, AA101993, AA134643, AA143525, AA176419, AA424269, AA555196, AA769107, AA987653, AI076212, N84624, N85006, AI084132, AI084154, AA094327
830696	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 816 of SEQ ID NO:301, b is an integer of 15 to 830, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:301, and where b is greater than or equal to a + 14.	
830706	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3286 of SEQ ID NO:302, b is an integer of 15 to 3300, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:302, and where b is	

	greater than or equal to $a + 14$.	
830743	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 461 of SEQ ID NO:303, b is an integer of 15 to 475, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:303, and where b is greater than or equal to $a + 14$.	N30323, N56655, N69079, N69946, N80244, N98327, W07371, W42660, W45185, W55989, W56279, W68387, W68503, W72685, W74708, W74677, W77791, W80647, AA010723, AA011171, AA033537, AA034221, AA035773, AA056334, AA062820, AA132021, AA132124, AA135594, AA135681, AA151293, AA151292, AA181331, AA186392, AA187084, AA228662, AA228680, AA229819, AA468802, AA470869, AA483684, AA491891, AA514852, AA533423, AA548946, AA563674, AA564612, AA594511, AA600707, AA622053, AA635767, AA639353, AA662887, AA664589, AA729365, AA747035, AA747774, AA814124, AA873167, AA886626, AA903495, AA903981, AA922807, AA969768, AA973174, AA974282, AA976458, AA977143, AA983332, AI025140, AI066527, F19035, F19464, C03984, C13986, C14221, C14299, C14336, C14341, C14380, C14385, C14396, C14434, C14483, C14504, C14513, C15788
830770	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2888 of SEQ ID NO:304, b is an integer of 15 to 2902, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:304, and where b is greater than or equal to $a + 14$.	
830830	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1539 of SEQ ID NO:305, b is an integer of 15 to 1553, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:305, and where b is greater than or equal to $a + 14$.	
830838	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1973 of SEQ ID NO:306, b is an integer of 15 to 1987, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:306, and where b is greater than or equal to $a + 14$.	
830851	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 771 of SEQ ID NO:307, b is an integer of 15 to 785, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:307, and where b is greater than or equal to a + 14.	
830853	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2164 of SEQ ID NO:308, b is an integer of 15 to 2178, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:308, and where b is greater than or equal to a + 14.	
830856	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 861 of SEQ ID NO:309, b is an integer of 15 to 875, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:309, and where b is greater than or equal to a + 14.	
830862	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 742 of SEQ ID NO:310, b is an integer of 15 to 756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:310, and where b is greater than or equal to a + 14.	T46908, T46909, T46921, T46922, T50921, T52918, T53038, T56001, T59028, T94115, T94204, R53898, R53908, H02747, H27523, H77792, H88026, H88248, H90255, H96065, H88248, N21994, N64072, N73723, N74262, N75815, N77939, W03894, W23887, AA081082, AA113423, AA115852, AA143290, AA143335, AA146868, AA157054, AA157208, AA179118, AA187792, AA188385, AA468513, AA468983, AA501970, AA523481, AA528461, AA533759, AA533618, AA535287, AA541570, AA558529, L44430, AA604961, AA568927, AA659814, AA661481, AA661996, AA731036, AA748135, AA847331, AA878667, AA885549, AA935403, AA938035, AI001062, F19242, N83489, N83646, N84328, N85002, N85167, N85223, N85325, N85833, N85949, N86287, N86329, N87923, N83150, AA642852, AA091775, AA093919
830879	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 837 of SEQ ID NO:311, b is an integer of 15 to 851, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:311, and where b is greater than or equal to a + 14.	T62074, T62130, T67747, T67857, R44816, R48904, R44816, H13822, H29311, W37451, N90567, AA128266, AA164552, AA235044, AA236012, AA746229, AA962194, AA987868, AA994828, AI000188, AI015557
830919	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1321 of SEQ ID NO:312, b is an integer of 15 to 1335, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:312, and where b is	

	greater than or equal to $a + 14$.	
830969	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 502 of SEQ ID NO:313, b is an integer of 15 to 516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:313, and where b is greater than or equal to $a + 14$.	
830991	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1819 of SEQ ID NO:314, b is an integer of 15 to 1833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:314, and where b is greater than or equal to $a + 14$.	
831002	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1340 of SEQ ID NO:315, b is an integer of 15 to 1354, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:315, and where b is greater than or equal to $a + 14$.	
831003	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2407 of SEQ ID NO:316, b is an integer of 15 to 2421, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:316, and where b is greater than or equal to $a + 14$.	T64373, N48387, W52748, W52754, W70187, AA029541, AA034463, AA058497, AA082001, AA082284, AA085967, AA088397, AA133444, AA133477, AA149568, AA187408, AA226818, AA226855
831021	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1078 of SEQ ID NO:317, b is an integer of 15 to 1092, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:317, and where b is greater than or equal to $a + 14$.	
831036	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1366 of SEQ ID NO:318, b is an integer of 15 to 1380, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:318, and where b is greater than or equal to $a + 14$.	
831071	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2598 of SEQ ID NO:319, b is an integer of 15 to 2612, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:319, and where b is greater than or equal to $a + 14$.	

831094	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 929 of SEQ ID NO:320, b is an integer of 15 to 943, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:320, and where b is greater than or equal to a + 14.	
831099	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2945 of SEQ ID NO:321, b is an integer of 15 to 2959, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:321, and where b is greater than or equal to a + 14.	T58120, T90056, T90158, T94290, T94639, R69200, R69590, R69678, R76031, H65424, H65425, N32273, N40465, N47619, N48504, N66482, N67212, N67243, N67881, N71915, N72302, N92538, N94512, W03004, W06930, W20370, W23962, W38380, W38525, W38716, W39486, W42582, W42594, W44824, W48665, W51898, W52474, W53040, W60142, N90075, N90423, AA025009, AA024962, AA029382, AA029726, AA031500, AA031546, AA037283, AA037749, AA039259, AA044145, AA044261, AA065061, AA070027, AA082386, AA083544, AA083757, AA088692, AA088829, AA099577, AA100236, AA100245, AA100517, AA112739, AA112091, AA116055, AA130509, AA130510, AA132145, AA135909, AA136308, AA136413, AA136528, AA136751, AA146853, AA146852, AA148049, AA156943, AA159808, AA165022, AA173867, AA181803, AA182563, AA182776, AA186553, AA186858, AA192463, AA194658, AA255837, AA261995, AA423999, AA493599, AA228337, AA228348, AA506755, AA506420, AA513968, AA514542, AA522900, AA524125, AA551485, AA553912, AA563900, AA594966, AA602651, AA610339, AA610361, AA614772, AA618333, AA576828, AA665045, AA714493, AA729997, AA738153, AA768641, AA804931, AA806122, AA827914, AA857664, AA876216, AA877173, AA877646, AA894385, AA922728, AA947835, AA977110, AA984009, AA988275, AA988567, N84005, N84600, N84939, N85553, A1084028, N86141, N88049, N89450, N89451, C02877, C02980, C03631, C05243, C05332, C05993, AA642453, AA090838, AA089614, AA091652, AA093130, AA093851
831113	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	AA122085, AA147371, A1005336

	where a is any integer between 1 to 788 of SEQ ID NO:322, b is an integer of 15 to 802, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:322, and where b is greater than or equal to a + 14.	
831120	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1710 of SEQ ID NO:323, b is an integer of 15 to 1724, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:323, and where b is greater than or equal to a + 14.	
831172	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2247 of SEQ ID NO:324, b is an integer of 15 to 2261, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:324, and where b is greater than or equal to a + 14.	
831178	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1199 of SEQ ID NO:325, b is an integer of 15 to 1213, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:325, and where b is greater than or equal to a + 14.	
831184	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2750 of SEQ ID NO:326, b is an integer of 15 to 2764, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:326, and where b is greater than or equal to a + 14.	
831203	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1750 of SEQ ID NO:327, b is an integer of 15 to 1764, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:327, and where b is greater than or equal to a + 14.	
831210	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 557 of SEQ ID NO:328, b is an integer of 15 to 571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:328, and where b is greater than or equal to a + 14.	AA057014, AA059289
831228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 459 of SEQ ID	

	NO:329, b is an integer of 15 to 473, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:329, and where b is greater than or equal to a + 14.	
831256	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1321 of SEQ ID NO:330, b is an integer of 15 to 1335, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:330, and where b is greater than or equal to a + 14.	R17500, R48877, H12160, R84358, H90367, N33987, AA161057
831257	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1032 of SEQ ID NO:331, b is an integer of 15 to 1046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:331, and where b is greater than or equal to a + 14.	T49922, T85470, R37545, H03610, AA005184, AA045346
831277	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1297 of SEQ ID NO:332, b is an integer of 15 to 1311, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:332, and where b is greater than or equal to a + 14.	
831317	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1430 of SEQ ID NO:333, b is an integer of 15 to 1444, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:333, and where b is greater than or equal to a + 14.	T39850, T47708, T47709, T47863, T51491, T52507, T53819, T53951, T55884, T60330, T60359, T60364, T60380, T60480, T60634, T61198, T61280, T61878, T62028, T67704, T67742, T67780, T67853, T67910, T68010, T68058, T68132, T68154, T68379, T68998, T68999, T69078, T69079, T69119, T69177, T69442, T70496, T71707, T72285, T72505, T72998, T73123, T73679, T73756, T73761, T73837, T74031, T74383, T74405, T74655, T74784, T74798, T74892, T85320, T85533, R83453, R88738, R90989, R90995, H58528, H59441, H60092, H60282, H60589, H67401, H67458, H72811, H79422, H80518, H80570, H91775, H91816, N57814, W60714, W60741, AA034367, AA040550, AA040667, AA242768, AA424551, AA424642, R29495, R29660, R29089, C21224
831339	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1016 of SEQ ID NO:334, b is an integer of 15 to 1030, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:334, and where b is	

	greater than or equal to $a + 14$.	
831363	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2113 of SEQ ID NO:335, b is an integer of 15 to 2127, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:335, and where b is greater than or equal to $a + 14$.	T58736, T58803, T61766, T64470, T64610, T67816, T68878, T68952, T72450, T72511, T72968, T73613, T73939, H41914, H41957, N75040, W05718, AA043436, AA043416, AA045231, AA058807, AA484773, AA502762, AA503811, AA527553, AA744171, AA902935, AA903099, A1002033
831367	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 833 of SEQ ID NO:336, b is an integer of 15 to 847, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:336, and where b is greater than or equal to $a + 14$.	
831379	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 688 of SEQ ID NO:337, b is an integer of 15 to 702, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:337, and where b is greater than or equal to $a + 14$.	R26001, R26804, R82629, R82630, H21598, H27310, H27309, H38082, H38083, H44451, H44494, H47613, R83356, R83791, R96066, R96103, H72512, H72910, H80449, H80450, H90511, H90607, N71766, N94349, W16956, W23496, W24351, W46455, W46523, W48658, W70263, W73002, W76239, W92963, W92964, AA157329, AA157426, AA458665, AA229554, AA280810, AA280936, AA490898, AA491084, AA493730, AA527336, AA534762, AA535794, F17720, AA603439, AA568655, AA659071, AA826699, AA872867, AA876999, AA932403, AA953149, AA953343, A1000023, A1017353, A1094807, N95548, C02063, C04109
831385	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 861 of SEQ ID NO:338, b is an integer of 15 to 875, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:338, and where b is greater than or equal to $a + 14$.	
831390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1434 of SEQ ID NO:339, b is an integer of 15 to 1448, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:339, and where b is greater than or equal to $a + 14$.	T53890, T54037, T81546, T81973, R20470, R21066, R45288, R46246, R45288, R46246, H13340, H17537, H30523, R85229, R85230, R94643, R94685, R94686, H52010, H52125, H71328, H71376, N25973, N28794, N30891, N36603, N41703, N62205, N63213, N76503, W45706, W44353, W52126, W74523, W79862, AA033566, AA034468, AA099015, AA099092, AA100315, AA129588, AA167137, AA194961, AA226935, AA226943, AA418898, AA428909,

		AA485083, AA485195, AA505107, AA506087, AA516109, AA525370, AA617946, AA627402, AA573848, AA574063, AA809830, AA834509, AA837985, AA862394, AA862989, AA974789, AA988779, A1000171, A1094917, W24010, N88026, C20972
831391	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 829 of SEQ ID NO:340, b is an integer of 15 to 843, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:340, and where b is greater than or equal to a + 14.	
831405	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1279 of SEQ ID NO:341, b is an integer of 15 to 1293, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:341, and where b is greater than or equal to a + 14.	T54632, T54714, T55384, T55812, T56220, T60613, T69578, R08164, R08219, T78003, T78164, R01577, R12676, R16414, H60551, N21984, N25878, N25887, N75352, W01648, W72541, W76166, W86984, W86811, W88909, W88788, AA022691, AA022784, AA193302, AA194256, AA235873, AA425660, AA573463, AA953249, R29055
831442	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1259 of SEQ ID NO:342, b is an integer of 15 to 1273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:342, and where b is greater than or equal to a + 14.	
831476	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1779 of SEQ ID NO:343, b is an integer of 15 to 1793, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:343, and where b is greater than or equal to a + 14.	R48303, R48405, R73778, H30456, H81254, W02773, W24831, W73089, W73194, AA034015, AA151153, AA151154, AA418429, AA424672, AA593592, AA910532, AA987246, A1001017, C02335, C04320
831488	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1658 of SEQ ID NO:344, b is an integer of 15 to 1672, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:344, and where b is greater than or equal to a + 14.	
831518	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2095 of SEQ ID NO:345, b is an integer of 15 to 2109, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:345, and where b is greater than or equal to a + 14.	

831519	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1700 of SEQ ID NO:346, b is an integer of 15 to 1714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:346, and where b is greater than or equal to a + 14.	
831521	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1658 of SEQ ID NO:347, b is an integer of 15 to 1672, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:347, and where b is greater than or equal to a + 14.	
831550	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1469 of SEQ ID NO:348, b is an integer of 15 to 1483, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:348, and where b is greater than or equal to a + 14.	
831560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1828 of SEQ ID NO:349, b is an integer of 15 to 1842, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:349, and where b is greater than or equal to a + 14.	T56438, R22852, R46063, R52365, R81781, R81879, H02958, H04256, H05743, H05849, H23235, H23349, H43210, H43260, H87699, H91571, W00708, W56717, W56762, W70251, W70252, AA026841, AA027043, AA041261, AA041495, AA043451, AA043452, AA054505, AA054366, AA055050, AA055129, AA147629, AA147667
831562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2994 of SEQ ID NO:350, b is an integer of 15 to 3008, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:350, and where b is greater than or equal to a + 14.	
831570	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2742 of SEQ ID NO:351, b is an integer of 15 to 2756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:351, and where b is greater than or equal to a + 14.	
831593	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1631 of SEQ ID NO:352, b is an integer of 15 to 1645, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:352, and where b is	

	greater than or equal to $a + 14$.	
831596	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1623 of SEQ ID NO:353, b is an integer of 15 to 1637, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:353, and where b is greater than or equal to $a + 14$.	
831627	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1105 of SEQ ID NO:354, b is an integer of 15 to 1119, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:354, and where b is greater than or equal to $a + 14$.	AA147578, AA156449, AA588796, AA863066, D80116
831649	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 724 of SEQ ID NO:355, b is an integer of 15 to 738, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:355, and where b is greater than or equal to $a + 14$.	R21047
831664	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:356, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:356, and where b is greater than or equal to $a + 14$.	R35205, H13039, R84255, W24589, W93157, AA186436, AA188774, AA227246, AA658889, AA838204, W22056, W25833, W28198, W28494, AA090436, AA089530, AA089667
831674	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1548 of SEQ ID NO:357, b is an integer of 15 to 1562, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:357, and where b is greater than or equal to $a + 14$.	
831684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1917 of SEQ ID NO:358, b is an integer of 15 to 1931, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:358, and where b is greater than or equal to $a + 14$.	T64083, R54664, R54665, W52888, W60096, W60162, AA009843, AA009870, AA236225, AA236291, AA459452, AA465675, AA554776, AA563899, AA583755, AA593849, AA596013, AA627978, AA573921, AA747840, AA828086, AA830260, AA837593, AA996154, C01662
831687	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 855 of SEQ ID NO:359, b is an integer of 15 to 869, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:359, and where b is greater than or equal to $a + 14$.	T49489, R05976, R55046, N21648, N31054, N48001, AA464953, AA426224, AA430556, AA600829, AA744708, AA747361, AA976473, A1097658

831726	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 547 of SEQ ID NO:360, b is an integer of 15 to 561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:360, and where b is greater than or equal to a + 14.	
831736	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1666 of SEQ ID NO:361, b is an integer of 15 to 1680, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:361, and where b is greater than or equal to a + 14.	T60384, T93026, T83297, R17403, R17423, R21319, H65765, N94506, W23956, W24344, W45068, W57786, W57860, W81343, AA058929, AA151788, AA151833
831762	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 726 of SEQ ID NO:362, b is an integer of 15 to 740, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:362, and where b is greater than or equal to a + 14.	
831801	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1310 of SEQ ID NO:363, b is an integer of 15 to 1324, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:363, and where b is greater than or equal to a + 14.	T39530, T64430, R36089, H12597, H12647, H19534, H20096, H26648, H26663, W15192, W45569, W45621, AA018144, AA018145, AA018470, AA039510, AA039529, AA047549, AA047837, AA057785, AA074201, AA075686, AA079138, AA135599, AA135658, AA147502, AA147931, AA156715, AA156811, AA188215, AA186362, AA425996, AA283917, AA514670, AA522463, AA714301, AA742700, AA872728, AA887841, AA971644, AI015637, AI053971, AI054233, AI074507, AI084901, W28363
831848	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2839 of SEQ ID NO:364, b is an integer of 15 to 2853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:364, and where b is greater than or equal to a + 14.	T77112, R13655, R19353, R19511, R24780, R35812, R36752, R38177, R43861, R44629, R45511, R43861, R45511, R44629, R71248, R71299, R82784, H00629, H01917, H04479, H45706, H45757, H94039, H94125, N30574, N57220, AA033684, AA114107, AA253260, AA461547, AA460619, AA715125, AI096588, C03714, AA092127
831861	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1823 of SEQ ID NO:365, b is an integer of 15 to 1837, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:365, and where b is greater than or equal to a + 14.	T57456, T58038, T58104, R08156, R27046, R28341, R28340, N32411, N56831, N78961, W16984, W16954, W17352, W74522, W79861, AA025882, AA025883, AA084109, AA100121, AA100060, AA132713

831866	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1809 of SEQ ID NO:366, b is an integer of 15 to 1823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:366, and where b is greater than or equal to a + 14.	
831878	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 884 of SEQ ID NO:367, b is an integer of 15 to 898, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:367, and where b is greater than or equal to a + 14.	
831899	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1103 of SEQ ID NO:368, b is an integer of 15 to 1117, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:368, and where b is greater than or equal to a + 14.	AA159048, AA768390, AA806956
831913	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2212 of SEQ ID NO:369, b is an integer of 15 to 2226, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:369, and where b is greater than or equal to a + 14.	
831972	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3622 of SEQ ID NO:370, b is an integer of 15 to 3636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:370, and where b is greater than or equal to a + 14.	
831985	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4025 of SEQ ID NO:371, b is an integer of 15 to 4039, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:371, and where b is greater than or equal to a + 14.	
831986	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1585 of SEQ ID NO:372, b is an integer of 15 to 1599, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:372, and where b is greater than or equal to a + 14.	
832010	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 450 of SEQ ID NO:373, b is an integer of 15 to 464, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:373, and where b is greater than or equal to a + 14.	
832016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 876 of SEQ ID NO:374, b is an integer of 15 to 890, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:374, and where b is greater than or equal to a + 14.	
832041	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1860 of SEQ ID NO:375, b is an integer of 15 to 1874, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:375, and where b is greater than or equal to a + 14.	R63637, R92994, N30838, N30844, N41366, N41372. AA639771
832044	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2004 of SEQ ID NO:376, b is an integer of 15 to 2018, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:376, and where b is greater than or equal to a + 14.	T56668, R09616, R20197, R44983, R52998, R52997, R44983, H06485, H06543, H09799, H09885, H24790, N57987, N62197, N76494, W02915, W78217, AA041290, AA041323, AA074236, AA075127, AA075212, AA075847, AA088708, AA088793, AA112359, AA121803, AA151677, AA166711, AA167069, AA181608, AA188478, AA194067, AA194182, AA221025, AA221037, AA228036, AA228145, AA557397, AA564567, AA582681, AA582151, AA601549, AA613841, AA832393, AA846987, AA865356, AA866164, AA872667, AA862962, AA911092, AA937359, A1000072, D83877
832049	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 804 of SEQ ID NO:377, b is an integer of 15 to 818, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:377, and where b is greater than or equal to a + 14.	
832122	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2551 of SEQ ID NO:378, b is an integer of 15 to 2565, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:378, and where b is greater than or equal to a + 14.	
832148	Preferably excluded from the present invention are	T78202, R37864, R62706, R78737,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1666 of SEQ ID NO:379, b is an integer of 15 to 1680, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:379, and where b is greater than or equal to a + 14.	R78736, H62109, N50394, N51659, N67973, N80394, W33108, W33107, AA016055, AA074831, AA075097, AA256793, AA256472, AA418825, AA418922, AA430755, AA280663, AA281049, AA467867, AA502148, H71558, AA721278, AA748880, AA809767, AA810852, AA832174, AA911263, AA938484, AA975282, D80672, D81573, D81746, A1096900, C02375
832197	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:380, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:380, and where b is greater than or equal to a + 14.	
832237	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1017 of SEQ ID NO:381, b is an integer of 15 to 1031, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:381, and where b is greater than or equal to a + 14.	R36943, R42259, R53230, R42259, H09607, AA150724, AA831055
832246	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1583 of SEQ ID NO:382, b is an integer of 15 to 1597, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:382, and where b is greater than or equal to a + 14.	H13698, H13750, R91283, R91322, H97506, N64810, N75659, W61290, W65386, H54890, AA568261, AA830860, AA863239, AA873329, AA938701, D82264, C18047
832256	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 161 of SEQ ID NO:383, b is an integer of 15 to 175, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:383, and where b is greater than or equal to a + 14.	
832280	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2157 of SEQ ID NO:384, b is an integer of 15 to 2171, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:384, and where b is greater than or equal to a + 14.	H09977, H09978, R89392, R94438, H93033, H93466, H93904, N29334, N53767, N57027, N71868, N71879, N73126, W24652, AA026682, AA047124, AA127259, AA224396, AA224473, AA227220, AA236734, AA236763, AA236910, AA236919
832285	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2350 of SEQ ID NO:385, b is an integer of 15 to 2364, where both a and b correspond to the positions of nucleotide	R12740, R14184, R15171, R26447, R28455, R34165, R35396, R39792, R40473, R49696, R41588, R40473, R49696, R70668, R70669, R79640, R79833, H02312, H08199, H08297, R99351, H84241, H84567, H85554,

	residues shown in SEQ ID NO:385, and where b is greater than or equal to a + 14.	N24354, N25230, N32462, N33863, N64676, N70374, N80109, W47526, W47527, W80678, W80934, W93668, AA082195, AA223758, AA243624, AA255527, AA256711, AA262387, AA281015, AA281094, AA281183, AA281203, AA287927, AA287991, AA505084, AA505086, AA525301, AA553559, AA564243, AA582189, AA737010, AA808271, AA872481, AA937541, A1015987, C01015, C20842
832294	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2850 of SEQ ID NO:386, b is an integer of 15 to 2864, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:386, and where b is greater than or equal to a + 14.	
832326	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2669 of SEQ ID NO:387, b is an integer of 15 to 2683, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:387, and where b is greater than or equal to a + 14.	
832333	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1432 of SEQ ID NO:388, b is an integer of 15 to 1446, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:388, and where b is greater than or equal to a + 14.	
832346	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 709 of SEQ ID NO:389, b is an integer of 15 to 723, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:389, and where b is greater than or equal to a + 14.	T88928, R12446, R37113, R42462, H15692, H18859, N34664, AA132220, AA224337, AA460720, AA492479
832370	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1032 of SEQ ID NO:390, b is an integer of 15 to 1046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:390, and where b is greater than or equal to a + 14.	
832381	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 685 of SEQ ID NO:391, b is an integer of 15 to 699, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:391, and where b is greater than or equal to a + 14.	
832394	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1531 of SEQ ID NO:392, b is an integer of 15 to 1545, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:392, and where b is greater than or equal to a + 14.	
832454	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 735 of SEQ ID NO:393, b is an integer of 15 to 749, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:393, and where b is greater than or equal to a + 14.	T57094, T58711, T68990, T71879, R92183, H93778, N63977, N80768, AA034382, AA034383, AA057664, AA235744, AA425865, AA524693, AA551804, AA523604, AA614639, AA740316, AA872373, AA938571, AA947337, R28997, AA640968, C21135
832465	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 597 of SEQ ID NO:394, b is an integer of 15 to 611, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:394, and where b is greater than or equal to a + 14.	R36004, R36378, H71881, H96279, N50049, N63692, W74426, W79180, W87805, AA421015, AA527679, AA833773, AA987375, F19351, AA642491, C14893, C14937
832475	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1842 of SEQ ID NO:395, b is an integer of 15 to 1856, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:395, and where b is greater than or equal to a + 14.	
832495	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2637 of SEQ ID NO:396, b is an integer of 15 to 2651, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:396, and where b is greater than or equal to a + 14.	
832498	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2493 of SEQ ID NO:397, b is an integer of 15 to 2507, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:397, and where b is greater than or equal to a + 14.	T67126, T67127, R13516, R20638, H64071, N22361, N25516, N39506, N75609, N78204, W40313, W45344, AA074739, AA074803, AA143509, AA523999, AA552542, AA554032, N20483, AA588804, AA617733, AA577150, AA577309, AA579423, AA740813, AA835721, AA836640, AA909766, AA936979, AA947310, N26815, A1085484, D78707, W67520, W68152
832501	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1259 of SEQ ID NO:398, b is an integer of 15 to 1273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:398, and where b is greater than or equal to a + 14.	
832505	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3760 of SEQ ID NO:399, b is an integer of 15 to 3774, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:399, and where b is greater than or equal to a + 14.	T50501, T50636, T92136, R52390, R59648, H06170, H28886, H28885, R96577, R96600, H84171, H94122, H98228, N36866, N36872, N46136, N46142, N63589, N66323, W48779, W49798, AA029033, AA054487, AA058524, AA084466, AA086177, AA098967, AA099485, AA100345, AA147008, AA147009, AA146910, AA146909, AA160346, AA159865, AA192832, AA203513, AA252521, AA252553, AA463513, AA463570, AA421250, AA425704, AA427774, AA278328, AA278999, AA280712, AA281733, AA281871, AA282407, AA282626, AA283639, AA542810, AA557893, AA568486, AA569759, AA577522, AA659517, AA659737, AA664537, AA713950, AA805488, AA835999, AA876619, AA931568, AA935758, AA946722, A1000603, D82640
832539	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1508 of SEQ ID NO:400, b is an integer of 15 to 1522, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:400, and where b is greater than or equal to a + 14.	H72563, AA160114, AA159654, AA161261, AA165097, AA223618, AA243203
832554	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1356 of SEQ ID NO:401, b is an integer of 15 to 1370, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:401, and where b is greater than or equal to a + 14.	
832569	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1398 of SEQ ID NO:402, b is an integer of 15 to 1412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:402, and where b is greater than or equal to a + 14.	
832578	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1736 of SEQ ID NO:403, b is an integer of 15 to 1750, where both a and b correspond to the positions of nucleotide	R09545, R09658, R09967, R11471, R16714, R16910, R16965, R19372, R80788, R80988, H28725, H63085, H63169, H75499, H75500, N33554, N41536, N52961, N52966, N74070, W01039, W57770, W57843, W60109,

	residues shown in SEQ ID NO:403, and where b is greater than or equal to a + 14.	W91978, W92107, AA001984, AA004653, AA027155, AA418427, AA281395, AA532870, AA564737, AA588889, AA631841, AA639548, AA765363, AA877896, AA887900, AA974026, AI057270, AI084214, AI094490, AI096750, AI097632, AI096745
832615	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1325 of SEQ ID NO:404, b is an integer of 15 to 1339, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:404, and where b is greater than or equal to a + 14.	
832620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 468 of SEQ ID NO:405, b is an integer of 15 to 482, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:405, and where b is greater than or equal to a + 14.	
832632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1399 of SEQ ID NO:406, b is an integer of 15 to 1413, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:406, and where b is greater than or equal to a + 14.	
832633	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1679 of SEQ ID NO:407, b is an integer of 15 to 1693, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:407, and where b is greater than or equal to a + 14.	R69173, AA053085, AA053597, AA427705, AA730380, AA865757, AA911497, AI083906
833483	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1328 of SEQ ID NO:408, b is an integer of 15 to 1342, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:408, and where b is greater than or equal to a + 14.	
834574	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2403 of SEQ ID NO:409, b is an integer of 15 to 2417, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:409, and where b is greater than or equal to a + 14.	
834859	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1387 of SEQ ID NO:410, b is an integer of 15 to 1401, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:410, and where b is greater than or equal to a + 14.	
834861	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3002 of SEQ ID NO:411, b is an integer of 15 to 3016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:411, and where b is greater than or equal to a + 14.	
834890	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 944 of SEQ ID NO:412, b is an integer of 15 to 958, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:412, and where b is greater than or equal to a + 14.	T40255, T40256, T40770, T40778, T40803, T41118, T94280, T94627, R13201, R32388, R32389, R53769, H28669, H39502, H42532, H42533, R82957, R85205, R85206, R88749, R90730, R90754, R91006, R92221, H56130, H56210, H58500, H57659, H69479, H69882, N22547, N31579, N42592, N45537, N48687, N56654, N58050, N69059, N73728, N80748, N92927, N94545, W20471, W30838, W52039, W60171, W68292, W93085, W93140, N91563, AA010850, AA011289, AA054592, AA054780, AA081135, AA081214, AA081655, AA081936, AA082127, AA082262, AA088665, AA088804, AA102560, AA100239, AA114237, AA115714, AA115715, AA127304, AA127303, AA147789, AA148021, AA149821, AA152050, AA160878, AA169126, AA171659, AA172131, AA172285, AA194597, AA243129, AA419357, AA425135, AA426203, AA244212, AA505963, AA508221, AA527434, AA527878, AA565036, F17736, AA582605, AA582728, AA583851, AA586421, AA601920, AA570580, AA574367, AA577515, AA577538, AA565998, AA657417, AA659655, AA662658, AA665113, AA714991, AA770684, AA808865, AA826971, AA838507, AA876809, AA877842, AA878025, AA886042, AA886643, AA877950, AA937751, AA948428, AA947036, AA973473, AA983150, AA989361, A1082367, D78922, D82096, N83321, C04115, R29685, C17110, C18023, C18068, AA093539, AA094947, AA151399, AA654145, AA654136
835079	Preferably excluded from the present invention are	N25566, W00985, AA081340,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 486 of SEQ ID NO:413, b is an integer of 15 to 500, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:413, and where b is greater than or equal to a + 14.	AA152231, AA164282, AA171619, AA187113, A1073932
835554	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3383 of SEQ ID NO:414, b is an integer of 15 to 3397, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:414, and where b is greater than or equal to a + 14.	
835560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2866 of SEQ ID NO:415, b is an integer of 15 to 2880, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:415, and where b is greater than or equal to a + 14.	
835723	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1602 of SEQ ID NO:416, b is an integer of 15 to 1616, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:416, and where b is greater than or equal to a + 14.	T71562, R11480, R19383, R25309, R46659, R48802, R48913, R50038, R50376, R54963, R46659, R70030, R70077, R70161, R71380, R72303, R72352, R72772, R72773, R73386, R73387, H15775, H15776, H25239, H27204, H30499, H42026, H42613, H43207, H43254, H44314, H44936, H44975, R98394, R98395, R99071, R99271, H58902, H58903, H73590, H73436, H75566, H80599, N40440, N48475, N59703, AA515035, AA515043, AA515450, AA515650, AA515746, AA551788, AA551943, AA554602, AA557281, AA581549, AA581554, AA587399, AA593890, AA593997, AA593998, AA568878, AA568962, AA622458, AA714206, AA728962, AA737738, AA738036, AA738486, AA847538, AA865069, AA872029, AA886612, AA903381, AA916458, AA916464, AA922563, AA928617, AA928314, AA934581, AA973769, AA973767, AA983480, AA991199, AA994932, AA995182, AA999704, A1028371, AA643041
835791	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1801 of SEQ ID NO:417, b is an integer of 15 to 1815, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:417, and where b is greater than or equal to a + 14.	

835817	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:418, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:418, and where b is greater than or equal to a + 14.	
835840	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2838 of SEQ ID NO:419, b is an integer of 15 to 2852, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:419, and where b is greater than or equal to a + 14.	T66583, R15957, R22860, R62339, R62341, R62856, AA210836, AA214633, AA256340, AA732582, AA740735
836048	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2691 of SEQ ID NO:420, b is an integer of 15 to 2705, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:420, and where b is greater than or equal to a + 14.	
836898	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1887 of SEQ ID NO:421, b is an integer of 15 to 1901, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:421, and where b is greater than or equal to a + 14.	
836927	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2463 of SEQ ID NO:422, b is an integer of 15 to 2477, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:422, and where b is greater than or equal to a + 14.	
837344	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 763 of SEQ ID NO:423, b is an integer of 15 to 777, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:423, and where b is greater than or equal to a + 14.	
837789	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1635 of SEQ ID NO:424, b is an integer of 15 to 1649, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:424, and where b is greater than or equal to a + 14.	
838549	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1594 of SEQ ID NO:425, b is an integer of 15 to 1608, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:425, and where b is greater than or equal to a + 14.	
838754	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1780 of SEQ ID NO:426, b is an integer of 15 to 1794, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:426, and where b is greater than or equal to a + 14.	
838768	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 756 of SEQ ID NO:427, b is an integer of 15 to 770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:427, and where b is greater than or equal to a + 14.	
839486	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 498 of SEQ ID NO:428, b is an integer of 15 to 512, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:428, and where b is greater than or equal to a + 14.	
839561	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1456 of SEQ ID NO:429, b is an integer of 15 to 1470, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:429, and where b is greater than or equal to a + 14.	R61634, AA135004, AA159213
839816	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 420 of SEQ ID NO:430, b is an integer of 15 to 434, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:430, and where b is greater than or equal to a + 14.	
840068	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1809 of SEQ ID NO:431, b is an integer of 15 to 1823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:431, and where b is greater than or equal to a + 14.	
840279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 3377 of SEQ ID NO:432, b is an integer of 15 to 3391, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:432, and where b is greater than or equal to a + 14.	
840489	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2539 of SEQ ID NO:433, b is an integer of 15 to 2553, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:433, and where b is greater than or equal to a + 14.	
840538	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2518 of SEQ ID NO:434, b is an integer of 15 to 2532, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:434, and where b is greater than or equal to a + 14.	T47551, T47552, T64522, T65947, R70190, H97064, N25641, N34240, N48063, N53261, N67904, N92702, N98774, W16899, W20316, W31028, W40137, W45371, W48722, W48577, W68670, W68773, W74242, AA033573, AA033574, AA063270, AA063271, AA065213, AA064894, AA082200, AA083707, AA085441, AA085694, AA088302, AA088303, AA099844, AA099984, AA102604, AA111894, AA112981, AA115039, AA115800, AA115799, AA122221, AA126905, AA126955, AA127109, AA127548, AA127549, AA128933, AA129152, AA129743, AA133290, AA135251, AA151963, AA156321, AA156382, AA160182, AA165104, AA164688, AA173757, AA180038, AA182644, AA190866, AA190959, AA191561, AA191637, AA197348, AA195895, AA258593, AA258622, AA262173, AA464978, AA465047, AA417938, AA418116, AA292727, AA523585, AA525020, AA548516, AA551816, AA554642, AA581720, AA568802, AA579801, AA738216, AA832441, AA903391, AA938688, AA977201, AA987552, AI095102, AI084149, W27768, C05889, C06263, AA089556, AA652586, AA213999, AA213977, AA219123, AA219290, AA435695, D12383, D12389, AA451677, AA453222, AA485641, AA485768, AA488670, AA485947, AA486053, AA486197, AA489511, AA489512, AA489558, AA491452, AA489876, AA600130, AA608644, AA620481, AA664307, AA629754, AA629909, AA677148, AA722910, AA772440, AA773550, AI038219, AI075755, AI081932, AI084706, TI0852, T24678, F00208, F00897

840545	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1808 of SEQ ID NO:435, b is an integer of 15 to 1822, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:435, and where b is greater than or equal to a + 14.	
840549	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1016 of SEQ ID NO:436, b is an integer of 15 to 1030, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:436, and where b is greater than or equal to a + 14.	R10733, T86298, R55182, R55183, H00476, H00530, H25856, H25909, H25910, N50923, W84600, W84452, AA227897, D78774, AA486440, AA629249
840551	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1618 of SEQ ID NO:437, b is an integer of 15 to 1632, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:437, and where b is greater than or equal to a + 14.	
840557	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1002 of SEQ ID NO:438, b is an integer of 15 to 1016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:438, and where b is greater than or equal to a + 14.	
840561	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 580 of SEQ ID NO:439, b is an integer of 15 to 594, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:439, and where b is greater than or equal to a + 14.	
840562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1566 of SEQ ID NO:440, b is an integer of 15 to 1580, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:440, and where b is greater than or equal to a + 14.	R08937, R09046, R14796, R18307, R31150, R42283, R51828, R54224, R42283, R72104, R72156, R73118, R73171, R73943, H25904, H27191, H27192, H30471, H72478, H72879, H88214, H98231, W45061, W45071, W49842, W67423, W67424, W93880, W94151, AA023007, AA022473, AA032224, AA032282, AA034411, AA035691, AA040428, AA046861, AA046994, AA046313, AA046139, AA053780, AA101657, AA101658, AA167298, AA227543, AA227684, AA458877, AA459067, AA463656, AA464047, AA464754, AA225370, AA225425, AA225400, AA558796, AA582089, AA565830, AA713907,

		AA864510, AA936117, C01002, N86320, C04277, AA652714, AA402391, AA402565, AA479073, AA621791, AA670200, AA456544, AA676732, AA707089, A1014599, A1022852, A1023739, A1091873, A1094288, Z39517, Z43438
840564	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1068 of SEQ ID NO:441, b is an integer of 15 to 1082, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:441, and where b is greater than or equal to a + 14.	
840572	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1227 of SEQ ID NO:442, b is an integer of 15 to 1241, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:442, and where b is greater than or equal to a + 14.	T87514, T87515, H84879, AA001503, AA506411, AA508167, AA715396, AA931268, AA292666, AA478036, AA478193, AA478194, AA707886, AA724969, AA725050, AA779127, AA843885
840600	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 954 of SEQ ID NO:443, b is an integer of 15 to 968, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:443, and where b is greater than or equal to a + 14.	R38172, AA226748, AA484320, AA831852
840604	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1346 of SEQ ID NO:444, b is an integer of 15 to 1360, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:444, and where b is greater than or equal to a + 14.	
840608	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1821 of SEQ ID NO:445, b is an integer of 15 to 1835, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:445, and where b is greater than or equal to a + 14.	
840620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1341 of SEQ ID NO:446, b is an integer of 15 to 1355, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:446, and where b is greater than or equal to a + 14.	R17303, R41982, R41982, H43756, N62762, AA053677, AA053697, AA084224, AA084019, AA084952, AA419123, AA419160, AA426014, AA425077, AA427847, AA524035, AA565019, AA632254, AA745726, AA835832, AA931712, AA932520, AA937139, AA961716, AA995607, AA453838, AA455030, AA476981, AA479615, AA482659, AA455837,

		AA488554, AA620470, AA781416, AA844227, AI090902, T19161
840625	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 361 of SEQ ID NO:447, b is an integer of 15 to 375, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:447, and where b is greater than or equal to a + 14.	
840626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1379 of SEQ ID NO:448, b is an integer of 15 to 1393, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:448, and where b is greater than or equal to a + 14.	
840638	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1649 of SEQ ID NO:449, b is an integer of 15 to 1663, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:449, and where b is greater than or equal to a + 14.	H01158, H01159, H05751, H05858, H83341, H83695, N47512, N47513, W39756, W79733, W90027, W90155, AA047691, AA047741, AA086374, AA100549, AA159315, AA159414, AA282525, AA282633, AA595381, AA688093, AA744757, AA865203, AA933811, AA969838, AA975917, F18424, D12197, D12219, AA478596, AA665540, AA909221, AA969720, AI049820
840649	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1366 of SEQ ID NO:450, b is an integer of 15 to 1380, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:450, and where b is greater than or equal to a + 14.	R00133, R22651, R44356, R44356, R56353, R93194, N47106, N50316, N50780, N55139, AA010596, AA010597, AA012940, AA012888, AA013216, AA013313, AA017544, AA017417, AA047814, AA047792, AA235545, AA262268, AA262879, AA563873, AA570239, AA573586, AA827412, AA862337, AA902472, AA962409, AA971292, AA973596, AI056509, AI080455, AA410833, T23822, T16761
840651	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 912 of SEQ ID NO:451, b is an integer of 15 to 926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:451, and where b is greater than or equal to a + 14.	
840666	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1628 of SEQ ID NO:452, b is an integer of 15 to 1642, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:452, and where b is greater than or equal to a + 14.	N32778, N34353, N34537, N41780, N42818, N93337, W25190, AA035229, AA035230, AA044070, AA044162, AA195074, AA195174, AA419441, AA731906, AA761315, AA761330, AA766382, AA766593, AA769537, AA805515, AA806516, AA809893, AA814954, AA857917, N44554,

		AA393941, A1074651, T10618, Z35722
840681	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2240 of SEQ ID NO:453, b is an integer of 15 to 2254, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:453, and where b is greater than or equal to a + 14.	
840682	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1917 of SEQ ID NO:454, b is an integer of 15 to 1931, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:454, and where b is greater than or equal to a + 14.	
840684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 757 of SEQ ID NO:455, b is an integer of 15 to 771, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:455, and where b is greater than or equal to a + 14.	
840697	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1155 of SEQ ID NO:456, b is an integer of 15 to 1169, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:456, and where b is greater than or equal to a + 14.	R00751, R02584, R02703, R69879, R69927, H13156, H29249, H29248, H41216, R83398, H54666, H54667, H73551, H73552, H90468, H91760, H97869, N31729, N31735, N51232, W32147, W32175, W44313, W45660, W57760, W57761, W68386, W68502, W68752, W68835, W72538, W76163, AA035740, AA043246, AA043585, AA044419, AA043053, AA047593, AA047601, AA088798, AA147253, AA155747, AA160105, AA165689, AA172386, AA173747, AA189005, AA189006, AA471066, AA507210, AA513086, AA516406, AA514685, AA635861, AA657400, AA668796, AA737126, AA768005, AA768358, AA887459, AA977176, D80509, D81008, D81471, D81800, D82666, N83795, AA643662, AA284937, AA290823, AA447984, AA448126, AA676807, AA709464, AA780333, AA843801, AA853391, AA868403, AA917460, T17166, T17177, T16671, T48481, T48507
840698	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3235 of SEQ ID NO:457, b is an integer of 15 to 3249, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:457, and where b is	

	greater than or equal to $a + 14$.	
840708	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1902 of SEQ ID NO:458, b is an integer of 15 to 1916, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:458, and where b is greater than or equal to $a + 14$.	R21272, R45362, R45362, H06049, H13385, AA082768, AA101114, AA131634, AA131718, AA152290, AA150232, AA418083, AA418230, AA422115, AA424919, AA426139, AA741277, AA749290, AA811505, AA836102, AA411231, AA453804, AA453890, AA758905, AA769817, AA770192, AA904708, AA905158, AA969156, AI093952, Z42470, Z41665, Z44053
840714	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2759 of SEQ ID NO:459, b is an integer of 15 to 2773, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:459, and where b is greater than or equal to $a + 14$.	
840716	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2017 of SEQ ID NO:460, b is an integer of 15 to 2031, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:460, and where b is greater than or equal to $a + 14$.	
840721	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1825 of SEQ ID NO:461, b is an integer of 15 to 1839, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:461, and where b is greater than or equal to $a + 14$.	
840735	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 765 of SEQ ID NO:462, b is an integer of 15 to 779, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:462, and where b is greater than or equal to $a + 14$.	IT47277, T56085, T93319, T85388, H57620, H58465, N77902, N80219, N93978, W19715, W37380, W37643, W38508, W38722, W47048, W68079, W67976, W69349, W69350, AA025313, AA024560, AA063371, AA063370, AA463222, AA463223, AA424422, AA469264, AA480510, AA507733, AA524348, AA557233, AA602394, AA603318, AA631014, AA569554, AA575944, AA688112, AA911131, AA932225, AA937015, AA994856, AI077707, N92552, W00604, C00184, AA292823, AA401683, AA663906, AA664122, AA771943, AA779608, AA812529, AI028120, AI027559, AI032511, AI033880, AI034204, AI078458, AI041685, D31473, T64469
840738	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1703 of SEQ ID NO:463, b is an integer of 15 to 1717, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:463, and where b is greater than or equal to a + 14.	
840745	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 814 of SEQ ID NO:464, b is an integer of 15 to 828, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:464, and where b is greater than or equal to a + 14.	
840747	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1159 of SEQ ID NO:465, b is an integer of 15 to 1173, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:465, and where b is greater than or equal to a + 14.	
840756	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 507 of SEQ ID NO:466, b is an integer of 15 to 521, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:466, and where b is greater than or equal to a + 14.	AA074254
840776	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1414 of SEQ ID NO:467, b is an integer of 15 to 1428, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:467, and where b is greater than or equal to a + 14.	T47069, T47068, T63511, T63587, T79637, T79722, R36141, R36419, R65831, R65934, R69612, R69701, H00464, H00514, H04572, H04575, H12602, H12652, H13166, H66218, H67195, H67868, H67868, N62959, W92249, W92250, W92609, W95234, AA007598, AA193373, AA195360, AA195359, AA425046, AA430627, AA428172, AA484871, AA557201, AA902998, AA927360, N79862, AA479674, AA477192, AA481418, AA481651, AA495983, AA496377, AA496655, AA912146, AA912181, AI049805, AA693485
840784	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3449 of SEQ ID NO:468, b is an integer of 15 to 3463, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:468, and where b is greater than or equal to a + 14.	
840788	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 607 of SEQ ID	

	NO:469, b is an integer of 15 to 621, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:469, and where b is greater than or equal to a + 14.	
840794	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1819 of SEQ ID NO:470, b is an integer of 15 to 1833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:470, and where b is greater than or equal to a + 14.	
840797	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3188 of SEQ ID NO:471, b is an integer of 15 to 3202, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:471, and where b is greater than or equal to a + 14.	
840799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 927 of SEQ ID NO:472, b is an integer of 15 to 941, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:472, and where b is greater than or equal to a + 14.	
840818	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1265 of SEQ ID NO:473, b is an integer of 15 to 1279, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:473, and where b is greater than or equal to a + 14.	
840822	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3195 of SEQ ID NO:474, b is an integer of 15 to 3209, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:474, and where b is greater than or equal to a + 14.	T47621, T77305, T83423, R18484, R51973, R51974, R73192, H06082, H12940, H27135, H45895, H45904, N72089, W00342, W52213, W96404, AA045488, AA058907, AA062768, AA069032, AA081439, AA082427, AA084417, AA101216, AA234022, AA534011, AA565390, AA588319, AA588430, AA568701, AA635907, AA579930, AA827039, AA857519, AA872490, AA904077, AA995057, AI073336, N95359, C15883, AA781445, AA906492, AI037943, AI039428
840830	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 819 of SEQ ID NO:475, b is an integer of 15 to 833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:475, and where b is	N33920, N33932, N49642, N49629, AA508747, AA514767, AA583465, AA805203, AA878968, U37231, T24573

	greater than or equal to $a + 14$.	
840846	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1127 of SEQ ID NO:476. b is an integer of 15 to 1141, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:476, and where b is greater than or equal to $a + 14$.	T68706, T68719, T68771, T68784, T73424, T73431, T73486, T73492, T73499, T73535, T89865, R11465, T79345, T79774, T81799, T82119, T82855, T96198, T96454, T96686, T96802, T96920, T97027, T99996, T99997, R00156, R00157, R83404, R85816, R91357, R93314, R94713, R94794, R97348, R99024, R99798, H48280, H48369, H48754, H54738, H54739, H55985, H55984, H56050, H56244, H57662, H57872, H57873, H58502, H60170, H60211, H62933, H69203, H69228, H69229, H71630, H73011, H73012, H81193, H81194, H90826, H91385, N33963, N49672, N49822, N52577, N54836, N58435, N64440, N66934, N69249, N69373, N74062, N75759, N78025, N78145, N94249, N95116, W03303, W01169, W01912, N91401, AA025243, AA026028, AA193126, AA194255, AA236507, AA242995, AA622239, AA575858, AA575872, AA576026, AA576150, AA576597, AA864932, AA877934, AA969761, AA994970, AI017867, D82634, C21067, AA431221, AA779655, AA782374, AA812640, AA923315, AA962377, AA993251, AI018445, AI025584, AI092470, T79311
840848	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1088 of SEQ ID NO:477, b is an integer of 15 to 1102, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:477, and where b is greater than or equal to $a + 14$.	R10066, R10163, T26606, R61067, R72646, H08322, H47858, H47859, R86048, H68866, H68867, H69098, H82364, N58491, N78080, W52876, W60083, AA043086, AA045865, AA045866, AA055712, AA057298, AA058743, AA079887, AA079888, AA099233, AA099234, AA102153, AA113213, AA115932, AA121000, AA131067, AA143412, AA146598, AA155632, AA155688, AA160447, AA173257, AA173248, AA195987, AA196375, AA233537, AA463552, AA503072, AA551794, AA586410, AA594814, AA613123, AA573356, AA580449, AA731195, AA742856, AA827930, AA863440, AA865529, AA876847, AA953614, AA976924, N84278, N88762, C17112, AA219765, AA284503, AA293437, AA293046, AA669435, AA722103, AI027785, AI073617, AI092707, T17392, F08770, D12026
840860	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T89645, T89919, T93704, R21871, R22387, R78094, R78181, R78515,

	<p>sequence described by the general formula of a-b, where a is any integer between 1 to 4187 of SEQ ID NO:478, b is an integer of 15 to 4201, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:478, and where b is greater than or equal to a + 14.</p>	<p>R78560, H40124, H41731, N28359, N42893, N62851, N64787, N67463, N76199, N77065, N77758, W67341, W68381, AA034244, AA044935, AA045056, AA057392, AA057684, AA071214, AA071442, AA081937, AA082360, AA082229, AA082230, AA082708, AA083297, AA083188, AA127585, AA149575, AA151791, AA167113, AA173360, AA191227, AA195437, AA223329, AA223614, AA243268, AA261939, AA262815, AA262816, AA422160, AA426276, AA225924, AA504466, AA504634, AA522823, AA554566, AA632813, AA576873, AA662886, AA730326, AA748669, AA828942, AA837197, AA857065, AA857683, AA862276, AA864246, AA873317, AI083733, D82604, D82635, N81179, N85023, N85166, N85712, C00193, C00199, C02425, N87331, N88683, N88852, N89408, C02916, C05151, C06382, AA642209, C21319, AA091285, AA091688, AA094300, AA205974, AA206268, AA206598, AA205324, AA649340, AA247212, AA404505, AA421263, AA421361, D11545, AA441853, AA441826, AA463350, AA463858, AA487271, AA487388, AA496439, AA496488, AA634627, AA663685, AA665466, AA456144, AA722996, AA772136, AA772153, AA774179, AA992418, AI076734, T10506, Z30218, Z38961, T16262, T48571, D31110, D45597, F06042, F00682</p>
840861	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 773 of SEQ ID NO:479, b is an integer of 15 to 787, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:479, and where b is greater than or equal to a + 14.</p>	<p>T52180, T52256, T57048, T60934, T60993, T94137, T94228, T91060, T85924, R23216, R23292, R31316, R31576, R62640, R62693, H03198, H18231, H18269, H22414, H26112, H26116, H26378, H40754, H38895, H47721, H48072, R89134, R89141, R91829, R91836, R98452, H65626, H65627, H69728, H71913, H71914, H78844, H80090, H83062, H84585, H87467, H87577, H93457, H93458, N23179, N30549, N32644, N39052, N40455, N48060, N48244, N53258, N53755, N63557, N94559, N94883, N94981, N95791, N42987, W19445, W19573, W23831, W24902, W30850, W32700, W32701, W37523, W56867, W60497, W60972, W61219, W69268, W69346, W80426, W80556, W94817, W95832, W95966, W96035, W96092,</p>

		<p>N90310, AA010147, AA010148, AA025440, AA025757, AA027347, AA027822, AA027874, AA029650, AA029651, AA037779, AA039260, AA046801, AA046818, AA054707, AA058654, AA062684, AA063287, AA074876, AA074979, AA084381, AA085264, AA085328, AA085598, AA122190, AA120978, AA133892, AA129630, AA172403, AA172206, AA190489, AA190525, AA464455, AA464996, AA225769, AA259210, AA483109, AA483741, AA493542, AA502162, AA516183, AA522567, AA526813, AA557654, AA588882, AA593799, AA576216, AA659530, AA662308, AA688246, AA688254, AA687457, AA687516, AA689236, AA728852, AA729032, AA747479, AA747979, AA831447, AA887348, AA903105, AA916516, AA934714, AA953363, AA976759, AA991410, AA991434, AI002147, AI028033, N83338, C02469, R29174, AA090669, AA092066, AA648634, AA443968, AA444149, AA482243, AA482340, AA485406, AA598458, AA644566, AA664032, AA680199, AA676482, AA629708, AA630110, AA457100, AA431269, AA405296, AA405332, AA721997, AA724146, AA774657, AA781529, AA781641, AA781838, AA782849, AA813171, AA843229, AA846744, AA846814, AA854299, AA854765, AA789029, AA993047, AI023973, AI027725, AI031943, AI038463, AI041602, AI085085, AI086504, AI088189</p>
840871	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 717 of SEQ ID NO:480, b is an integer of 15 to 731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:480, and where b is greater than or equal to a + 14.</p>	<p>H42821, AA028094, AA099211, AA160368, AA223572, AA232552, AA252811</p>
840874	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1105 of SEQ ID NO:481, b is an integer of 15 to 1119, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:481, and where b is greater than or equal to a + 14.</p>	
840878	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,</p>	<p>T40405, T41252, T47240, T47241, T50233, T52891, T57110, T58359, R19508, R43858, R43858, R75598,</p>

	where a is any integer between 1 to 2042 of SEQ ID NO:482, b is an integer of 15 to 2056, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:482, and where b is greater than or equal to a + 14.	R75665, H13192, H13193, N25264, N31900, N42683, N72995, N93388, W25360, W47628, W47629, AA009691, AA009410, AA045777, AA045910, AA063040, AA063076, AA130044, AA149205, AA149206, AA191678, AA252698, AA464304, AA225264, AA514845, AA526726, AA548411, AA548704, AA552050, AA552558, AA568675, AA827017, AA834447, AA838450, AA886357, AA886653, AA887879, AA916602, AA928685, AA968793, A1005016, W28859, AA134038, AA455118, AA496380, AA496656, AA598830, AA653270, AA725217, AA733068, A1004394, A1023815, A1026954, A1040891, Z25388, Z28470, AA702322
840880	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 873 of SEQ ID NO:483, b is an integer of 15 to 887, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:483, and where b is greater than or equal to a + 14.	H02306, H02418, N48196, N53344, AA059013, AA506159, AA613938, AA662759, AA976725, AA854631
840884	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1864 of SEQ ID NO:484, b is an integer of 15 to 1878, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:484, and where b is greater than or equal to a + 14.	
840907	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1552 of SEQ ID NO:485, b is an integer of 15 to 1566, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:485, and where b is greater than or equal to a + 14.	
840926	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3032 of SEQ ID NO:486, b is an integer of 15 to 3046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:486, and where b is greater than or equal to a + 14.	
840932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1890 of SEQ ID NO:487, b is an integer of 15 to 1904, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:487, and where b is	

	greater than or equal to $a + 14$.	
840940	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 813 of SEQ ID NO:488, b is an integer of 15 to 827, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:488, and where b is greater than or equal to $a + 14$.	
840947	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1912 of SEQ ID NO:489, b is an integer of 15 to 1926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:489, and where b is greater than or equal to $a + 14$.	
840959	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1447 of SEQ ID NO:490, b is an integer of 15 to 1461, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:490, and where b is greater than or equal to $a + 14$.	
840964	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 791 of SEQ ID NO:491, b is an integer of 15 to 805, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:491, and where b is greater than or equal to $a + 14$.	R79226, H12332, H51062, H83364, H89523, N27508, N30527, N40233, N52503, N53855, N94367, AA055215, AA055306, AA188169, AA468498, AA470473, AA563662, AA622643, AA579613, AA668790, AA748160, AA765447, AA873430, AA879079, AA903275, AA970424, N73354, AA402259, AA883758, AA890505, AA906005, AI023931
840979	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2255 of SEQ ID NO:492, b is an integer of 15 to 2269, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:492, and where b is greater than or equal to $a + 14$.	
840984	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4094 of SEQ ID NO:493, b is an integer of 15 to 4108, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:493, and where b is greater than or equal to $a + 14$.	
840986	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2195 of SEQ ID NO:494, b is an integer of 15 to 2209, where both a and b correspond to the positions of nucleotide	H25393, H25394, H25511, H25512, R95750, R95794, H64076, H64131, H68715, H80548, H80604, H94681, H95039, H99481, N28293, N30167, N35782, W47389, W47262, W61304, W65368, AA054346, AA054383.

	residues shown in SEQ ID NO:494, and where b is greater than or equal to a + 14.	AA058320, AA058448, AA512954, AA558416, AA588459, AA935690, AI097565, N87339, AA993027, AA993568, AA701454, AA702350
840988	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1663 of SEQ ID NO:495, b is an integer of 15 to 1677, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:495, and where b is greater than or equal to a + 14.	T87048, R24473, R43337, R43337, N75007, W05750, AA182467, AA227466, AA504464, AA504538, AA923479, AA648887, AA663889, AI027636, AI028506, AI026720, Z42717
840990	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1688 of SEQ ID NO:496, b is an integer of 15 to 1702, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:496, and where b is greater than or equal to a + 14.	
840992	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2362 of SEQ ID NO:497, b is an integer of 15 to 2376, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:497, and where b is greater than or equal to a + 14.	
841009	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 826 of SEQ ID NO:498, b is an integer of 15 to 840, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:498, and where b is greater than or equal to a + 14.	T40334, T41195, T79150, T79231, T85615, T98895, T99485, R25796, H03311, H03312, H11314, H21245, R91754, R91755, R93025, R97834, R97886, R99577, R99583, R99683, R99689, H88057, H97799, H97870, N34019, N35363, N42786, N44738, N52502, N70158, N72884, N74746, N93542, N95357, N98354, W01181, W03108, W15165, W19587, W21350, W24700, W24805, W39226, W48682, W49637, W49739, W51977, W67546, W67528, W67665, W79731, W93828, W93829, AA025348, AA025356, AA024401, AA024402, AA029589, AA029588, AA099331, AA099865, AA121627, AA126717, AA126816, AA126817, AA133155, AA165162, AA165163, AA557332, AA640015, AA579505, AA665011, AA665221, AA738009, AA830748, AA918150, AA918992, AA947223, AA974955, AI083731, N56157, N89240, AA092060, AA094384, AA650291, AA292814, AA402491, F20671, F21115, D11655, D11564, D11605, D12048, AA634049, U54738, AA732766, AA782030, AA843638, AA860477, AA861482, AI018649,

841012	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 447 of SEQ ID NO:499, b is an integer of 15 to 461, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:499, and where b is greater than or equal to a + 14.	AI092171, Z28714, T23956, AA694568
841016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2768 of SEQ ID NO:500, b is an integer of 15 to 2782, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:500, and where b is greater than or equal to a + 14.	R21854, R21868, R23349, R27518, R63726, R63775, R65731, R65957, R65958, R66192, R66977, R66978, R67072, R69600, R69690, H12415, H12416, N46541, N47260, N47778, N48572, N51984, N95008, W25613, W31713, W32142, W38029, W38650, W38655, AA034256, AA037658, AA037660, AA039268, AA042908, AA042921, AA063533, AA126558, AA130121, AA130157, AA137270, AA136020, AA232954, AA233044, AA429346, AA429872, AA565520, AA604780, AA610435, AA631349, AA631518, AA740206, AA770618, AA912228, AI079705, N84191, N85956, N92894, W38030, C00380, N83173, C03262, AA092010, U82782, AA247592, AA284977, AA283619, AA291890, AA293636, AA410312, AA410537, AA453566, AA487623, AA626442, AA628932, AA629190, AA629753, AA629916, AA719528, AA843073, AA844228, AA890492, AI024670, AI051881, AI061324, T11149
841017	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1235 of SEQ ID NO:501, b is an integer of 15 to 1249, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:501, and where b is greater than or equal to a + 14.	R21764, R21815, N71125, W17312, AA112660, AA179538, AA179507, AA902202, AA907419, AA913594, AA994481, AI049652
841021	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1344 of SEQ ID NO:502, b is an integer of 15 to 1358, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:502, and where b is greater than or equal to a + 14.	R23836, W38704, AA033686, AA176734, AA192268, AA525913, AA531505, AA532666, AA533781, AA533827, AA533949, AA554396, AA576754, AA906883, N24273, C14272, C14285, C14286, C18998
841032	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 487 of SEQ ID NO:503, b is an integer of 15 to 501, where both a and b correspond to the positions of nucleotide	T41136, T52990, T52991, T61494, T63001, T63145, T87321, T87328, T89480, T84361, R05264, N75935, W05120, W25352, AA191627, AA258512, AA418549, AA224774, AA225253, AA229538, AA229537,

	residues shown in SEQ ID NO:503, and where b is greater than or equal to a + 14.	AA229951, AA230318, AA468106, AA468170, AA482814, AA482855, AA482894, AA482906, AA483676, AA491563, AA491627, AA492175, AA501375, AA502205, AA505498, AA508058, AA508125, AA512979, AA513165, AA523347, AA528170, AA531497, AA542840, AA551430, AA553992, AA554420, AA582164, AA583205, AA593192, AA593362, AA602125, AA603378, AA603728, AA617691, AA622865, AA630937, AA631991, AA570802, AA569520, AA654990, AA664728, AA664864, AA665278, AA729616, AA729639, AA729652, AA730512, AA730705, AA730910, AA737300, AA737303, AA736808, AA736909, AA738098, AA740165, AA740553, AA742574, AA742885, AA746988, AA747057, AA747094, AA747099, AA747961, AA748108, AA804727, AA805835, AA834105, AA838466, AA864527, AA872303, AA875939, AA876612, AA876936, AA879219, AA885735, AA886033, AA888159, AA888528, AA888683, AA903652, AA935001, AA948734, AA947836, AA978250, AA994661, AI073926, AI085517, N83676, N86451, N87989, AA642538, AA090432, AA090481, AA092225, AA091643, AA094678, AA094818, AA095214, AA648652, AA649783, AA650377, AA401641, F21163, AA411822, AA442212, AA609798, AA679909, F22052, AA679265, AA722456, AI003421, AI028430, AI077884, AI086743, T89286, R05321, AA694044
841051	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1997 of SEQ ID NO:504, b is an integer of 15 to 2011, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:504, and where b is greater than or equal to a + 14.	AA427363
841064	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1975 of SEQ ID NO:505, b is an integer of 15 to 1989, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:505, and where b is greater than or equal to a + 14.	R95695, H49073, H61707, H61911, H68517, H89719, H89781, H89828, H90680, N76870, W88654, W88898, AA046748, AA053076, AA053592, AA127256, AA127257, AA187351, AA188218, H67307, AA602545, AA720701, AA742288, N87596, AA094084, AA204976, AA676787, AA703221, AA779414, AI038609, AI074626, AI088527, T17364,

		AA702787
841069	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1071 of SEQ ID NO:506, b is an integer of 15 to 1085, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:506, and where b is greater than or equal to a + 14.	
841072	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1471 of SEQ ID NO:507, b is an integer of 15 to 1485, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:507, and where b is greater than or equal to a + 14.	
841078	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1916 of SEQ ID NO:508, b is an integer of 15 to 1930, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:508, and where b is greater than or equal to a + 14.	T39937, T68962, T84426, R20697, R36425, R45643, R45643, R68137, R70943, R70957, R70996, R71011, H02222, H05658, H05659, H25177, H29362, H54732, H54733, H60311, H60310, H77561, H77562, H78245, H78446, H82436, H82699, N20477, N57742, N59418, N59709, N76617, AA029237, AA055009, AA055434, AA236337, AA425703, AA427773, AA482193, AA482287, AA612777, AA729757, AA737276, AA744359, AA872776, AA972581, C06045, AA446583, AA449748, AA707197, AA757691, AA774691, AA992571, A1003756, A1027513, A1039704, A1042272, A1052652, A1077380, A1083949, AA774036
841080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1120 of SEQ ID NO:509, b is an integer of 15 to 1134, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:509, and where b is greater than or equal to a + 14.	
841088	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1368 of SEQ ID NO:510, b is an integer of 15 to 1382, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:510, and where b is greater than or equal to a + 14.	R00895, R21561, R42090, R42090, H05080, N79589, N94381, W16578, W42724, W42813, W46346, W46347, W47346, W57707, W57783, AA070469, AA490938, AA586820, AA580196, AA745683, AA809239, AA931405, D11601, AA725448, AA992145, A1023735, A1025359, A1031575, A1033697, A1038145, A1093535, F00072
841092	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1727 of SEQ ID	

	NO:511, b is an integer of 15 to 1741, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:511, and where b is greater than or equal to a + 14.	
841095	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1516 of SEQ ID NO:512, b is an integer of 15 to 1530, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:512, and where b is greater than or equal to a + 14.	W20114, AA255840, AA568302, AA406006, AA434170
841096	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2985 of SEQ ID NO:513, b is an integer of 15 to 2999, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:513, and where b is greater than or equal to a + 14.	
841102	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2034 of SEQ ID NO:514, b is an integer of 15 to 2048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:514, and where b is greater than or equal to a + 14.	
841104	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3286 of SEQ ID NO:515, b is an integer of 15 to 3300, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:515, and where b is greater than or equal to a + 14.	T93851, R05295, R05354, R71097, R71445, R99396, N53129, W38359, W38417, W38418, W39384, W44785, W44786, W69719, W69847, W73703, AA134718, AA164646, AA164647, AA418958, AA420439, AA420440, AA548241, AA548224, AA558195, W73847, Z19840, AA707354, AA868898, AA917430, A1073454, F09131, F11469, AA700476
841108	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3411 of SEQ ID NO:516, b is an integer of 15 to 3425, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:516, and where b is greater than or equal to a + 14.	T89709, T89806, T91163, T93774, T93819, T95226, R06420, R06475, R23277, R23370, R32742, R32743, R52354, R52355, R64095, R64184, R65984, R65985, R70225, R70226, R76344, R76672, R80205, H00679, H00770, H04254, H24758, H24803, H40273, H38053, H38054, H47116, H47210, R92478, R94873, R94872, H57866, H57867, H59353, H61105, H63261, H63535, H63938, H67759, H67760, H77384, H77385, H82932, H87435, H87541, H88753, H88754, N59081, N59489, N63682, N63939, N66851, N70709, N92122, N99845, W32595, W88585, W90769, W90327, W93082, W93137, AA025425, AA041232, AA114914, AA114913, AA128525, AA235362, AA235944,

		AA235945, AA425197, AA636023, AA639557, AA729723, AA907495, AI056355, AI089809, AA448599, AA449742, AA476262, AA478567, AA478700, AA599706, AA634117, AA677126, AA716562, AA923333, AA948589, AI051569, AI073816, AI074666, AI080341, AI084428, AI090962, AI096407
841118	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1344 of SEQ ID NO:517, b is an integer of 15 to 1358, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:517, and where b is greater than or equal to a + 14.	R20815, R36529, R38448, R46586, R46586, R71122, R71625, R77658, R80438, R80643, H12595, H12644, H99733, N20132, N25939, N29738, N57157, N59874, N67154, N67834, W03438, W04625, W31524, AA044199, AA044996, AA135739, AA135782, AA146912, AA146911, AA173589, AA224431, AA232224, AA256600, AA256599, AA419270, AA419321, AA425195, AA484744, AA507823, AA513832, AA584296, AA600955, AA614813, AA807248, AA904059, AA937796, AA973678, AA983325, AA991604, W01284, C16969, AA476260, AA476318, AA476367, AA609550, AA678511, AA722726, AA904676, AA954468, AI001869, AI031538, Z41297
841119	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1354 of SEQ ID NO:518, b is an integer of 15 to 1368, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:518, and where b is greater than or equal to a + 14.	R18472, W39766, AA076303, AA985235
841124	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 919 of SEQ ID NO:519, b is an integer of 15 to 933, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:519, and where b is greater than or equal to a + 14.	
841137	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1416 of SEQ ID NO:520, b is an integer of 15 to 1430, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:520, and where b is greater than or equal to a + 14.	T65560, R52978, R59392, H24368, H25185, N33308, AA016160, AA019434, AA082036, AA099724, AA099725, AA101466, AA100553, AA100634, AA100635, AA143046, AA150250, AA151129, AA165491, AA172129, AA176104, AA176248, AA176272, AA197310, AA227454, AA232220, AA243156, AA261904, AA262541, AA458854, AA459044, AA481155, AA493247, AA514323, AA522820, AA558368, AA582973, AA604489, AA640528, AA569125,

		AA569824, AA737640, AA743846, AA808232, AA812222, AA847813, AA865060, AA872242, AA872353, AA922866, AA933823, AA988358, AI056397, AI085865, AI088865, AA205921, AA205923, AA205997, AA204887, AA205731, D11887, AA634040, AA703823, AA703893, Z20424, AA707344, AA707416, AA716243, AA683201, AA890456, AI003274, AI076618, AI090177, T10877, Z28746, T25145, Z40353, F11026, F09670, AA699695, AA701137
841143	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1155 of SEQ ID NO:521, b is an integer of 15 to 1169, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:521, and where b is greater than or equal to a + 14.	T52948, T57468, T59332, T91403, T84637, R69314, R69315, R77481, R77675, R77676, H30692, H70576, N24036, N24905, N26173, N35858, N36029, W39771, W45303, W80648, W80649, AA029895, AA029983, AA036639, AA036850, AA043430, AA043431, AA046109, AA046196, AA076106, AA076107, AA083131, AA083181, AA083285, AA083293, AA147761, AA147804, AA155831, AA155741, AA430082, AA581553, AA593886, AA594233, AA604399, AA576339, AA715836, AA730946, AA737298, AA768251, AA872423, AA888276, AA961744, AA962699, AA975874, AI000132, R29417, AA640954, AA094702, AA398483, AA402600, AA489817, AA489948, AA496290, AA663953, AA663986, AA725581, AA771972, AA781165, AA845829, AA772618, AA773208, AA907551, AI003883, AI004593, AI031669, AI052123, AI085380
841148	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2148 of SEQ ID NO:522, b is an integer of 15 to 2162, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:522, and where b is greater than or equal to a + 14.	
841149	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 785 of SEQ ID NO:523, b is an integer of 15 to 799, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:523, and where b is greater than or equal to a + 14.	AA812937
841151	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1708 of SEQ ID NO:524, b is an integer of 15 to 1722, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:524, and where b is greater than or equal to a + 14.	
841155	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 548 of SEQ ID NO:525, b is an integer of 15 to 562, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:525, and where b is greater than or equal to a + 14.	
841161	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2009 of SEQ ID NO:526, b is an integer of 15 to 2023, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:526, and where b is greater than or equal to a + 14.	H81836, AA015599, AA099033, AA099034, AA211818, AA741499, AA748367, AA768854, AA805297, AA804217, A1000120, A1090415, D79280, D79875, AA628397, AA628438, AA889584, Z36757
841162	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2833 of SEQ ID NO:527, b is an integer of 15 to 2847, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:527, and where b is greater than or equal to a + 14.	T54529, T54568, T39916, T40885, T64421, T64740, T94433, T94519, T94763, T94764, T67443, T67536, T69533, R08782, R08783, T84049, T86084, R18023, R19657, R33054, R33948, R52119, R52216, R53248, R53249, R71311, H04393, H04418, H23196, H23309, H47118, R95161, H54791, H54843, H66487, H66488, H87522, H87523, H92220, H97204, H97637, H98041, N25008, N27036, N32850, N32940, N41677, N41803, N52911, N55243, N55603, N59425, N62367, N67146, N67527, N68040, N68109, N69439, N79136, W03264, W02511, W16533, W16511, W16949, W19590, W20032, W25683, W56022, W57870, W58141, W84752, W84757, W96458, W96558, N89892, N91494, AA035714, AA040577, AA040675, AA043889, AA052991, AA053277, AA053702, AA062923, AA063530, AA074314, AA074909, AA074744, AA076274, AA098982, AA099025, AA146894, AA146893, AA160127, AA160126, AA160195, AA160196, AA169764, AA169385, AA179301, AA223348, AA233558, AA235471, AA460676, AA420533, AA506563, AA523418, AA527621, AA528362, AA531060, AA532619, AA541282, AA552184, AA564466, AA564790, H98795, AA583450, AA613483, AA622733, AA627809, AA577550, AA578980, AA579413, AA714153, AA721494, AA721786, AA737104,

		AA738062, AA745852, AA746662, AA748113, AA814512, AA814515, AA848156, AA858182, AA877787, AA886219, AA886814, AA908510, AA919073, AA953828, AA971838, AA974669, AA974937, AA975070, AA978156, AA985412, AA985429, AA989103, AA989168, AA975750, AI053418, AI053736, AI053892, AI053967, AI053988, AI054073, AI054111, F18748, AI096767, W16689, F17979, W26593, W74635, R29761, AA090571, AA090284, AA092279, AA092676, AA174176, AA206002, AA206857, AA206939, AA204847, AA204862, AA205665, AA205777, C17805, AA215924, AA284942, AA285094, AA292514, AA293872, AA398296, AA401676, AA412021, AA450108, AA450173, AA477960, AA478675, AA479216, AA482218, AA608548, AA634838, AA634910, AA634951, AA644321, AA664196, AA665979, AA668238, AA668579, AA669764, AA669856, AA676279, AA630300, Z20366, AA716371, AA716380, Z19906, AA777040, AA778451, AA781061, AA845834, T25435, Z21568, AA772588, AA917780, AI003327, AI016140, AI024969, AI032559, AI056850, AI088269, AI090536, AI092597, AI093387, T15364, D29035, T27400, T27473, F02321, F06069, T69476, AA773898, AA694154
841163	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 802 of SEQ ID NO:528, b is an integer of 15 to 816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:528, and where b is greater than or equal to a + 14.</p>	T70512, W58177, W58266, AA027003, AA047260, AA057146, AA076110, AA150122, AA150030, AA424246, AA425670, AA523788, AA554661, AA582491, AA587000, AA633476, AA578397, AA662364, AA687611, AA729856, AA741041, AA806947, AA894899, AA922687, AA934486, AA946779, AA954606, AA962108, AA988276, AI054171, AA436000, AA436099, AA442324, AA451996, AA722958, AA780203, T25797, AI018410, AI024726, AI074321
841169	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 871 of SEQ ID NO:529, b is an integer of 15 to 885, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:529, and where b is greater than or equal to a + 14.</p>	
841172	<p>Preferably excluded from the present invention are</p>	T47968, H14181, H26893, N40884,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 728 of SEQ ID NO:530, b is an integer of 15 to 742, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:530, and where b is greater than or equal to a + 14.	Z42735
841174	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 511 of SEQ ID NO:531, b is an integer of 15 to 525, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:531, and where b is greater than or equal to a + 14.	
841179	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1911 of SEQ ID NO:532, b is an integer of 15 to 1925, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:532, and where b is greater than or equal to a + 14.	
841183	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 488 of SEQ ID NO:533, b is an integer of 15 to 502, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:533, and where b is greater than or equal to a + 14.	
841186	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1786 of SEQ ID NO:534, b is an integer of 15 to 1800, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:534, and where b is greater than or equal to a + 14.	
841204	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2483 of SEQ ID NO:535, b is an integer of 15 to 2497, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:535, and where b is greater than or equal to a + 14.	
841206	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4076 of SEQ ID NO:536, b is an integer of 15 to 4090, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:536, and where b is greater than or equal to a + 14.	
841207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	AA215286

	sequence described by the general formula of a-b, where a is any integer between 1 to 572 of SEQ ID NO:537, b is an integer of 15 to 586, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:537, and where b is greater than or equal to a + 14.	
841211	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1236 of SEQ ID NO:538, b is an integer of 15 to 1250, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:538, and where b is greater than or equal to a + 14.	
841225	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1336 of SEQ ID NO:539, b is an integer of 15 to 1350, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:539, and where b is greater than or equal to a + 14.	
841229	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2495 of SEQ ID NO:540, b is an integer of 15 to 2509, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:540, and where b is greater than or equal to a + 14.	
841237	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1729 of SEQ ID NO:541, b is an integer of 15 to 1743, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:541, and where b is greater than or equal to a + 14.	H39746, H38765, H53680, H84385, H84386, H95751, H96427, H96428, N22709, N24033, N27417, N27531, N31183, N34699, N35427, N40348, N46995, N47385, W47664, W52613, W58021, AA020909, AA032219, AA032277, AA036745, AA053732, AA055872, AA057318, AA062713, AA070398, AA134055, AA132315, AA132625, AA149601, AA149602, AA494458, AA516430, AA534386, AA582804, AA581987, AA588838, AA631158, AA635970, AA577392, AA577494, AA857008, AA894813, AA933084, AI000994, N47386, D11495, D11593, D12071, D11877, D11882, D11902, AA456436, AA683214, AA890528, AA983938, AI074406, AI084728
841241	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2196 of SEQ ID NO:542, b is an integer of 15 to 2210, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:542, and where b is greater than or equal to a + 14.	T64820, R18486, R48571, R48670, R51358, R51464, R70428, R71854, R77389, R77390, H18251, H18293, H18401, H18402, H19764, H19765, H21210, H21526, H24560, H25150, H26985, H28104, H30240, H30297, H30868, H30871, H40890, H41878, H41879, H43721, H43811, H43814,

		R84543, R85932, R87323, R93828, H49042, H49101, H51175, H51188, H68511, H75818, H80551, H80607, N41005, N45017, N56601, N70611, N74891, N93043, N93044, N94350, N98497, W04932, W21511, W21512, W24020, W31043, W47411, W47607, W47659, W47660, W48851, W48618, W52281, W56619, W56649, W68334, W68375, W70156, W70195, W84467, W84552, W90400, W94826, W96342, W96343, N91167, AA016293, AA017674, AA025151, AA025152, AA027955, AA031264, AA031395, AA031855, AA031854, AA035782, AA037318, AA040025, AA056359, AA069269, AA069418, AA069509, AA101608, AA114873, AA114837, AA115697, AA133516, AA220968, AA458530, AA460966, AA463596, AA419091, AA428836, AA507951, AA582836, AA640114, AA659114, AA836669, AA903136, AA903220, AA918099, AA928492, AA971856, AA973427, AA994099, AI016016, AI057267, AA069497, AA206877, AA218868, AA284783, AA284712, AA293434, AA293042, AA402851, AA454608, AA496283, AA609652, AA708123, AA757619, AA757695, AA774425, AA774630, AA775465, AA852435, AA852436, AA852604, AA852605, AA868271, AA884190, T03362, AI042345, AI042606, AI066399, AI086541, AI086967, AI091380, AI091725, AI092820, AI092945, T23722, F03416, F04814, F07127, F08608, F12341
841259	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1701 of SEQ ID NO:543, b is an integer of 15 to 1715, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:543, and where b is greater than or equal to a + 14.</p>	
841260	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3095 of SEQ ID NO:544, b is an integer of 15 to 3109, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:544, and where b is greater than or equal to a + 14.</p>	T93673, R01175, R01287, R72262, R72263, H53584, H53905, N57686, N59657, N63715, N98804, W86302, W86653, W87312, AA055614, AA058962, AA058961, AA149239, AA180323, AA460554, AA460555, AA492261, AA596073, AA604012, AA612811, AA617927, AA631804, AA767954, AA769298, AA804811, AA814647, AA833776, AA872768, AA873458, AA876551, AA886069,

		AA932445, AA976417, AA989268, AI055853, D80933, AI088938, AI096484, AA215901, AA393250, AA435612, AA449044, AA449758, AA653318, AA678103, AA678744, AA705036, AA854081, AA789188, AA813062, AA868902, AI023192, AI033456, AI090508, Z28555, T25877, D30980, D31048, D31377, F00724, AA682530, AA694353
841264	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1162 of SEQ ID NO:545, b is an integer of 15 to 1176, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:545, and where b is greater than or equal to a + 14.	
841275	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1721 of SEQ ID NO:546, b is an integer of 15 to 1735, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:546, and where b is greater than or equal to a + 14.	
841311	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1034 of SEQ ID NO:547, b is an integer of 15 to 1048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:547, and where b is greater than or equal to a + 14.	
841313	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 722 of SEQ ID NO:548, b is an integer of 15 to 736, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:548, and where b is greater than or equal to a + 14.	
841317	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2217 of SEQ ID NO:549, b is an integer of 15 to 2231, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:549, and where b is greater than or equal to a + 14.	T78127, R31279, R31890, R38014, R68187, R68186, R68960, R81444, R81647, H03085, H42975, N22228, N35405, N40226, N52138, N66461, N66470, W48764, W49783, W58388, AA044222, AA044341, AA131687, AA131731, AA224224, AA224527, AA469092, AA580878, AA573581, AA863153, AA903745, AA971415, C03879, AA249392, AA448556, AA449703, F22605, AA723322, AA904943, Z18868, AA971554, AA991799, AI015846, AI037913, AI056007, AI082497, AI090170, AI095394

841322	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1802 of SEQ ID NO:550, b is an integer of 15 to 1816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:550, and where b is greater than or equal to a + 14.	R21970, R83459, H65911, W76286, AA182592, AA281797, AA281874, AA291943, H65824, AA580660, AA748474, AA829390, AA293389, AA401755, AA910004, AA994494, AI005165, AI081877
841331	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2596 of SEQ ID NO:551, b is an integer of 15 to 2610, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:551, and where b is greater than or equal to a + 14.	
841332	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4007 of SEQ ID NO:552, b is an integer of 15 to 4021, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:552, and where b is greater than or equal to a + 14.	
841338	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1766 of SEQ ID NO:553, b is an integer of 15 to 1780, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:553, and where b is greater than or equal to a + 14.	
841345	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3699 of SEQ ID NO:554, b is an integer of 15 to 3713, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:554, and where b is greater than or equal to a + 14.	
841349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1983 of SEQ ID NO:555, b is an integer of 15 to 1997, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:555, and where b is greater than or equal to a + 14.	
841355	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 892 of SEQ ID NO:556, b is an integer of 15 to 906, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:556, and where b is greater than or equal to a + 14.	
841417	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3470 of SEQ ID NO:557, b is an integer of 15 to 3484, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:557, and where b is greater than or equal to a + 14.	
841548	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 776 of SEQ ID NO:558, b is an integer of 15 to 790, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:558, and where b is greater than or equal to a + 14.	AA223588
841632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 544 of SEQ ID NO:559, b is an integer of 15 to 558, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:559, and where b is greater than or equal to a + 14.	
841662	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 520 of SEQ ID NO:560, b is an integer of 15 to 534, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:560, and where b is greater than or equal to a + 14.	H15850, H99706, N78646, W74702, W94916, AA809695
841771	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3029 of SEQ ID NO:561, b is an integer of 15 to 3043, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:561, and where b is greater than or equal to a + 14.	T50029, T67900, T74699, T74819, T88802, T81298, T84439, T95656, R06092, R06196, R14563, R14966, R14970, R16465, R38948, R40957, R40957, R63975, R64085, R66362, R66363, R67505, H17644, H17758, R92097, H48240, H48331, H49625, H49715, H61167, H62068, H69147, N25753, N36472, N69035, N71493, N92970, N98567, N99536, W00665, W24251, W40582, W45462, W45538, W45525, W45687, W44315, W57971, W57944, W70012, W70013, W86733, AA044684, AA071192, AA071199, AA190325, AA191520, AA533197, AA558210, AA581106, AA581161, AA577119, AA857551, AA878885, AA936839, AA975697, D78980, W28535, C02075, C17857
841827	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1372 of SEQ ID NO:562, b is an integer of 15 to 1386, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:562, and where b is	

	greater than or equal to $a + 14$.	
841835	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2624 of SEQ ID NO:563, b is an integer of 15 to 2638, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:563, and where b is greater than or equal to $a + 14$.	
842259	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 677 of SEQ ID NO:564, b is an integer of 15 to 691, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:564, and where b is greater than or equal to $a + 14$.	
842463	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1953 of SEQ ID NO:565, b is an integer of 15 to 1967, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:565, and where b is greater than or equal to $a + 14$.	
842595	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1320 of SEQ ID NO:566, b is an integer of 15 to 1334, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:566, and where b is greater than or equal to $a + 14$.	
842722	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1596 of SEQ ID NO:567, b is an integer of 15 to 1610, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:567, and where b is greater than or equal to $a + 14$.	
842815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1398 of SEQ ID NO:568, b is an integer of 15 to 1412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:568, and where b is greater than or equal to $a + 14$.	
842818	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1111 of SEQ ID NO:569, b is an integer of 15 to 1125, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:569, and where b is greater than or equal to $a + 14$.	

843251	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1902 of SEQ ID NO:570, b is an integer of 15 to 1916, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:570, and where b is greater than or equal to a + 14.	
843422	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1239 of SEQ ID NO:571, b is an integer of 15 to 1253, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:571, and where b is greater than or equal to a + 14.	
843784	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1999 of SEQ ID NO:572, b is an integer of 15 to 2013, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:572, and where b is greater than or equal to a + 14.	
844017	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 655 of SEQ ID NO:573, b is an integer of 15 to 669, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:573, and where b is greater than or equal to a + 14.	AA075932
844138	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2418 of SEQ ID NO:574, b is an integer of 15 to 2432, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:574, and where b is greater than or equal to a + 14.	T54096, T54187, T54360, T39143, T40432, T90493, T90589, T89428, T89794, T80000, R00221, R00327, R25952, R26450, R26761, R28459, R55293, R55390, R73233, H42630, H44454, H44498, R83525, R86282, H85785, N33586, N34419, N36244, N48653, N49430, W51915, AA055530, AA055939, AA069732, AA100817, AA122084, AA121407, AA126332, AA133329, AA134151, AA134152, AA134714, AA136470, AA136960, AA157850, AA157906, AA157976, AA159365, AA171854, AA187219, AA186342, AA250818, AA464565, AA464666, AA428826, AA429361, AA491863, AA505512, AA524490, AA558038, AA581979, AA588712, AA593885, AA601110, AA573930, AA577156, AA578735, AA689519, AA730155, AA768486, AA805061, AA826981, AA865985, AA931167, AA947324, AA953202, AA961105, AA962413, AA976440, AA977760, AI032134, AI053416, AI053575,

		AI054013, AI054146, AI054281, U46376, W22126, C00371, C05283, AA641416, AA643346, AA292261, AA421818, AA496452, AA496521, AA653437, AA664399, AA680123, AA431832, AA434143, AA678582, AA705952, AA679763, AA733019, AA781645, AA813232, AA833597, AA844624, AI024151, AI038232, AI042551, AI080152, AI086490, T24101, F03522, F07244
844166	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1358 of SEQ ID NO:575, b is an integer of 15 to 1372, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:575, and where b is greater than or equal to a + 14.	
844194	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2006 of SEQ ID NO:576, b is an integer of 15 to 2020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:576, and where b is greater than or equal to a + 14.	
844394	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3147 of SEQ ID NO:577, b is an integer of 15 to 3161, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:577, and where b is greater than or equal to a + 14.	
844450	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2032 of SEQ ID NO:578, b is an integer of 15 to 2046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:578, and where b is greater than or equal to a + 14.	
844534	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 288 of SEQ ID NO:579, b is an integer of 15 to 302, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:579, and where b is greater than or equal to a + 14.	
844535	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3053 of SEQ ID NO:580, b is an integer of 15 to 3067, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:580, and where b is greater than or equal to a + 14.	
844644	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1560 of SEQ ID NO:581, b is an integer of 15 to 1574, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:581, and where b is greater than or equal to a + 14.	
844653	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 946 of SEQ ID NO:582, b is an integer of 15 to 960, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:582, and where b is greater than or equal to a + 14.	
844659	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 527 of SEQ ID NO:583, b is an integer of 15 to 541, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:583, and where b is greater than or equal to a + 14.	
844796	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2954 of SEQ ID NO:584, b is an integer of 15 to 2968, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:584, and where b is greater than or equal to a + 14.	
844812	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2594 of SEQ ID NO:585, b is an integer of 15 to 2608, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:585, and where b is greater than or equal to a + 14.	
844894	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1879 of SEQ ID NO:586, b is an integer of 15 to 1893, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:586, and where b is greater than or equal to a + 14.	
845361	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2449 of SEQ ID NO:587, b is an integer of 15 to 2463, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:587, and where b is	T93072, T93161, T69748, T70732, R01200, R01312, R05457, R05477, R05584, R43190, R43190, R65942, R75719, R78234, H03875, H03876, H15845, H16155, H17787, H40269, H45881, R84787, R92493, R92931, H58301, H58912, H58913, H62257,

	greater than or equal to $a + 14$.	H67051, H68135, H81385, H83681, H91363, H96711, N20348, N22509, N27952, N28616, N31997, N32005, N36007, N39356, N40718, N70011, N70094, N92576, N99870, W00896, W00925, W04623, W25220, W31522, W37278, W37791, W38868, W52654, W51751, AA017158, AA019458, AA022914, AA022915, AA037370, AA037502, AA045696, AA045697, AA046013, AA054565, AA054625, AA069778, AA079736, AA081087, AA081144, AA100055, AA100504, AA100334, AA115581, AA115554, AA126149, AA126373, AA133101, AA130558, AA136439, AA151673, AA151821, AA151822, AA159031, AA165200, AA165201, AA176477, AA176498, AA176771, AA176830, AA182601, AA176736, AA187943, AA188578, AA188675, AA190342, AA190343, AA195091, AA213662, AA213715, AA232222, AA426516, AA424760, AA483564, AA490859, AA491042, AA505249, AA507988, AA508858, AA513433, AA514771, AA514785, AA514980, AA527545, AA534100, AA554008, AA557148, AA584946, AA586481, AA587849, AA588781, AA593916, AA605049, AA604893, AA617650, AA568567, AA621979, AA627588, AA578585, AA578744, AA661910, AA729355, AA729902, AA736994, AA738388, AA740375, AA741213, AA760943, AA830401, AA834201, AA834208, AA834250, AA864864, AA888527, AA906940, AA922073, AA927272, AA931625, AA933055, AA932772, AA936861, AA938504, AA975187, AA977857, AA975594, AI000724, AI014600, AI017381, AI066441, D82733, U47688, N83708, N83790, N85010, W22533, W23255, N86314, N87393, N88971, AA642249, AA642903, AA090403, AA091011, AA095990, AA205824, AA204931, AA643262, AA648446, AA216706, AA219615, AA249170, C75338, AA599187, AA668746, AA670340, AA405611, AA405150, AA708635, AA716044, AA722076, AA722829, AA725716, AA781064, AA844379, AI037987, AI039577, AI078722, AI077655, AI080306, AI084320, AI085219, AI093296, AI093479, AI095168, AI095267, D29018, F02782,
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		F06502, F00762, F00966
845620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1931 of SEQ ID NO:588, b is an integer of 15 to 1945, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:588, and where b is greater than or equal to a + 14.	
845639	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 802 of SEQ ID NO:589, b is an integer of 15 to 816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:589, and where b is greater than or equal to a + 14.	
845660	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2293 of SEQ ID NO:590, b is an integer of 15 to 2307, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:590, and where b is greater than or equal to a + 14.	
845720	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1424 of SEQ ID NO:591, b is an integer of 15 to 1438, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:591, and where b is greater than or equal to a + 14.	
845785	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1064 of SEQ ID NO:592, b is an integer of 15 to 1078, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:592, and where b is greater than or equal to a + 14.	
845897	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2478 of SEQ ID NO:593, b is an integer of 15 to 2492, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:593, and where b is greater than or equal to a + 14.	
845922	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1890 of SEQ ID NO:594, b is an integer of 15 to 1904, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:594, and where b is greater than or equal to a + 14.	

846016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 323 of SEQ ID NO:595, b is an integer of 15 to 337, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:595, and where b is greater than or equal to a + 14.	
846040	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1274 of SEQ ID NO:596, b is an integer of 15 to 1288, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:596, and where b is greater than or equal to a + 14.	
846073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1038 of SEQ ID NO:597, b is an integer of 15 to 1052, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:597, and where b is greater than or equal to a + 14.	T83567, T83771, R51147, N26938, N32715, N36666, W57781, W74108, AA082091, AA425613
846257	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2079 of SEQ ID NO:598, b is an integer of 15 to 2093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:598, and where b is greater than or equal to a + 14.	

Polynucleotide and Polypeptide Variants

The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, and/or the cDNA sequence contained in a cDNA clone contained in the deposit.

- 5 The present invention also encompasses variants of the cancer polypeptide sequence disclosed in SEQ ID NO:Y, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

- 10 "Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

- 15 The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the related cDNA contained in a deposited library or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polypeptides encoded by these nucleic acid molecules are also encompassed by the invention. In another embodiment, the invention encompasses nucleic acid molecules which comprise or alternatively consist of, a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under low stringency conditions, to the nucleotide coding sequence in SEQ ID NO:X, the nucleotide coding sequence of the related cDNA clone contained in a deposited library, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which
- 20
- 25
- 30

hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

The present invention is also directed to polypeptides which comprise, or alternatively
5 consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%,
99% or 100% identical to, for example, the polypeptide sequence shown in SEQ ID NO:Y, a
polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide
sequence encoded by the cDNA in the related cDNA clone contained in a deposited library,
and/or polypeptide fragments of any of these polypeptides (e.g., those fragments described
10 herein). Polynucleotides which hybridize to the complement of the nucleic acid molecules
encoding these polypeptides under stringent hybridization conditions, or alternatively, under
lower stringency conditions, are also encompassed by the invention, as are polypeptides
encoded by these polynucleotides.

By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical"
15 to a reference nucleotide sequence of the present invention, it is intended that the nucleotide
sequence of the nucleic acid is identical to the reference sequence except that the nucleotide
sequence may include up to five point mutations per each 100 nucleotides of the reference
nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid
having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to
20 5% of the nucleotides in the reference sequence may be deleted or substituted with another
nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference
sequence may be inserted into the reference sequence. The query sequence may be, for
example, an entire sequence referred to in Table 1, an ORF (open reading frame), or any
fragment specified as described herein.

25 As a practical matter, whether any particular nucleic acid molecule or polypeptide is
at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of
the present invention can be determined conventionally using known computer programs. A
preferred method for determining the best overall match between a query sequence (a
sequence of the present invention) and a subject sequence, also referred to as a global
30 sequence alignment, can be determined using the FASTDB computer program based on the
algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment
the query and subject sequences are both DNA sequences. An RNA sequence can be

compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other

manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that
5 the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur
10 at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence in SEQ ID
15 NO:Y or a fragment thereof, the amino acid sequence encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present
20 invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237- 245(1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a
25 FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal
30 deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences

truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C- terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which less than 50, less

than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, as discussed herein, one or more amino acids can be deleted from the N-terminus or C-terminus of the polypeptide of the present invention without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., *J. Biotechnology* 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (*J. Biol. Chem* 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, as discussed herein, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more

biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show a functional activity (e.g., biological activity) of the polypeptide of the invention of which they are a variant. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity.

The present application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein or fragments thereof, (e.g., including but not limited to fragments encoding a polypeptide having the amino acid sequence of an N and/or C terminal deletion), irrespective of whether they encode a polypeptide having functional activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having functional activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having functional activity include, inter alia, (1) isolating a gene or allelic or splice variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the gene, as described in Verma et al., Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York (1988); and (3) Northern Blot analysis for detecting mRNA expression in specific tissues.

Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, which do, in fact, encode a polypeptide having a functional activity of a polypeptide of the invention.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to, for example, the nucleic acid sequence of the cDNA in the related cDNA clone contained in a

deposited library, the nucleic acid sequence referred to in Table 1 (SEQ ID NO:X), or fragments thereof, will encode polypeptides "having functional activity." In fact, since degenerate variants of any of these nucleotide sequences all encode the same polypeptide, in many instances, this will be clear to the skilled artisan even without performing the above
5 described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having functional activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as
10 further described below.

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid
15 sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have
20 been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For
25 example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly
30 tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side

chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly. Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a polypeptide having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid substitutions. Of course it is highly preferable for a polypeptide to have an amino acid sequence which comprises the amino acid sequence of a polypeptide of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library which contains, in order of ever-increasing preference, at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1

amino acid substitutions. In specific embodiments, the number of additions, substitutions, and/or deletions in the amino acid sequence of SEQ ID NO:Y or fragments thereof (e.g., the mature form and/or other fragments described herein), an amino acid sequence encoded by SEQ ID NO:X or fragments thereof, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or fragments thereof, is 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, conservative amino acid substitutions are preferable.

Polynucleotide and Polypeptide Fragments

The present invention is also directed to polynucleotide fragments of the cancer polynucleotides (nucleic acids) of the invention. In the present invention, a "polynucleotide fragment" refers, for example, to a polynucleotide having a nucleic acid sequence which: is a portion of the cDNA contained in a deposited cDNA clone; or is a portion of a polynucleotide sequence encoding the polypeptide encoded by the cDNA contained in a deposited cDNA clone; or is a portion of the polynucleotide sequence in SEQ ID NO:X or the complementary strand thereto; or is a polynucleotide sequence encoding a portion of the polypeptide of SEQ ID NO:Y; or is a polynucleotide sequence encoding a portion of a polypeptide encoded by SEQ ID NO:X or the complementary strand thereto. The nucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, at least about 100 nt, at least about 125 nt or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from, for example, the sequence contained in the cDNA in a related cDNA clone contained in a deposited library, the nucleotide sequence shown in SEQ ID NO:X or the complementary strand thereto. In this context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., at least 150, 175, 200, 250, 500, 600, 1000, or 2000 nucleotides in length) are also encompassed by the invention.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900,

901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-
5 2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, and 3551 to the end of SEQ ID NO:X, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3,
10 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of the polypeptide encoded by the polynucleotide of which the sequence is a portion. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these nucleic acid molecules under stringent hybridization
15 conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or fragments.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-
20 400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-
25 2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, and 3551 to the end of the cDNA nucleotide sequence contained in the deposited cDNA clone, or the complementary strand thereto. In this context "about" includes the particularly
30 recited range, or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of the polypeptide encoded by the cDNA

nucleotide sequence contained in the deposited cDNA clone. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these fragments under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as
5 are polypeptides encoded by these polynucleotides or fragments.

In the present invention, a "polypeptide fragment" refers to an amino acid sequence which is a portion of that contained in SEQ ID NO:Y, a portion of an amino acid sequence encoded by the polynucleotide sequence of SEQ ID NO:X, and/or encoded by the cDNA contained in the related cDNA clone contained in a deposited library. Protein (polypeptide)
10 fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, an amino acid sequence from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, 161-180,
15 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100,
20 1101-1120, 1121-1140, 1141-1160, 1161-1180, and 1181 to the end of SEQ ID NO:Y. Moreover, polypeptide fragments of the invention may be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, or ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either terminus or at both
25 termini. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

Even if deletion of one or more amino acids from the N-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still
30 be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are

removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, polypeptide fragments of the invention include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

The present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in the related cDNA clone contained in a deposited library). In particular, N-terminal deletions may be described by the general formula m-q, where q is a whole integer representing the total number of amino acid residues in a polypeptide of the invention (e.g., the polypeptide disclosed in SEQ ID NO:Y), and m is defined as any integer ranging from 2 to q-6. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example the ability of the shortened mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic

activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

5 Accordingly, the present invention further provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in deposited cDNA clone referenced in Table I). In particular, C-terminal deletions may be
10 described by the general formula 1-n, where n is any whole integer ranging from 6 to q-1, and where n corresponds to the position of an amino acid residue in a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention.

 In addition, any of the above described N- or C-terminal deletions can be combined to
15 produce a N- and C-terminal deleted polypeptide. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of a polypeptide encoded by SEQ ID NO:X (e.g., including, but not limited to, the preferred polypeptide disclosed as SEQ ID NO:Y), and/or the cDNA in the related cDNA clone contained in a deposited library, where n
20 and m are integers as described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

 Any polypeptide sequence contained in the polypeptide of SEQ ID NO:Y, encoded by the polynucleotide sequences set forth as SEQ ID NO:X, or encoded by the cDNA in the related cDNA clone contained in a deposited library may be analyzed to determine certain
25 preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ ID NO:X, or the cDNA in a deposited cDNA clone may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA; <http://www.dnastar.com/>).⁹

 Polypeptide regions that may be routinely obtained using the DNASTAR computer
30 algorithm include, but are not limited to, Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Eisenberg alpha- and

beta-amphipathic regions, Karplus-Schulz flexible regions, Emini surface-forming regions and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides of the invention in this regard are those that encode polypeptides comprising regions that combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out
5 above.

Additionally, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Emini surface-forming regions, and Jameson-Wolf regions of high antigenic index (i.e., containing four or more contiguous amino acids having an antigenic index of greater than or equal to 1.5, as identified using the default parameters of the Jameson-Wolf program) can routinely be
10 used to determine polypeptide regions that exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from data by DNASTAR analysis by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

15 Preferred polypeptide fragments of the invention are fragments comprising, or alternatively consisting of, an amino acid sequence that displays a functional activity of the polypeptide sequence of which the amino acid sequence is a fragment.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length
20 (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

25 Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

In preferred embodiments, polypeptides of the invention comprise, or alternatively
30 consist of, one, two, three, four, five or more of the antigenic fragments of the polypeptide of SEQ ID NO:Y, or portions thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Table 4.

Sequence/ Contig ID	Epitope
507291	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 843 as residues: Pro-12 to Pro-20, Lys-27 to Gly-34, Pro-67 to Arg-72, Asp-102 to Thr-111, Asp-136 to Gly-142, Ser-153 to Pro-158.
508000	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 844 as residues: Ala-16 to Trp-35.
518325	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 845 as residues: Glu-60 to Asp-67.
523111	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 846 as residues: Ser-1 to Gln-10.
532211	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 848 as residues: Cys-17 to Arg-22.
532247	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 849 as residues: Val-4 to His-10.
537932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 850 as residues: Ser-62 to Gly-68.
540117	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 851 as residues: Pro-24 to Arg-30, Met-101 to Phe-106, Thr-138 to Asn-153.
547710	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 852 as residues: Asp-1 to Arg-7, Glu-25 to His-31, Ile-51 to Lys-56, Pro-61 to Pro-67, Gly-113 to Thr-119, Lys-125 to Asp-130, His-335 to Gly-340, Arg-364 to Pro-371.
551747	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 853 as residues: Lys-79 to Ala-88, Ser-109 to Leu-125, Asp-155 to Lys-163, Tyr-211 to Thr-219, Pro-221 to Ala-226.
552799	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 854 as residues: Gln-81 to Thr-114, Gln-200 to Arg-206.
553243	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 855 as residues: Ala-43 to Asp-48, Asp-64 to Lys-69, His-88 to Thr-94, Ala-107 to Phe-113, Leu-117 to Ser-125, Thr-132 to Glu-138, Ser-169 to Trp-181, Ser-194 to Thr-200.
553368	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 856 as residues: Ser-52 to Arg-57, Leu-76 to Gly-82, Ser-91 to Glu-96, Tyr-132 to Ala-147.
554349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 857 as residues: Ala-31 to Gly-36, Ala-68 to Tyr-75, Gln-121 to Asp-127.
558491	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 858 as residues: Pro-1 to Arg-10.
558983	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 859 as residues: Pro-37 to Gly-42, Val-67 to Lys-84, Gln-122 to Gly-127.
589390	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 862 as residues: Glu-14 to Asn-19, Arg-68 to Ser-74, Ser-79 to Ala-84, Lys-95 to Ile-101, Lys-125 to Glu-138.
596882	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 863 as residues: Lys-15 to Lys-23, Pro-29 to Gly-34.
616289	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 864 as residues: Leu-1 to Pro-13, Thr-64 to Gly-70, Lys-119 to Arg-130.
622140	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 865 as residues: Ser-1 to Lys-6, Pro-16 to Ser-23, Arg-49 to Glu-58.
647714	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 867 as residues: Arg-1 to Gly-9, Glu-27 to Gly-36, Pro-72 to Phe-86, Pro-104 to Cys-111, Gln-145 to Lys-162, Arg-226 to Trp-233.
652156	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 871 as residues: Asn-30 to Ile-43, Ile-76 to Lys-81.
653010	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 872 as

	residues: Ser-1 to Ala-10.
655904	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 873 as residues: Ala-21 to Cys-27, Ser-76 to Gly-87, Ser-112 to Trp-121, Trp-128 to Asn-133, Glu-225 to Cys-231, Tyr-238 to Cys-248, Lys-269 to Asp-279, Phe-292 to Thr-298, Cys-357 to Ala-362, Pro-383 to Pro-388, Lys-412 to Lys-420.
657852	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 874 as residues: Arg-10 to Lys-22, Gln-48 to Glu-53, Arg-73 to Asn-86.
666414	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 875 as residues: Asn-9 to Lys-19, Arg-27 to Gly-32, Ser-58 to Thr-70, Ala-81 to Pro-86.
670188	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 877 as residues: Asn-68 to Ser-75.
670279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 878 as residues: Lys-86 to Lys-91, Glu-101 to Val-120, Ala-130 to Glu-136.
670729	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 879 as residues: Ala-116 to Asp-134.
676496	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 881 as residues: Ile-1 to Arg-8.
678248	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 883 as residues: Ala-16 to Lys-22, Tyr-30 to Asn-35, Asp-61 to Val-70, Arg-129 to Asn-135, Thr-142 to Gly-148.
683668	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 884 as residues: Ser-3 to Gly-28, Gly-46 to Pro-56, Gly-70 to Ile-92, Gln-102 to Ser-117, Ala-123 to Pro-129, Pro-135 to Leu-140, Pro-150 to Asp-158, Pro-165 to Pro-177, Gln-188 to Asp-205, Ile-230 to Arg-245, His-251 to Trp-260, Asp-262 to Cys-267, Asn-296 to Arg-307, Glu-322 to Pro-330, Ile-351 to Asn-357, Asp-363 to Leu-369, Glu-386 to Phe-391, Lys-415 to Ser-420.
693172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 885 as residues: Arg-11 to Arg-18, Pro-51 to Lys-58.
694303	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 886 as residues: Pro-12 to Ser-17, Leu-30 to Cys-39, Val-49 to Pro-54, Pro-67 to Leu-73, Pro-84 to Gln-90, His-99 to Leu-109.
695042	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 887 as residues: Ser-4 to Trp-28, Pro-51 to Leu-56, Asn-64 to His-70.
699799	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 888 as residues: Gln-17 to Phe-25, Glu-42 to Tyr-48, Val-52 to Gly-57, Pro-67 to Ser-73, Thr-97 to Gln-106, Gln-113 to Leu-123, Arg-171 to Asp-178, Arg-184 to Leu-191, Ile-195 to Phe-203, Lys-212 to Glu-217, Ala-236 to Asp-244, Arg-255 to Leu-260, Lys-266 to His-273, Glu-357 to Glu-363.
703015	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 890 as residues: Pro-27 to Asp-37, Gly-55 to Pro-61, His-96 to Ala-101, Glu-151 to Asn-156, Tyr-166 to Cys-178.
706391	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 891 as residues: Pro-22 to Ala-34, Pro-40 to Glu-52.
706924	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 893 as residues: Gly-1 to Gly-9, Gln-21 to Met-27.
707642	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 894 as residues: Glu-33 to Lys-40, Asn-55 to Lys-64, Tyr-104 to Cys-110, Ser-138 to Arg-148, Arg-157 to Gly-163, Lys-165 to Asn-172.
710369	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 895 as residues: Asn-1 to Thr-10.
718826	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 896 as residues: Ser-57 to Pro-63, Lys-93 to Ser-99.
719790	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 897 as residues: Phe-4 to Gln-23, Glu-47 to Ala-56, Asn-95 to Gln-102, Gln-109 to Glu-115, Arg-168 to Glu-175, Thr-196 to Arg-201, Lys-209 to Asp-215, Val-236 to Val-243.
720222	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 898 as

	residues: Glu-37 to Arg-43, Gly-62 to Pro-67, Gly-95 to Val-101, Gln-109 to Asp-114, Ala-137 to Phe-145, Asp-181 to Ser-188.
724033	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 899 as residues: Glu-55 to Glu-60, Asp-76 to Ser-85, Lys-106 to Asp-111, Gln-131 to Arg-137, Ala-172 to Gly-218.
724767	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 900 as residues: Leu-49 to Tyr-56, Tyr-114 to Glu-136, Arg-142 to Gly-148.
727065	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 901 as residues: Asn-41 to Gly-46, Lys-82 to His-88, Glu-107 to His-112, Leu-127 to Asp-132, Phe-163 to Phe-175, Thr-202 to Ile-209, Lys-229 to Gly-237, Ala-239 to Tyr-245.
727246	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 902 as residues: Pro-2 to Gly-10.
739448	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 908 as residues: His-2 to Leu-8, Gln-33 to Glu-40, Ala-44 to Glu-55, Gly-57 to Ser-67, Glu-70 to Ala-84, Glu-95 to Lys-111, Ile-186 to Asp-205, Leu-232 to Asp-238.
740060	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 910 as residues: Pro-44 to Thr-50, Arg-72 to Lys-80, Tyr-241 to Asn-251, Lys-273 to Gly-282, Ser-302 to Asn-312, Pro-337 to Ser-343, Ile-367 to Asp-376, Gly-395 to Tyr-417, Ser-442 to Gln-448.
741560	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 911 as residues: Gln-33 to Tyr-39, Pro-42 to Phe-47.
742543	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 912 as residues: Phe-10 to Tyr-15, Glu-139 to Asp-144, Glu-166 to Asn-171, Lys-175 to Glu-181.
742831	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 913 as residues: Val-64 to Glu-69.
745327	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 914 as residues: Arg-1 to Pro-13, Pro-54 to Ala-61.
745695	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 915 as residues: Trp-130 to Ser-135, Leu-199 to Thr-210, Ser-221 to Gln-229, Ala-249 to Tyr-255, Pro-257 to Pro-267, Ser-309 to Arg-314.
750316	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 916 as residues: Pro-18 to Asn-24, Thr-65 to Asp-70.
750522	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 917 as residues: Gln-10 to Lys-15.
750583	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 918 as residues: Lys-9 to Thr-15, Gln-32 to Gln-40.
751020	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 919 as residues: Arg-39 to Leu-47, Ser-107 to Ile-117, Pro-135 to Gln-144.
752196	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 920 as residues: Lys-20 to Lys-28.
753084	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 921 as residues: Lys-84 to Thr-98, Arg-128 to Ser-134, Arg-244 to Asn-252, Lys-365 to His-372.
754957	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 922 as residues: Pro-101 to Glu-106, Glu-116 to Asp-127, Ser-199 to Ile-210, Asp-217 to Asp-229, Ser-239 to Gly-244, Gln-262 to Asn-273, Pro-279 to Ser-284, Lys-318 to Arg-326, Lys-334 to Ile-341.
756557	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 923 as residues: Val-13 to Phe-21, Ile-55 to Pro-63, Ser-69 to Leu-74, Arg-82 to Leu-96, Asn-131 to Leu-139, Ile-156 to Thr-164, Thr-241 to Leu-249, Gly-273 to Ser-279, Thr-282 to Arg-289.
756712	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 924 as residues: Ile-4 to Thr-37, Gln-42 to Ser-48, Asn-56 to Lys-69, Ser-79 to Ser-85.
757414	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 925 as residues: Glu-14 to Thr-23, His-50 to Arg-62, Tyr-72 to Cys-78, Gly-121 to Pro-128.

757614	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 926 as residues: Gly-13 to Cys-19, Thr-32 to Glu-38, Val-44 to Gln-53, Lys-55 to Asp-60, Gln-65 to Glu-70, Lys-89 to Glu-105, Glu-112 to Asp-142, Glu-147 to Arg-152, Glu-211 to Leu-216, Leu-227 to Ser-232, Lys-245 to Lys-255, Glu-278 to Tyr-291, Gln-297 to Arg-303.
759878	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 928 as residues: Trp-16 to Glu-21, Trp-45 to Pro-54, Ile-154 to Phe-162, Gly-174 to Leu-181.
760227	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 929 as residues: Arg-99 to Asp-104.
766051	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 931 as residues: Asp-10 to Lys-19.
768053	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 933 as residues: Ile-1 to Tyr-7, Phe-52 to Cys-61, Val-118 to Ser-125.
768055	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 934 as residues: Asp-39 to Ser-46, Lys-92 to Lys-99, Val-165 to Phe-172, Lys-252 to Ala-261, Asn-268 to Ala-273.
769685	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 935 as residues: Pro-129 to Arg-135.
771920	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 936 as residues: Pro-47 to Val-53, Asp-85 to Phe-97, Val-136 to Gly-144, Pro-166 to Glu-172, Leu-190 to Ser-197.
772790	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 937 as residues: Leu-5 to Trp-13, Met-20 to Leu-39, Ile-50 to Pro-63, Glu-66 to Ser-72, Leu-112 to Gln-120, Ala-141 to Lys-146, Tyr-165 to Asp-173.
772916	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 938 as residues: Lys-16 to Arg-25.
773632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 940 as residues: Arg-1 to His-33.
774364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 941 as residues: Ser-97 to Asn-103.
775355	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 942 as residues: Ser-40 to Ala-46.
775844	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 943 as residues: Leu-20 to Ser-31, Thr-38 to Val-47.
777760	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 944 as residues: Thr-22 to Ser-28, Thr-35 to Glu-42, Met-47 to Thr-55.
779837	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 945 as residues: Thr-26 to Arg-31, Leu-75 to Lys-100.
780769	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 946 as residues: Gly-1 to Asp-7, Lys-25 to Lys-31, Tyr-65 to Gly-70, Thr-100 to Arg-106, Pro-118 to Glu-124, Lys-162 to Ser-172, Leu-176 to Leu-182.
781445	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 947 as residues: Asn-33 to Lys-38, Leu-67 to Met-73, Ser-111 to Lys-121, Lys-127 to Leu-134, Pro-153 to Trp-158, Lys-237 to Met-249, Pro-280 to Tyr-292.
781531	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 948 as residues: Ala-8 to Pro-23, Gln-56 to Cys-61, Asn-66 to Pro-72.
783018	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 949 as residues: Asn-4 to Leu-17, Gly-19 to Phe-26, Pro-37 to Glu-43, Val-58 to Ser-64, Gln-80 to Gly-85.
783097	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 950 as residues: Pro-1 to Asp-9, Pro-24 to Gly-40, Pro-47 to Thr-55, Gln-62 to Ser-76.
784198	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 951 as residues: Met-1 to Arg-15, Leu-43 to Glu-48, Asp-55 to Asp-62, Ser-111 to Lys-160.
784868	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 952 as residues: Trp-8 to Gly-17, Glu-20 to Arg-35, Gly-40 to Cys-45, Ser-59 to Ser-64, Ala-73 to Leu-78, Val-85 to Leu-91, Arg-130 to Lys-135, Leu-138 to Glu-146, Pro-188 to

	Pro-194, Ser-206 to Cys-212, Ser-232 to Ala-246, Asp-293 to Ser-298.
785428	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 953 as residues: Arg-9 to Met-20, Glu-28 to Gly-33, Asn-49 to Lys-57, Thr-67 to Arg-75, Ser-81 to Leu-87, Glu-103 to Thr-109, Pro-115 to Ile-120, Asn-146 to Ser-174, Ser-177 to His-195, Met-197 to Ile-221, Asp-232 to Glu-240, Glu-289 to Phe-302, Cys-306 to Arg-314, Ser-357 to Ser-366, Lys-385 to Glu-401, Val-419 to Asp-427.
785845	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 954 as residues: Arg-41 to Asp-52, Pro-82 to Arg-94, Pro-102 to Gln-107, Gln-170 to Tyr-181, Glu-248 to Lys-254, Asp-277 to Gly-287, Ala-302 to Arg-308, Thr-367 to Gly-374.
785854	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 955 as residues: Asp-1 to Asp-17, Cys-59 to Asp-65.
787279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 958 as residues: Lys-13 to Lys-20.
789002	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 959 as residues: Met-20 to Glu-29.
789008	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 960 as residues: Ser-24 to Arg-33, Ile-44 to Gly-57, Arg-63 to Asn-72, Ile-76 to Pro-82.
789555	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 961 as residues: Trp-106 to Thr-117, Trp-156 to Gln-163, Gln-173 to Asp-178, Gln-227 to Glu-233, Gln-255 to Glu-261, Glu-297 to Tyr-306, Thr-339 to Val-345, Leu-378 to Ile-385, Asp-414 to Lys-420, Cys-437 to Ile-444, Thr-491 to Gln-497, Glu-509 to Ser-515, Lys-526 to Glu-538.
789631	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 962 as residues: Thr-10 to Gly-18.
789779	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 963 as residues: Glu-1 to Ala-13, Leu-103 to Ser-109.
790387	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 964 as residues: His-1 to Ala-12.
790461	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 965 as residues: Glu-14 to Gly-23, Asp-47 to Met-53, Ala-55 to Thr-60, Pro-67 to Thr-73, Pro-78 to Gly-86, Tyr-91 to Pro-101, Ala-133 to Asn-139, Glu-169 to Gln-182, Glu-189 to Thr-195, Asn-197 to Arg-203, Gln-265 to Asp-271.
790931	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 966 as residues: Val-3 to Glu-13, Pro-29 to Pro-35, Glu-116 to Arg-125.
791176	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 967 as residues: Pro-1 to Pro-10, Pro-17 to Phe-28, Ser-61 to Pro-67.
792539	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 969 as residues: Ser-12 to Trp-17, Gln-20 to Lys-29, Asp-45 to Glu-51, Tyr-75 to Lys-83, Arg-103 to Gly-119, Gln-145 to Lys-155, Lys-166 to Leu-180, Thr-195 to Gly-203, Gln-209 to Val-219, Ser-222 to Ala-244, Leu-251 to Leu-260, Lys-277 to Lys-285.
792749	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 970 as residues: Ala-22 to Asp-41, Thr-61 to Met-66, Asp-191 to Lys-198, Arg-280 to Phe-287, Thr-289 to Lys-299, Pro-325 to Asp-332, Ser-351 to Arg-357.
793206	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 972 as residues: Gly-1 to Arg-6, Gln-11 to Arg-22, Glu-86 to Asp-91.
793626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 974 as residues: Ser-1 to Gly-13, Gly-17 to Asn-26.
794417	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 975 as residues: Ser-7 to Trp-16.
795197	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 976 as residues: Ser-67 to Glu-73, Arg-129 to Gly-136, Phe-154 to Ala-161, Tyr-198 to Tyr-203, Pro-206 to Asp-212, Glu-222 to Cys-231.
795251	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 977 as residues: Phe-44 to Ser-50, Asp-57 to Pro-62, Asn-80 to His-90, Ser-110 to Ala-115, Ile-141 to Val-148, Glu-155 to Thr-173, Val-202 to Pro-217, Ile-221 to Val-229, Thr-

	233 to Ser-243, Val-253 to Thr-259, Ala-290 to Asn-320, Pro-322 to Ile-330, Ala-333 to Met-344, Val-362 to Leu-367, Asp-397 to Val-402, Glu-422 to Gly-448, Met-453 to Gly-460.
795752	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 978 as residues: Pro-52 to Asn-63, Pro-70 to Ile-79, Arg-93 to Gln-111.
796261	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 979 as residues: His-1 to Val-6, Cys-10 to Ser-15, Gly-26 to Ser-34, Trp-36 to Pro-58, Pro-96 to Thr-102, Pro-111 to Tyr-116, Phe-131 to Gly-138, Pro-184 to Leu-190, Glu-237 to Gly-244, Pro-255 to Lys-267, Lys-271 to Leu-280.
796933	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 980 as residues: Arg-1 to Pro-14, Gln-47 to Cys-52, Asn-57 to Pro-63, Ser-277 to Lys-282.
799424	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 981 as residues: Tyr-18 to Leu-27, Met-50 to Met-60, Leu-169 to His-178, Ser-233 to Ser-241.
799698	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 982 as residues: Pro-16 to Pro-21, Ala-54 to Glu-61, Ala-96 to Gly-105.
800351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 983 as residues: Gly-21 to Gln-34, His-39 to Lys-53, Ser-63 to Tyr-71.
800573	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 984 as residues: Asp-33 to Arg-39, Ala-43 to Leu-48, Glu-256 to Gln-266, Gly-305 to Ile-311, Pro-314 to Ala-320, Gln-388 to Asn-394.
805815	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 985 as residues: Arg-1 to Lys-22, Ser-34 to Arg-48, Thr-64 to Arg-70, Pro-81 to Phe-89, Arg-148 to Asn-154, Tyr-172 to Asp-185, Ser-205 to Asp-216, Tyr-278 to His-285, His-294 to Pro-299, Glu-326 to Gly-333, Gly-336 to Ser-345.
806445	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 986 as residues: Arg-15 to Gly-24, Lys-26 to Trp-32.
810309	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 987 as residues: Pro-33 to Phe-50, Ile-57 to Gly-62, Gln-72 to Asn-85, Ala-87 to Thr-172.
811022	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 988 as residues: Ala-1 to Met-11, Gln-62 to Trp-68, Ala-89 to Val-99.
811023	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 989 as residues: Tyr-54 to Lys-61, Met-64 to Thr-70.
811143	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 990 as residues: Ala-1 to Ser-7, Ser-19 to Gly-36, Arg-53 to Pro-58, Thr-87 to Glu-102, Arg-115 to Tyr-120, Thr-159 to Thr-164, Ala-171 to Ser-179, Ala-206 to Pro-217, Pro-224 to Ala-233, Arg-253 to Ser-259.
813000	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 993 as residues: Tyr-25 to Lys-30, Lys-36 to Ile-43, Lys-52 to Gln-69, Glu-76 to Asp-81, Arg-92 to Trp-104, Leu-120 to Lys-126, Ser-129 to Ser-135, Ser-139 to Thr-156, Pro-165 to Glu-178, Ser-181 to Thr-186, Tyr-196 to Lys-201, Cys-225 to Lys-230, Glu-234 to Ser-242.
813431	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 995 as residues: Leu-23 to His-29, Pro-38 to Leu-46, Ser-59 to Gly-68, Pro-85 to Lys-108, Arg-119 to Phe-124, Ser-139 to Lys-156.
813450	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 996 as residues: Asn-1 to Trp-10.
813478	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 997 as residues: Ala-8 to Arg-14, Ile-64 to Thr-69, Val-94 to Asp-101, His-112 to Gln-117, Tyr-139 to Glu-145, Tyr-195 to Cys-208, Gly-216 to Gly-223, Asp-297 to Ser-307, Gly-378 to Leu-383, Ile-391 to Pro-404, Asn-451 to Ser-466.
813505	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 998 as residues: Thr-1 to Ala-20, Pro-22 to Lys-27, His-44 to Thr-51, Pro-53 to Thr-60, Arg-62 to Lys-79, Lys-97 to Asn-103, Pro-139 to Lys-144.
815552	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 999 as residues: Pro-1 to Ser-6, Pro-25 to Cys-31, Arg-142 to Lys-150.

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815606	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1000 as residues: Arg-1 to Ala-11.
816048	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1001 as residues: Ala-13 to Thr-24, Glu-30 to Gln-39, Arg-69 to Gly-77, Gln-119 to Gly-126, Tyr-156 to Asn-162, Ser-184 to Gly-191.
823981	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1004 as residues: Lys-1 to Cys-7, Ala-11 to Lys-17, Glu-90 to Ile-95, Asn-141 to Arg-148, Leu-158 to Ala-163, Ala-171 to Thr-177.
824364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1005 as residues: Gln-43 to Gly-54.
824423	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1006 as residues: Cys-33 to Arg-42, Val-53 to Met-63, Lys-71 to Lys-78, Gly-107 to Pro-118, Ala-159 to Leu-165, Val-272 to Arg-284, Pro-422 to Pro-427, Arg-437 to Gln-443, Ala-474 to Asp-482, His-519 to Cys-525, Ala-529 to Gln-535, Arg-540 to Gln-548.
825279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1007 as residues: Ser-8 to Arg-14, Asp-23 to Gly-28, Ser-30 to Pro-37, His-52 to Ala-57, Pro-65 to Ser-74, Pro-112 to Ser-118, Ala-181 to Pro-189.
825548	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1009 as residues: Pro-2 to Ser-9.
825725	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1010 as residues: Pro-1 to Gly-8, Leu-95 to Lys-100, Glu-118 to Thr-125, Ser-162 to Lys-167, Arg-201 to Tyr-206.
827079	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1012 as residues: Arg-9 to Ser-17.
827153	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1013 as residues: Val-32 to Ala-44, Pro-49 to Ser-57, Gln-77 to Gly-82, Asp-116 to Gly-127, Arg-165 to Asn-172.
827351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1014 as residues: Gly-5 to Lys-11, Ser-59 to Lys-67, Glu-130 to Arg-136, Asn-176 to Leu-183.
827503	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1015 as residues: Asp-61 to Val-67, Arg-113 to Asp-119, Ser-180 to Gly-191, Pro-199 to Ser-211, Ser-228 to Asn-238, Gly-276 to Ser-286, His-343 to Gly-351, Gln-354 to Arg-366, Leu-368 to Gln-382, Pro-393 to Ser-400, Asp-412 to Cys-418, Gly-430 to Leu-435, Gln-445 to Asp-450, Lys-484 to Val-491, Leu-513 to Gly-520.
827563	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1016 as residues: Pro-69 to Ala-81, Pro-84 to Gly-91, Ala-106 to Leu-112, Arg-216 to Lys-224, Trp-239 to Gly-250.
827565	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1017 as residues: Ala-1 to Ser-8, Ser-88 to Gly-96, Asn-121 to Asp-128, Cys-191 to Gly-196, Met-242 to Thr-248.
827893	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1018 as residues: Ser-41 to Ala-50, Glu-72 to His-77, Ala-120 to Glu-125, Thr-144 to Ile-153.
828072	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1019 as residues: Lys-30 to Leu-35.
828241	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1021 as residues: Gly-35 to Phe-45, Pro-47 to Arg-55, Glu-62 to Leu-70, Arg-102 to Tyr-111, Phe-128 to Gln-134, Val-139 to Met-144, Ser-180 to Gly-188, Lys-214 to Leu-219, Ser-241 to Glu-246, Phe-292 to Thr-298.
828287	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1022 as residues: Ala-12 to Thr-21, Ala-23 to Gly-31, Leu-43 to Gly-51, Lys-127 to Val-134.
828371	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1024 as residues: Gln-1 to Ala-6, Lys-50 to Pro-71, Pro-98 to Ser-111, Asp-148 to His-164, Asp-185 to Arg-191, Asp-238 to Gly-244, Pro-262 to Cys-274.
828403	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1025 as residues: Gly-1 to Trp-15, Arg-73 to Leu-82.
828501	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1026 as

	residues: Arg-99 to Arg-105, Pro-171 to Ser-176, Lys-189 to Val-195, Lys-291 to Ala-296.
828527	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1028 as residues: Glu-58 to Cys-63.
828538	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1029 as residues: Pro-9 to Thr-24, Thr-46 to Gly-52, Ser-70 to Thr-76, Ser-142 to Thr-149, Pro-154 to Ser-171, Glu-189 to Ser-196.
828541	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1030 as residues: Arg-9 to Pro-23, Gln-64 to Leu-69, Asp-76 to Asn-83, Lys-88 to Gln-93, Pro-129 to Thr-135, Gly-194 to Gly-203, Asp-223 to Gly-231, Thr-265 to Ile-281, Leu-287 to Lys-297.
828549	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1031 as residues: Pro-22 to Asn-28.
828562	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1032 as residues: Arg-26 to Asp-33, Asp-42 to Pro-58, Thr-63 to Lys-70, Thr-103 to Asp-114.
828576	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1033 as residues: Arg-11 to Gly-17, Pro-26 to Gly-31, Ala-48 to His-58.
828602	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1034 as residues: Tyr-1 to Met-8, Leu-10 to Lys-26, Pro-47 to Pro-54, Lys-128 to Ser-133.
828628	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1035 as residues: Thr-124 to Thr-129, Gly-136 to Phe-142, Asp-164 to His-171, Asp-180 to Tyr-194.
828684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1037 as residues: Ser-16 to Thr-22, Arg-39 to Ala-51, Arg-60 to Gly-65, Thr-67 to Arg-90, Lys-109 to Gln-125, Ser-146 to Arg-159, Gln-166 to Thr-176, Glu-192 to Tyr-197, Val-267 to His-279, Ala-351 to Gly-356, Phe-363 to Gly-368, Gly-387 to Arg-392, Asp-488 to Ala-498.
828727	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1038 as residues: Gly-14 to Val-21, Asp-40 to Gln-57, Gln-86 to Tyr-93, Gln-98 to Asp-104, Lys-124 to Asp-130, Gln-138 to Cys-156, Tyr-170 to Gln-175, Gln-196 to Ala-201.
828734	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1039 as residues: Asp-5 to Trp-19, Ile-37 to Pro-42, Asp-52 to Asp-72, Glu-85 to Ser-92, Ser-107 to Leu-117, Asp-128 to His-147.
828842	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1041 as residues: Ala-25 to Phe-32, Glu-54 to Ser-61, Thr-74 to Glu-79, Glu-99 to Lys-105, Glu-112 to Glu-121.
828843	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1042 as residues: Pro-3 to Asn-11, Gln-46 to Ala-51, Asn-62 to Lys-74, Val-108 to Gln-113, Arg-119 to Gly-163, Ala-223 to Lys-237.
828851	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1043 as residues: Thr-3 to Lys-8, Leu-63 to Val-70, Lys-141 to Val-149, Ile-326 to Thr-333.
828856	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1044 as residues: Leu-1 to Gly-10.
828862	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1045 as residues: Pro-1 to Pro-9, Arg-81 to Glu-87, Gln-114 to Glu-119.
828870	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1046 as residues: Ser-1 to Gly-18, Trp-25 to Gly-31, Arg-46 to Ser-52, Ala-103 to Ala-108, Ser-154 to Gly-165, Gln-228 to Pro-236, Ser-284 to Gly-291, Ala-321 to Asp-327, Lys-377 to Asn-394, Asp-406 to Ser-416.
828873	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1047 as residues: Tyr-15 to Gly-20, Asn-72 to Asp-80, Pro-105 to Pro-110, Gln-149 to Arg-154, Glu-161 to Gly-167, Ile-312 to Asp-318, Lys-353 to Leu-361, Arg-379 to Thr-385, Pro-423 to Trp-435, Pro-437 to Cys-444, Asn-450 to Met-466.
828892	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1048 as residues: Asp-19 to Asn-25, Gly-67 to Glu-79.
828893	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1049 as

	residues: Ser-55 to Thr-60, Glu-97 to Ser-103, Thr-164 to Glu-170, Gly-192 to Gly-197, Leu-204 to Ser-218, Ala-238 to Ser-250, Asp-265 to Tyr-292, Gly-298 to Gly-307, Gly-351 to Met-359, Phe-389 to Glu-400.
828897	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1050 as residues: Phe-28 to Arg-33.
828910	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1051 as residues: His-1 to Ile-13, Arg-20 to Glu-64, Arg-83 to Gln-89, Tyr-145 to Asp-152.
828927	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1052 as residues: Glu-10 to Pro-21, Thr-54 to Gly-60, Cys-79 to Glu-90, Lys-154 to Lys-159.
828932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1053 as residues: Arg-1 to Arg-9, Phe-54 to Pro-60, Gln-74 to Gly-90, Asn-114 to Gly-119, Cys-124 to Ser-132, Thr-139 to Leu-151, Asp-171 to Lys-182, Ala-188 to Leu-193, Val-203 to Trp-222, Lys-230 to Glu-236, Glu-244 to Asp-250, Leu-258 to Gly-268, Gly-283 to Asp-288, Ser-291 to Trp-297, Gly-300 to Ala-308.
828933	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1054 as residues: Glu-21 to Ser-34, Thr-130 to Tyr-138.
828941	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1055 as residues: Gly-1 to Ala-6, Pro-15 to Gly-22, Asn-160 to Gln-177, Asn-193 to Asp-199, Glu-205 to Leu-211.
828963	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1057 as residues: Pro-48 to Gly-54, Ser-56 to Ser-76, Lys-102 to Pro-107, Ser-146 to Gly-153, Ser-208 to Arg-213, Tyr-285 to Leu-299, Pro-314 to Phe-319, Asn-322 to Asn-327.
828964	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1058 as residues: Thr-36 to Cys-47.
828966	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1059 as residues: Gly-1 to Ser-16, Met-26 to Pro-31, Lys-128 to Glu-134, His-165 to Gln-170, Asp-207 to Asn-216, Pro-348 to Arg-359, Lys-433 to Ala-439, Gly-448 to Tyr-457.
828967	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1060 as residues: Met-135 to Arg-141, Gly-149 to Lys-166, Ile-188 to Ser-196, Gly-203 to Tyr-213, Gln-267 to Asp-278, Arg-298 to Trp-317, Leu-319 to Leu-326, Gln-344 to Thr-349, Pro-410 to Ser-419, Ala-500 to Ala-510.
828977	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1061 as residues: Gly-32 to Tyr-42, Asn-52 to Glu-58, Ser-78 to Gly-87, Lys-97 to Gly-109, Glu-116 to Arg-127, Pro-147 to Pro-152, Pro-162 to Asn-171, Leu-179 to Glu-185, Ile-203 to Glu-208, Val-222 to Gln-228.
828978	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1062 as residues: Asp-24 to Lys-30, Arg-49 to Lys-62, Arg-121 to Thr-149, Gly-163 to Leu-171, Ala-186 to Glu-195, Glu-216 to Ser-221, Ile-229 to Ser-236, Lys-258 to Lys-264, Lys-305 to Arg-313.
829001	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1064 as residues: Thr-11 to Cys-24, Arg-48 to His-55, Arg-62 to Gly-70.
829003	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1065 as residues: Lys-14 to Gly-22, Ser-61 to Asp-66, Cys-80 to Lys-91, Lys-97 to Arg-107, Gly-135 to Asn-146, Lys-198 to Lys-208, Met-221 to Thr-227, Phe-244 to Gly-256, Asp-292 to Gln-300.
829016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1066 as residues: Arg-1 to Asp-11, Ala-17 to Gln-25, Glu-30 to His-37, Cys-39 to Thr-44, Asn-86 to Phe-93.
829027	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1067 as residues: Pro-1 to Ser-7, Thr-45 to Leu-63, Arg-113 to Thr-118, Pro-172 to Gly-182.
829028	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1068 as residues: Ser-1 to Gln-19, Gly-32 to Phe-39, Ala-95 to Arg-116, Lys-122 to Glu-142, Ile-148 to Asn-156, Ser-168 to Asn-191, Ala-196 to Thr-204, Ser-289 to Lys-304, Leu-308 to Ser-314, Thr-332 to Ile-341.
829034	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1070 as residues: Ser-32 to Ala-43, Thr-62 to Glu-69, Phe-128 to Thr-156, Thr-179 to His-188,

	Gly-196 to Glu-203, Pro-205 to Ala-219, Gln-221 to Ile-230, Pro-246 to Thr-255, Thr-271 to His-276, Asn-324 to Thr-344, Pro-364 to Ala-370, Tyr-427 to Arg-434, Gly-440 to Pro-445.
829036	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1071 as residues: Leu-16 to Phe-21, Thr-69 to Lys-74, Asn-87 to His-92, Thr-126 to Leu-137, Phe-154 to Lys-164, Ala-171 to Asp-178, Ile-192 to Thr-203, Glu-261 to Ser-273.
829049	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1072 as residues: Gly-50 to Tyr-59.
829073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1073 as residues: Asn-1 to Met-6, Asn-26 to Ser-35, Pro-43 to Ile-54.
829075	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1074 as residues: Gly-14 to Pro-30, Ser-64 to Ser-69, Asn-97 to Arg-109.
829076	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1075 as residues: Lys-84 to Gly-94, Asn-142 to Ile-147.
829080	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1076 as residues: Gly-13 to Trp-23, Pro-39 to Gly-44.
829087	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1077 as residues: Pro-13 to Arg-24.
829095	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1079 as residues: Pro-8 to Pro-13.
829118	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1081 as residues: Arg-7 to Val-12, Ile-52 to Thr-70, Ser-86 to Asp-91, Thr-126 to Ser-138.
829152	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1082 as residues: Asp-12 to Ser-19.
829160	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1083 as residues: Ala-7 to Arg-20.
829163	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1084 as residues: Ser-23 to Asp-32, Val-36 to Glu-59, Ser-65 to Asn-76, Cys-91 to Ser-102, Pro-108 to Leu-115, Thr-151 to Gln-164, Glu-167 to Lys-176.
829176	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1085 as residues: His-1 to Asn-8, Cys-22 to Arg-27, Gly-34 to Ser-44, Tyr-60 to Ser-65, Ser-118 to Gln-123, Ser-149 to Trp-154, Pro-159 to Gly-168, Gln-207 to Leu-220.
829204	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1086 as residues: Ala-11 to Ser-19, Thr-104 to Lys-133.
829207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1087 as residues: Lys-5 to Ser-11, Pro-31 to Ser-37, Pro-87 to Asp-92, Asp-115 to Lys-123, Ser-149 to Arg-155, Thr-243 to Pro-253.
829228	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1088 as residues: Pro-1 to Trp-6, Leu-73 to Tyr-79, Glu-108 to Thr-117, Asp-136 to Asp-142, Ser-201 to Pro-207, Leu-224 to Pro-233, Val-242 to Ala-248, Ser-312 to Leu-319, Val-349 to Ser-359, Ala-362 to His-368, Thr-370 to Gly-376, Lys-403 to Tyr-409, Glu-426 to Arg-431, Lys-455 to Asp-460, Arg-499 to Thr-505, Asp-561 to Ser-570, Ser-665 to Ser-673.
829252	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1089 as residues: Thr-9 to Val-16.
829269	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1091 as residues: Ser-1 to Glu-7, Lys-76 to Gln-83.
829277	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1092 as residues: Lys-88 to Phe-97, Thr-106 to Leu-120, Thr-147 to Pro-152, Pro-173 to Met-179.
829290	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1093 as residues: Pro-1 to Pro-19, Pro-25 to Lys-30.
829308	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1096 as residues: Met-26 to Asn-37, Glu-42 to Gln-51, Thr-68 to Ser-95, Ala-97 to Lys-113, Asp-156 to Val-161, Val-208 to Asp-215, Pro-217 to Ala-228.
829349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1097 as

	residues: Asn-18 to Lys-24, Asp-87 to Asn-94, Glu-116 to Gly-125.
829354	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1098 as residues: Ala-1 to Asn-16, Pro-36 to Arg-43.
829388	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1099 as residues: Glu-91 to Pro-100, Tyr-122 to Thr-127, Thr-168 to Val-173, Thr-210 to Asp-215, Leu-219 to Gly-224, Gly-232 to Val-237.
829626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1101 as residues: Gly-145 to Ala-151.
829730	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1102 as residues: Pro-22 to His-27, Pro-87 to Asp-93, Arg-109 to Lys-115, Arg-172 to Glu-177, Glu-219 to Asp-226.
829892	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1103 as residues: Tyr-36 to Ala-46, Val-58 to Asn-63, Glu-73 to Asn-78, Asn-90 to Asn-95, Ser-125 to Leu-133, Glu-143 to Pro-150, Phe-186 to Leu-191, Leu-274 to Glu-281, Lys-303 to Phe-308, Thr-323 to Gly-330.
829938	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1105 as residues: Thr-1 to Pro-14, Ser-36 to Thr-57, Ser-81 to Thr-91, Glu-103 to Leu-110, Glu-124 to Tyr-130, Ala-135 to Lys-140, Leu-146 to Glu-162, Lys-167 to Glu-172, Glu-199 to Val-213.
829969	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1106 as residues: Arg-12 to His-21, Arg-77 to Ser-88.
829982	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1107 as residues: Arg-6 to His-14, Ser-40 to Met-47, Thr-68 to Cys-74, Ile-97 to His-115, Gly-118 to Pro-124.
830007	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1108 as residues: Ala-7 to Ala-16.
830019	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1109 as residues: Leu-21 to Pro-27.
830073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1110 as residues: Gly-16 to Val-22, Pro-45 to Lys-50, Phe-58 to Arg-65, Ser-135 to Gly-141, Gly-153 to Ser-158, Pro-160 to Tyr-168.
830148	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1114 as residues: Asp-63 to Lys-81, Gly-101 to Gly-108, Pro-182 to Ala-200, Pro-210 to Met-216, Pro-235 to Gly-243.
830183	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1117 as residues: Pro-29 to Lys-37, Pro-40 to Val-47, Tyr-62 to His-67.
830194	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1118 as residues: Ala-43 to Lys-51, Glu-66 to Leu-74, His-81 to Glu-88, Arg-98 to Ser-105, Gly-111 to Gln-116, Leu-166 to Lys-182, Leu-261 to Ala-273, Glu-294 to Arg-302, Glu-335 to Asp-347.
830207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1119 as residues: Pro-14 to Pro-48, Asp-55 to Gly-61, Lys-94 to Asn-99, Ala-107 to Ser-115, Ile-117 to Asn-124, Thr-133 to Cys-139, Thr-142 to Ile-147, Gly-163 to Ser-169.
830242	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1120 as residues: Glu-29 to Lys-34, Leu-151 to Gln-157, Arg-160 to Ser-171, Gln-177 to Pro-190.
830328	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1121 as residues: Pro-18 to Met-24, Glu-66 to Gln-78, Ala-85 to Arg-93, Glu-99 to His-108, Leu-114 to Asp-137, Pro-171 to Gln-176, Gly-205 to Leu-213.
830340	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1122 as residues: Gly-12 to Lys-18, Arg-46 to Glu-56, Leu-67 to Gly-73, Ala-91 to Tyr-112.
830341	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1123 as residues: Leu-14 to Gln-20, Asn-34 to Glu-41, Lys-193 to Asn-198.
830351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1124 as residues: Pro-1 to Leu-13, Gly-42 to Pro-51, Arg-64 to Ala-69, Met-104 to Asp-109, Cys-125 to Trp-132, Asp-161 to Trp-175, Glu-206 to Glu-218.

830358	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1125 as residues: Cys-75 to Thr-81.
830400	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1127 as residues: Pro-1 to Gly-6, Arg-17 to Arg-33, Glu-151 to Trp-157, Ile-187 to Tyr-193, Lys-249 to Glu-258, Asn-289 to Ser-294, Pro-340 to Lys-353.
830437	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1128 as residues: Ala-87 to Ser-94, Asp-104 to Arg-112, Leu-114 to Asp-119, Ser-186 to Thr-202.
830466	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1130 as residues: Pro-14 to Ile-24, Thr-35 to Phe-42, Ser-45 to Asn-57, Pro-65 to Trp-89.
830497	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1131 as residues: Thr-1 to Leu-9, Ser-46 to Leu-56, Glu-117 to Lys-124, Pro-129 to Asp-135, Ala-144 to Gln-150, Gly-156 to Lys-162, Phe-182 to Pro-187, Pro-196 to Gln-201, Lys-217 to Asp-227.
830511	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1132 as residues: Lys-13 to Cys-44, Lys-101 to Arg-109, Gln-120 to Gly-129.
830540	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1135 as residues: Leu-31 to Lys-37, Arg-48 to Asn-54.
830550	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1136 as residues: Pro-8 to Cys-15, Val-80 to Cys-85.
830567	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1137 as residues: Lys-28 to Leu-33, Pro-60 to Ser-66.
830586	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1138 as residues: Pro-1 to Gln-15, Arg-33 to Leu-40, Arg-72 to Ser-78, Leu-98 to Asp-103, Phe-116 to Gly-124, Pro-152 to Arg-158, Thr-193 to Pro-200, Leu-213 to Phe-219, Asp-229 to Lys-237, Lys-246 to Lys-258, Arg-275 to Thr-280, Thr-306 to Lys-312, Leu-320 to Arg-328, Ala-335 to Asn-340, Gly-342 to Trp-349, Cys-364 to Pro-372.
830632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1139 as residues: Ala-6 to Thr-14, Arg-143 to Lys-148.
830659	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1142 as residues: Thr-32 to Tyr-40, Ala-67 to Gln-82, Arg-128 to Thr-133, Leu-137 to Thr-146, Pro-187 to Ser-193.
830696	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1143 as residues: Glu-83 to Lys-91.
830743	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1145 as residues: Pro-11 to Phe-16, Thr-48 to Ser-60.
830770	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1146 as residues: Thr-36 to Thr-44.
830830	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1147 as residues: Lys-73 to Thr-78, Pro-84 to Pro-96, Lys-107 to Glu-124, Ile-142 to Cys-153, Asp-179 to Asn-184.
830838	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1148 as residues: Ser-17 to Arg-22, Gly-48 to Val-56, Asn-217 to Asp-223, Thr-238 to Asn-243.
830851	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1149 as residues: Arg-1 to Val-7, Ala-156 to Phe-162, Arg-216 to Lys-239.
830856	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1151 as residues: Trp-29 to Gly-35, Thr-41 to His-47, Val-95 to Lys-111.
830862	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1152 as residues: Arg-14 to Val-22, Ala-24 to Gly-35, Arg-37 to Lys-58, Ala-88 to Ala-94, Lys-164 to Ser-172.
830879	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1153 as residues: Cys-34 to Leu-44, Ser-60 to Gly-69, Asp-118 to Gly-123, Cys-148 to Gln-154.
830919	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1154 as residues: Pro-1 to Ser-41, Arg-53 to Pro-61, Arg-66 to Gln-132.

830969	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1155 as residues: His-17 to Pro-27, Phe-31 to Val-38, Gly-53 to Thr-62.
830991	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1156 as residues: Arg-1 to Pro-14, Ala-44 to Ser-56, His-69 to Lys-75, Gly-89 to Lys-98, Tyr-101 to Tyr-121, Pro-123 to Thr-131, Pro-149 to Gly-171, Tyr-186 to Glu-192.
831002	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1157 as residues: Glu-63 to Asn-73, Pro-114 to Tyr-122, Ser-194 to Glu-201, Ile-263 to Ser-269.
831003	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1158 as residues: Ile-9 to Leu-17, Asp-63 to Gly-70, Leu-112 to Ala-128.
831021	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1159 as residues: Asn-6 to Asp-12.
831036	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1160 as residues: Ser-6 to Ser-25, Tyr-37 to Lys-42, Arg-49 to Tyr-54, Pro-56 to Glu-61, Gln-72 to Cys-77, Lys-104 to Glu-110, Lys-134 to Met-142, Asp-147 to Arg-158, Arg-189 to Asn-194.
831071	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1161 as residues: Thr-41 to Arg-49, Glu-137 to Asp-142, Tyr-158 to Glu-163, Arg-184 to Thr-199, Arg-239 to Gly-253, Pro-297 to Gly-304, Pro-319 to Ile-327, Leu-347 to Val-356, Asn-435 to Leu-441, Asp-443 to Ser-452, Ala-457 to Thr-462, Asp-479 to Arg-484, Gly-510 to His-516, Glu-555 to Thr-565, Asp-597 to Ser-602, Thr-615 to Asp-622, Val-653 to Leu-661, Ala-684 to Arg-697, Ser-704 to Glu-712, Ala-731 to Ala-737, Lys-800 to Met-805.
831099	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1163 as residues: Leu-12 to Gly-18, Leu-93 to Ile-98, Lys-165 to Ser-183, Thr-198 to Lys-211, Glu-232 to Gly-237, Pro-239 to Gly-249, Arg-257 to Asp-278, Cys-292 to Glu-297, Arg-306 to Ser-316, Asp-323 to Asn-331, Glu-347 to Gly-354, Thr-365 to Asn-370, Pro-390 to Thr-396, Asn-420 to Ser-433, Val-440 to Gln-451, His-457 to Asp-465, Phe-533 to Met-538, Ala-540 to Tyr-550, Pro-560 to Lys-565.
831113	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1164 as residues: Ser-26 to Arg-33, Pro-51 to Thr-56, Cys-82 to Asp-94, Pro-104 to Gly-128.
831120	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1165 as residues: Ala-39 to Leu-47, Val-49 to Lys-55, Thr-66 to Asp-75, Thr-85 to Gly-104, Ala-114 to Gly-147, Pro-176 to Thr-199, Ser-205 to Ser-221, Glu-233 to Lys-240, Lys-246 to Asp-251, Glu-256 to Ser-267, Ser-291 to Leu-302, Thr-305 to Asp-324, Cys-336 to Val-345, Phe-367 to Cys-375.
831172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1166 as residues: Pro-1 to Gly-7, His-119 to Gly-125, His-145 to Asp-151, Leu-173 to Leu-178.
831178	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1167 as residues: Glu-37 to Asn-42, Ser-48 to Thr-54, Pro-101 to Glu-106.
831184	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1168 as residues: Gln-1 to Pro-29.
831203	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1169 as residues: Thr-1 to Ser-6, Leu-10 to Asn-23, Gln-31 to Arg-36, Arg-43 to His-49, Ala-58 to Leu-63, Gln-81 to Asp-105, Glu-113 to Ile-122, Pro-132 to Lys-137, Ser-175 to Gln-181.
831257	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1173 as residues: Arg-87 to Leu-96, His-104 to Lys-112, Asp-144 to Pro-150.
831277	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1174 as residues: Arg-1 to Gly-13.
831317	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1175 as residues: Ser-97 to Lys-102, Thr-108 to Gly-119, Lys-151 to Gly-157, Pro-204 to Glu-210, Gln-224 to Gly-230, Val-238 to Cys-245, Met-279 to Asn-284, Gly-332 to Glu-349.
831339	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1176 as

	residues: Met-1 to His-19, Pro-21 to Pro-27, Ala-49 to Gly-59, Pro-82 to Ala-104.
831363	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1177 as residues: Thr-1 to Ser-14, Thr-82 to Pro-89, Met-102 to Ala-109, Phe-117 to Ile-124, Asp-142 to Arg-148, Thr-196 to Trp-205, Gln-304 to Leu-310, Gln-325 to Ser-331, Gly-387 to Thr-393, Ala-415 to Lys-430, Pro-469 to Pro-477, Gly-500 to Ile-506, Arg-521 to Gly-529, Pro-534 to Gly-541, Gln-553 to Lys-558, Ala-571 to Glu-579.
831385	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1180 as residues: Ser-1 to Thr-9, Ala-32 to Asn-37, Thr-40 to Tyr-49, Gln-71 to Thr-80.
831390	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1181 as residues: Trp-50 to Gly-55, Leu-109 to Val-119, Phe-146 to Asp-158, Ser-165 to Trp-172, Phe-192 to Ile-197, Leu-241 to Asp-252, Lys-268 to Pro-273, Ser-310 to Lys-315, Asp-334 to Ala-342, Pro-348 to Tyr-353.
831391	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1182 as residues: Ser-28 to Pro-38, Pro-45 to Cys-55, Leu-70 to Ser-77, Glu-98 to Phe-104, Asp-112 to Ser-122, Thr-152 to Lys-158.
831405	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1183 as residues: Asp-47 to Ser-55, Glu-86 to Cys-95, Glu-105 to Gly-113, Gln-133 to Asn-138, Arg-144 to Asp-156.
831476	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1185 as residues: Gln-28 to Gly-33, Asp-41 to Trp-47, Asn-51 to Ser-56, Ser-73 to Asn-83, Trp-111 to Asn-117, Leu-133 to Gln-138, Arg-143 to Tyr-150, Thr-156 to Glu-165.
831488	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1186 as residues: Glu-53 to Asn-59, Lys-97 to Phe-104, Lys-133 to Ala-138.
831519	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1188 as residues: Ser-17 to Gly-25, Thr-47 to Leu-59, His-71 to Arg-77, Pro-83 to Gln-90, Tyr-133 to Ser-143, Arg-160 to Gly-169, Pro-188 to Val-193, Glu-202 to Glu-208, Leu-283 to Arg-288, Glu-295 to Leu-301, Ala-327 to Leu-333, Ala-426 to Pro-433, Leu-444 to Leu-456, Asn-492 to Ala-498.
831550	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1190 as residues: Arg-1 to Gly-15, Ser-42 to Trp-51, Pro-59 to Arg-64.
831560	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1191 as residues: Arg-58 to Asp-64.
831570	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1193 as residues: Thr-61 to Cys-74, Gly-92 to Cys-104, Cys-128 to Ser-133, Asn-179 to Gly-186, Ser-198 to Cys-226, Asn-265 to Ser-274, Ser-280 to Ile-285, Ser-291 to Asp-297, Leu-305 to Gly-315, Phe-317 to Gly-333, Asp-336 to Leu-344, Phe-354 to Cys-361.
831596	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1195 as residues: Gln-80 to Gly-85.
831627	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1196 as residues: Arg-1 to Ser-12, Gly-94 to Thr-106, Ser-161 to Leu-169, Ser-183 to Val-188, Glu-199 to Cys-205, Ser-246 to Ile-251, Leu-271 to Thr-276.
831649	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1197 as residues: Tyr-32 to Lys-39.
831664	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1198 as residues: Lys-1 to Asp-42, Arg-71 to Ala-76, Gln-138 to Phe-145, Lys-170 to Thr-178, Cys-186 to Asp-192.
831684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1200 as residues: Ile-135 to Ala-140, Tyr-151 to Asn-157, Ser-183 to Ile-190, Gly-196 to Lys-201, Lys-226 to Lys-232, Asn-246 to Thr-252, Asp-293 to Gly-300.
831687	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1201 as residues: Ala-56 to Tyr-63.
831726	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1202 as residues: Arg-3 to Arg-15, Lys-34 to Thr-39, Asn-41 to Lys-59, Ala-104 to Glu-110.
831762	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1204 as residues: Pro-83 to Leu-91, His-116 to Ala-122, Pro-141 to Ser-155.
831848	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1206 as

	residues: Gln-16 to Thr-23.
831861	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1207 as residues: Ala-20 to Lys-26, Pro-59 to Pro-67, Ser-104 to Thr-121, Gln-130 to Gln-136.
831866	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1208 as residues: Arg-11 to Ala-24, Ile-39 to Lys-45, Arg-76 to Pro-85, Lys-124 to Lys-130, Pro-139 to Ser-153, Ala-156 to Glu-170, Ser-179 to Thr-184, Asp-234 to Gly-244, Gly-321 to Lys-329.
831899	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1210 as residues: Asp-11 to Trp-16, Pro-37 to Thr-44, Pro-74 to Pro-82, Arg-112 to Gln-119, Cys-126 to Arg-138, Arg-199 to Thr-204.
831913	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1211 as residues: Pro-22 to Cys-27, Glu-54 to Glu-60, Asp-112 to Phe-117, Lys-183 to Asp-189, Gln-277 to Tyr-282, Pro-325 to Arg-331, Gly-336 to Tyr-346.
831985	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1213 as residues: Cys-7 to Asp-12, Pro-21 to Gly-26.
831986	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1214 as residues: Cys-1 to Ser-7, Ala-62 to Gly-72, Pro-83 to Ala-101.
832010	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1215 as residues: Leu-1 to Lys-21, Glu-39 to Cys-47, Lys-49 to Gln-61, His-64 to Gly-76, Thr-83 to Lys-90, His-92 to Ile-99.
832016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1216 as residues: Phe-28 to Asn-33, Leu-55 to Tyr-80, Pro-126 to Gly-132, Pro-162 to Gly-169, Pro-194 to Arg-201.
832041	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1217 as residues: Lys-55 to Met-63, Arg-120 to Asp-132, Gly-266 to Glu-281, Val-313 to Thr-319, Leu-361 to Ser-370, Tyr-406 to Met-412, Leu-465 to Trp-470.
832049	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1219 as residues: Leu-80 to Lys-87, Lys-102 to Thr-109, Glu-195 to Thr-200, Thr-203 to Asp-209.
832122	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1220 as residues: Asn-29 to Phe-36, Asp-41 to Ser-50.
832197	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1222 as residues: Glu-61 to Leu-70.
832237	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1223 as residues: Lys-28 to Val-35, Arg-41 to Arg-55, Pro-76 to Thr-87.
832246	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1224 as residues: Arg-17 to Asn-23, Arg-90 to Gly-95, Leu-114 to Glu-121, Pro-153 to Asp-158.
832256	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1225 as residues: Gly-15 to Asn-22.
832280	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1226 as residues: Glu-1 to Trp-16, Ala-32 to Glu-38, Ala-49 to Gln-55, Pro-61 to Gln-66, Ala-78 to Asp-100, Leu-107 to Thr-127, Pro-133 to Phe-157, Pro-160 to Thr-171, Leu-179 to Asp-196, Asp-201 to Lys-222, Pro-249 to Ile-254, Val-258 to Val-263, Thr-268 to Ser-277, Thr-279 to Ala-295, Gly-299 to Phe-327, Val-335 to Asp-346, Lys-366 to Asp-378.
832285	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1227 as residues: Phe-18 to Leu-23.
832294	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1228 as residues: Pro-21 to Gln-28, Pro-56 to Leu-64, Glu-79 to Pro-95, Met-125 to Gly-138.
832326	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1229 as residues: Ser-30 to Trp-45, Gln-64 to Cys-72, Pro-74 to Pro-80, Ala-92 to Arg-98, Trp-104 to Ser-112, Ser-129 to Asp-135, Pro-145 to Gln-152, Arg-168 to Gly-173, Gln-176 to Pro-183.
832370	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1232 as residues: Ala-5 to Ala-11, Pro-23 to Pro-36, Glu-72 to Gly-82, Pro-85 to Pro-91, Asp-

	98 to Glu-119, Pro-121 to Glu-127.
832381	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1233 as residues: Arg-1 to Glu-6, Arg-52 to Ala-58, Phe-72 to Leu-79, Gly-88 to Glu-93, Tyr-124 to Arg-134.
832454	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1235 as residues: Ala-23 to Asp-41.
832465	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1236 as residues: Ala-1 to Gly-7, Ala-32 to Val-45, Ile-65 to Ser-75, Ser-93 to Ser-108.
832475	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1237 as residues: Arg-1 to Val-10, Thr-65 to Ser-71, Arg-83 to Tyr-96, Trp-104 to Trp-111.
832495	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1238 as residues: Arg-9 to Arg-14.
832498	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1239 as residues: Pro-26 to Asp-31, Thr-113 to Gly-125, Asn-158 to Glu-163, Asn-288 to Val-293.
832501	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1240 as residues: Ser-8 to Glu-13.
832505	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1241 as residues: Ala-27 to Arg-46, Pro-54 to Arg-76, Arg-134 to Lys-140, Asn-148 to Ser-154, Lys-166 to Thr-172, Pro-175 to Gln-182, Asp-185 to Asp-192.
832554	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1243 as residues: Arg-26 to Val-31, Asn-122 to Thr-128.
832569	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1244 as residues: Gln-6 to Met-16.
832578	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1245 as residues: Arg-15 to Leu-27, Ser-62 to Gly-72, Pro-107 to His-112, Pro-122 to Gln-142, Glu-147 to Arg-158, Lys-177 to Lys-191, Leu-195 to Val-202, Leu-206 to Pro-218, Glu-228 to Gln-233, Asp-239 to Asp-244, Glu-258 to Gln-278.
832615	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1246 as residues: Gln-41 to Ala-48.
832632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1248 as residues: Asn-60 to Val-70, Glu-93 to Trp-107, Arg-116 to Gln-125, Leu-133 to Lys-141, Lys-162 to Glu-167.
832633	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1249 as residues: Gly-8 to Trp-13, Pro-36 to Gly-41, Pro-91 to Ala-96.
834859	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1252 as residues: Tyr-16 to Leu-22, Asp-24 to Asp-34, Gly-43 to Ala-48, Gly-57 to Thr-68, Gly-118 to Ser-127, Ile-129 to Tyr-134, Pro-139 to Asp-162.
834861	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1253 as residues: Glu-14 to Glu-50, Glu-67 to Asp-74, Leu-89 to Asn-95.
834890	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1254 as residues: Arg-8 to Lys-13, Gly-35 to Lys-42, Ala-48 to Lys-54, Ala-105 to Leu-110, Gly-150 to Val-157, Phe-164 to Asn-173.
835079	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1255 as residues: Ser-53 to Pro-60.
835554	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1256 as residues: Ile-31 to Ile-38, Asp-116 to Arg-121, Phe-246 to Leu-251, Lys-280 to Tyr-291, Met-363 to Arg-373, Gly-381 to Trp-386.
835723	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1258 as residues: Glu-20 to Thr-26, Trp-47 to Ser-57, Pro-98 to Asn-105, Pro-124 to Phe-129, Ala-173 to Val-183, Lys-190 to Ser-196, Asn-277 to Asn-284, Glu-297 to Phe-306, Thr-322 to Lys-327, Gln-372 to Val-383, Pro-387 to Gly-395, Ser-406 to Thr-415, Arg-432 to Thr-442.
835791	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1259 as residues: Ala-4 to Gly-10.
835817	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1260 as

	residues: Glu-37 to Leu-43.
835840	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1261 as residues: Gln-1 to Asn-6, Pro-18 to Ile-31.
836048	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1262 as residues: Lys-1 to Lys-11, Tyr-27 to Glu-35, Glu-61 to Gly-68.
836898	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1263 as residues: Gln-94 to Lys-102, Gly-140 to Thr-154, Arg-173 to Asp-196, Thr-201 to Asp-206, Glu-241 to Gly-248.
836927	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1264 as residues: His-1 to Arg-12.
837344	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1265 as residues: Pro-15 to Ile-24.
837789	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1266 as residues: Ser-1 to Trp-7, Asp-47 to Ile-52, Pro-70 to Ser-80, Cys-89 to Thr-98, Ala-131 to Ser-142, Phe-169 to Cys-176, Gly-183 to Ser-193, Phe-202 to Pro-209, Arg-243 to Ala-249, Ser-256 to Lys-265, Arg-277 to Asp-284.
838754	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1268 as residues: Phe-27 to Ser-37, Tyr-91 to Arg-96, Pro-156 to Gln-164, Cys-207 to Val-216, Met-242 to Tyr-251.
839561	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1271 as residues: Arg-2 to Gly-7, Arg-16 to Gln-22, Phe-41 to Gly-49, Ala-60 to Asn-74, Leu-125 to Gln-131, Asp-170 to Pro-175, Ala-209 to Arg-218, Glu-222 to Glu-258, Ala-265 to Ser-300.
839816	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1272 as residues: His-32 to Arg-37, Ser-42 to Ser-48, Glu-77 to Glu-88.
840068	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1273 as residues: Ala-1 to Gln-14.
840279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1274 as residues: Ala-1 to Asp-15.
840538	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1276 as residues: Ala-8 to Pro-13, Pro-18 to Gln-26, Lys-107 to Pro-114, Ala-149 to Arg-157, Ile-294 to Leu-299, Ser-356 to Pro-363, Pro-384 to Phe-392, Ala-474 to Gly-481, Ala-489 to Tyr-494, Pro-512 to Lys-517, Arg-623 to Thr-630, Lys-673 to Ser-678, Thr-703 to His-709, Arg-714 to Arg-720, Gly-755 to Glu-766.
840549	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1278 as residues: Ala-5 to Lys-15, Pro-28 to Gln-34, Tyr-105 to His-111, Gln-150 to Cys-157.
840557	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1280 as residues: Gly-34 to Leu-40, Thr-125 to Gly-134, Ala-148 to Arg-156, Lys-196 to Lys-215.
840561	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1281 as residues: Ser-21 to Phe-30.
840562	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1282 as residues: Gln-33 to Arg-41, Tyr-66 to Glu-71, Thr-112 to Gly-118, Thr-141 to Gly-148, Thr-160 to Cys-168, Arg-171 to Gly-177, Thr-180 to Pro-191, Glu-217 to Asp-225, Asp-236 to Lys-243.
840564	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1283 as residues: Val-13 to Pro-19, Gln-34 to Gly-39.
840600	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1285 as residues: Leu-26 to Ile-39.
840620	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1288 as residues: Ser-17 to Ser-26, His-32 to Gly-42, Thr-78 to Gln-83, Asp-130 to Leu-136, Arg-158 to Pro-164.
840626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1290 as residues: Phe-7 to Tyr-13, Pro-19 to Ala-35, Asp-87 to Leu-96, Lys-98 to Glu-105, Glu-120 to Leu-133.
840638	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1291 as

	residues: Gly-8 to Leu-13, Gly-21 to Ser-31, Arg-45 to Arg-54.
840649	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1292 as residues: Asn-30 to Thr-37, Asp-44 to Lys-52, Ser-71 to Asp-80, Glu-127 to Glu-133, Arg-162 to Ala-173, Glu-191 to Leu-199.
840651	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1293 as residues: Gly-14 to Glu-38, Asn-90 to Lys-100, Lys-150 to Val-158, Ser-166 to Gly-175.
840681	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1295 as residues: Thr-25 to Gly-31, Pro-86 to Trp-97, Ser-132 to Phe-138.
840682	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1296 as residues: Arg-12 to Lys-19, Asn-30 to Gly-36, Asp-50 to Gly-57, Glu-64 to Thr-69, Thr-79 to Lys-91, Gln-110 to Thr-115, Arg-223 to Gln-229, Asp-255 to Asp-260, Arg-278 to Gly-287, Glu-294 to Gln-300, Glu-433 to Glu-451, Leu-474 to Glu-479, Asp-490 to Leu-498, Gln-519 to Asp-527, Tyr-566 to Asp-575.
840684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1297 as residues: Pro-1 to Ala-9, Val-56 to Val-63, Gly-86 to Glu-91.
840697	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1298 as residues: Pro-9 to Arg-15, Pro-36 to Ser-42, Ser-65 to Phe-72, Gly-99 to Ser-105, Ala-122 to Phe-129.
840698	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1299 as residues: Thr-75 to Pro-84, His-94 to Met-99, Asp-149 to Ile-168, Asn-370 to Asn-375, Ser-384 to Lys-392, His-427 to Tyr-438.
840708	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1300 as residues: Ala-27 to Ser-36.
840714	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1301 as residues: Gly-1 to Gly-20, Arg-54 to His-59, Asn-89 to Leu-95, Ser-119 to Lys-125, Trp-127 to Cys-133, Gln-175 to Gln-185, Asp-213 to Lys-222, Pro-267 to Gln-275, Asp-306 to Asp-313, Thr-321 to Cys-331.
840716	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1302 as residues: Asn-40 to Thr-45, His-210 to Pro-215, Glu-369 to Thr-375, Lys-383 to Leu-397, Pro-438 to Ile-447, Pro-510 to Tyr-520, Arg-528 to Arg-533, Thr-549 to Thr-555.
840721	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1303 as residues: Arg-1 to Arg-7, Pro-29 to Lys-56, Asp-103 to Arg-108, Tyr-122 to Ser-127, Gly-219 to Glu-227, Asp-250 to Glu-255, Glu-294 to Pro-301, Ala-321 to Tyr-327, Arg-367 to Pro-373, Glu-396 to Asn-405, Gly-411 to Arg-418, Asn-433 to Lys-441.
840735	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1304 as residues: Glu-1 to Gly-11, Thr-20 to Asp-40, Gly-51 to Glu-61, Ala-64 to Leu-78, Leu-82 to Arg-94.
840738	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1305 as residues: Gln-26 to Asn-34.
840745	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1306 as residues: Gln-7 to Gly-12, Leu-60 to Pro-65, Arg-85 to Lys-99, Ser-132 to Pro-145, Pro-150 to Asp-155, Pro-183 to Asn-193, Arg-200 to Tyr-206.
840747	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1307 as residues: Gln-1 to Asp-15, Ile-35 to Glu-41, Leu-66 to Asn-71, Leu-73 to Pro-79, Gln-87 to Lys-94, Val-117 to Arg-123, Pro-144 to Tyr-150.
840756	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1308 as residues: Arg-8 to Gln-19, Arg-25 to Lys-38.
840776	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1309 as residues: Val-2 to Pro-10, Ser-28 to Ala-33, Pro-39 to Tyr-44, Thr-46 to Trp-55, Ser-64 to Ser-72, Ala-103 to Pro-109, Pro-111 to Gln-118.
840784	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1310 as residues: Pro-9 to Gly-20, Asn-32 to Leu-42, Asn-60 to Lys-70, Pro-76 to Gln-81, Glu-86 to Val-93, Arg-106 to Arg-111, Lys-176 to Asn-183.
840788	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1311 as residues: Ser-1 to Gln-8, Val-40 to Ser-49, Arg-105 to Lys-110.

840794	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1312 as residues: Arg-1 to Gln-14, Arg-43 to Glu-54.
840797	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1313 as residues: Gly-1 to Arg-9, Asn-31 to Asp-37, Arg-44 to Asn-53, Gly-62 to Lys-77, Thr-123 to Ile-137, Gly-389 to Thr-394, Lys-486 to Asn-493, Glu-512 to Phe-520, Met-555 to Lys-560, Leu-618 to Ser-623, Ile-698 to Glu-706, Gly-723 to Leu-730, Ala-773 to Gln-790.
840818	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1315 as residues: Pro-1 to Ile-12, Asp-30 to Tyr-35, Leu-38 to Pro-45, Lys-54 to Thr-60, Thr-75 to Leu-80, Asp-92 to Tyr-100, Ile-133 to Thr-138, Thr-194 to Glu-199, Asp-233 to Leu-239, Met-243 to Ala-251, Asp-254 to Glu-261.
840822	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1316 as residues: Val-100 to Tyr-106, Ala-127 to His-135, Gln-153 to Lys-158, Gly-214 to Glu-219, Gln-236 to His-244, Lys-253 to Tyr-258.
840846	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1318 as residues: Ala-20 to Thr-27, Glu-47 to Tyr-57, Tyr-87 to Lys-95, Pro-121 to Ala-127, Pro-208 to Ala-224.
840848	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1319 as residues: Arg-77 to Asn-82, Glu-119 to Arg-124, Gln-156 to Thr-162, Lys-209 to Lys-215.
840860	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1320 as residues: Ile-27 to Asp-41, Glu-43 to Ala-58, Glu-149 to Glu-154, Lys-158 to Ile-165, Glu-167 to Gly-189, Glu-242 to Phe-247, Arg-259 to Phe-268, Ile-283 to Val-291, Thr-295 to Thr-307, Glu-328 to Asp-338, Asp-372 to Gly-387.
840871	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1322 as residues: Gly-31 to Tyr-38, Leu-40 to Leu-45, Pro-203 to Trp-208.
840874	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1323 as residues: Ala-23 to Gly-28.
840878	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1324 as residues: Thr-40 to Glu-46, Pro-69 to Arg-76, Glu-108 to Asp-150.
840880	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1325 as residues: Ser-5 to Lys-14, Phe-32 to Gln-37.
840884	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1326 as residues: Leu-4 to Ser-10.
840926	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1328 as residues: Met-6 to Thr-15, Ser-17 to Phe-37, Ser-148 to Lys-154, Lys-260 to Phe-276, Glu-285 to Ile-292, Lys-410 to Asp-424.
840932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1329 as residues: Tyr-75 to Pro-83, Ile-181 to Gln-191, Glu-267 to Leu-275, Met-301 to Ala-307, Phe-322 to Gln-328, Met-371 to Gly-381, Gln-458 to Leu-463, Glu-474 to Lys-480, Lys-551 to Ser-558.
840940	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1330 as residues: Ser-26 to Thr-34, Thr-80 to Lys-88.
840947	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1331 as residues: Ile-1 to Arg-11, Pro-19 to Gln-46, Ala-55 to Pro-62, Cys-65 to Cys-82, Lys-93 to Pro-108.
840964	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1333 as residues: Ser-41 to Cys-46.
840979	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1334 as residues: Tyr-10 to His-27, Tyr-31 to Arg-41, Thr-44 to Leu-61, Cys-68 to Phe-73, Lys-98 to Glu-106, Gln-132 to Val-142, Glu-184 to Leu-191.
840984	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1335 as residues: Arg-38 to Gln-48, Met-137 to Asn-144, Gln-167 to Gln-172, Lys-182 to Gln-189, Gln-196 to Glu-206, Ile-210 to Glu-223, Gln-225 to Arg-246, Glu-250 to Thr-269, Gln-296 to Ile-318, Arg-323 to Glu-328, Tyr-337 to Lys-343, Glu-349 to Thr-357, Ser-393 to Glu-403, Arg-405 to Ile-427, Arg-431 to Glu-442, Leu-446 to Lys-473, Glu-475

	to Leu-486, Ile-488 to Asp-503, Ser-505 to Arg-623, Ala-625 to Asn-631, His-634 to Trp-792, Gly-799 to Gly-870, Arg-872 to Glu-929, Ser-931 to Pro-954, Ala-957 to Ala-977, Glu-982 to Trp-1000.
840986	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1336 as residues: Asp-41 to Tyr-51.
840988	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1337 as residues: Pro-17 to Leu-31, Ser-95 to Val-100, Lys-123 to Gly-129.
840990	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1338 as residues: Met-9 to Glu-16, Glu-41 to Trp-47, Arg-55 to Glu-62, Asp-135 to Ile-146, Gly-154 to Gly-160, Met-207 to Phe-214, Ser-245 to Lys-252, Gln-282 to Gln-288.
841009	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1340 as residues: Glu-12 to Thr-27, Met-45 to Asn-52, Tyr-79 to Thr-87, Asp-97 to Gly-102, Met-112 to Asp-120, Pro-141 to Tyr-155.
841012	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1341 as residues: Lys-36 to Ile-44, Arg-49 to Lys-69.
841016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1342 as residues: Cys-75 to His-82, Asp-126 to Tyr-135, Pro-144 to Tyr-155, Gly-179 to Trp-198, Tyr-201 to Met-208, Pro-226 to Lys-234, Gln-249 to Asp-267.
841017	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1343 as residues: Gln-1 to Trp-19.
841021	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1344 as residues: Glu-58 to Gly-63, Leu-75 to Leu-82.
841032	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1345 as residues: Pro-1 to Gly-13, Pro-30 to Ser-57, Gln-61 to Thr-77, Arg-82 to Thr-88, Pro-100 to Lys-105, Gly-119 to Gly-126.
841051	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1346 as residues: Asn-1 to Lys-6, Thr-16 to Glu-21, Asn-45 to Ser-58, Asp-68 to Ser-75.
841064	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1347 as residues: Asp-53 to Pro-58, Glu-78 to Lys-85, Pro-95 to Arg-102, Ser-142 to Arg-148, Lys-209 to Arg-214, Lys-241 to Gly-246, Ser-287 to Leu-292, Lys-307 to Val-313, Arg-389 to Gln-394.
841069	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1348 as residues: Thr-1 to Trp-14, Lys-27 to Leu-44, Glu-59 to Arg-73, Lys-87 to Phe-95, Pro-160 to Asn-166, Leu-212 to Ile-220, Arg-236 to Asp-243.
841072	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1349 as residues: Pro-7 to Arg-12, Phe-71 to Gln-76, Arg-82 to Asp-98, Ala-108 to Glu-128.
841078	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1350 as residues: Arg-32 to Ala-39.
841080	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1351 as residues: Glu-1 to Gly-7, Glu-25 to Gly-33, Ala-54 to Phe-60, Gly-64 to Gln-108, Glu-116 to Ser-122, Pro-130 to Asn-138, Gln-141 to Lys-153, Arg-164 to Ser-172, Leu-186 to Met-194, Pro-197 to Tyr-205, Asp-218 to Lys-229, Thr-236 to Ser-246, Ala-259 to Trp-266, Pro-281 to Pro-287, Cys-291 to Gln-298.
841092	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1353 as residues: Glu-45 to Lys-50.
841095	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1354 as residues: Lys-1 to Ser-19, Gly-33 to Gly-63, Gly-77 to Pro-89, Ser-164 to Ser-180, Ser-233 to Lys-238, Lys-267 to Leu-286.
841096	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1355 as residues: Gly-5 to Leu-12, Tyr-18 to Asp-25, Ile-88 to Ala-125, Ser-129 to Tyr-141, Gln-191 to Gln-196, Thr-290 to Asn-296, Thr-301 to Thr-309, Leu-360 to Ala-365, Leu-367 to Gly-378, Pro-398 to Gly-418, Pro-443 to Gly-454.
841102	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1356 as residues: Ser-61 to Leu-71.
841108	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1358 as residues: Ala-8 to Leu-20, Lys-27 to Arg-33, Arg-40 to Ala-50, Asp-77 to Glu-84,

	Asn-99 to Gly-109.
841119	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1360 as residues: Lys-6 to Ala-14, Ile-68 to Asn-73, Val-84 to Leu-90, Glu-110 to Val-116, Leu-182 to Gly-190, Tyr-264 to Phe-270, Ile-300 to Lys-306, Pro-354 to Glu-367.
841124	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1361 as residues: Ser-21 to Thr-26.
841143	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1363 as residues: Thr-1 to Lys-9, Pro-20 to Gly-27, Gly-29 to Gly-52, Arg-54 to Gly-61, Gly-69 to Gly-75, Ser-79 to Gly-96, Val-130 to Arg-135, His-207 to Asp-212, Val-296 to Leu-310, Arg-327 to Asn-334.
841148	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1364 as residues: Pro-1 to Met-43, Pro-55 to Ala-66, Pro-118 to Glu-128, Arg-181 to Lys-192, Tyr-197 to Thr-207, Trp-278 to Cys-284, Arg-334 to Asp-349.
841155	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1367 as residues: Gly-9 to Arg-24, Glu-69 to Met-74, Leu-86 to Leu-92, Asp-95 to Arg-115.
841163	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1370 as residues: Gly-29 to Gly-35, Ala-37 to Ala-48, Arg-97 to Thr-102, Arg-114 to Leu-119, Lys-144 to Lys-155.
841169	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1371 as residues: Ala-31 to Thr-69, Pro-90 to Pro-95, Pro-117 to Trp-126, Pro-128 to Arg-136.
841172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1372 as residues: Gly-17 to Arg-35, His-76 to Pro-90, Pro-92 to Cys-103.
841174	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1373 as residues: Arg-1 to Arg-8, Arg-14 to Phe-19.
841179	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1374 as residues: Leu-4 to Met-10, Leu-17 to Tyr-36, Arg-38 to Asp-63, Tyr-82 to Glu-90, Pro-97 to Gly-134, Arg-137 to Pro-148, Thr-160 to Lys-171, Tyr-183 to Asn-228, Gln-249 to Asn-258, Arg-263 to Glu-271, Arg-277 to Gln-296, Phe-298 to Asp-320, Glu-322 to Lys-329, Thr-337 to Thr-343, Glu-356 to Arg-363, Gly-371 to Asp-384.
841183	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1375 as residues: His-1 to Ser-27, Arg-60 to Arg-73, Arg-96 to Asp-124, Asp-131 to Gly-143, Lys-145 to Glu-150.
841186	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1376 as residues: Leu-7 to Val-18, Ser-27 to Pro-57, Arg-124 to Thr-135, Pro-212 to Ser-230, Gly-282 to Lys-287, Lys-441 to Lys-448.
841204	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1377 as residues: Lys-29 to Arg-35, Glu-81 to Arg-87, Ala-251 to Glu-261, Thr-266 to Gly-271, Thr-289 to Glu-295, Gly-328 to Tyr-334, Phe-432 to Lys-438, Asn-440 to Trp-458.
841206	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1378 as residues: Val-17 to Pro-25, Thr-55 to Asp-70, Lys-75 to Leu-81.
841207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1379 as residues: Pro-9 to Glu-15, Arg-22 to Trp-32, Ser-54 to Glu-62, Asn-92 to Gly-103.
841211	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1380 as residues: Arg-7 to Gly-12, Met-42 to Ser-58, Gln-65 to Asn-73, Glu-91 to Ala-99, Pro-103 to Tyr-109, Arg-174 to Ala-179, His-189 to Gln-196, Asn-208 to Pro-219.
841225	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1381 as residues: Ala-32 to Ala-40, Glu-93 to Phe-103, Lys-173 to Thr-189.
841237	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1383 as residues: Arg-2 to Gln-12, Lys-76 to Ala-86, Tyr-155 to Lys-163, Glu-228 to Leu-234, Lys-263 to Lys-273, Ile-286 to Lys-296.
841241	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1384 as residues: Asp-41 to Ile-52, Thr-59 to Lys-64, Glu-75 to Asn-89, Thr-99 to Thr-105.
841259	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1385 as residues: His-1 to Cys-22, Pro-24 to Pro-30, Tyr-84 to Ser-90, Ser-108 to Glu-118, Val-126 to Arg-143, Asp-175 to Gln-181, Ser-217 to Gly-224, Cys-262 to Cys-270.

	Tyr-296 to Glu-302, Thr-317 to Thr-324, Gln-341 to Gln-348, Trp-394 to Pro-399.
841260	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1386 as residues: Ala-25 to Glu-32, Ala-48 to Phe-53, Ser-69 to Ser-76, Asp-80 to Glu-86, Ser-125 to Ser-132, Ser-168 to Glu-179, Asn-201 to Ala-206, Lys-216 to Ile-246, Met-259 to Asn-272, Tyr-277 to Gln-287.
841264	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1387 as residues: Met-34 to Gly-50, Asp-69 to Trp-90, Asp-99 to Lys-107, Val-164 to Thr-170.
841311	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1389 as residues: Arg-4 to Val-15.
841313	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1390 as residues: His-6 to Gly-16, Gly-60 to Pro-95, Pro-125 to Gly-131, Gly-138 to Ala-147, Gln-173 to Glu-178.
841322	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1392 as residues: Lys-6 to Arg-23, Ser-74 to Arg-86, Lys-116 to Lys-122, Ser-127 to His-133, Ser-269 to Pro-275, Glu-344 to Phe-350, Gly-356 to His-362.
841331	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1393 as residues: Ser-45 to Lys-67, Asp-155 to Asp-172, Gln-193 to Ile-199, Gln-271 to Glu-285.
841332	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1394 as residues: Glu-8 to Ser-13, Lys-20 to Glu-27, Arg-81 to Ser-94, Thr-147 to Ile-154, Asn-200 to Glu-212, Asn-235 to Gly-244, Leu-433 to Thr-439, Pro-444 to Asn-455, Ser-470 to Asp-476, Ser-492 to Met-499, Glu-535 to Pro-547, Glu-703 to Thr-709, Glu-719 to Thr-726, Asn-802 to Leu-807, Asn-820 to Arg-825, Lys-830 to Tyr-836, Thr-838 to Thr-850, Ser-882 to Ser-894, Lys-944 to Gly-952, Gly-969 to Val-977, Glu-984 to Asn-990, Arg-996 to Lys-1001, Pro-1032 to Leu-1039, Thr-1050 to Gly-1058, Val-1103 to Arg-1108, Pro-1160 to His-1169, Tyr-1180 to Ser-1187, Glu-1211 to Ser-1217, Pro-1277 to Leu-1282.
841338	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1395 as residues: Ser-13 to Ser-18, Phe-48 to Ser-54.
841345	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1396 as residues: Trp-83 to Thr-89, Ser-135 to Asn-140, Ser-185 to Cys-190, Tyr-209 to Glu-220, Val-224 to Glu-232, Leu-258 to Asn-263, Ser-306 to Asn-312, Thr-319 to Glu-327, Thr-365 to Ile-373, Gly-417 to Cys-429, Lys-439 to Val-445, Lys-464 to Leu-469, Leu-477 to Asn-485, Arg-546 to Val-554, Glu-598 to Gly-607, Pro-634 to Ser-639, Asn-730 to Ala-746, Lys-812 to Gln-817, Glu-819 to Lys-835, Leu-867 to Asn-875, Leu-902 to Arg-910.
841349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1397 as residues: Asp-13 to Arg-18, Pro-36 to Arg-43, Gly-66 to Ser-74, Gly-87 to Lys-92, Asp-110 to Glu-115.
841417	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1399 as residues: Leu-102 to Ile-111, Pro-131 to Ile-337, Thr-339 to Asp-376.
841632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1401 as residues: Arg-13 to Gly-40, Arg-46 to Glu-52, Gln-55 to Lys-69.
841771	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1403 as residues: Pro-22 to Gly-30, Asp-45 to Gln-56, Ser-67 to Ser-73.
841827	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1404 as residues: Thr-1 to Ser-20.
841835	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1405 as residues: Tyr-5 to Lys-13, Cys-52 to Arg-61, Cys-85 to Ala-91, Gly-122 to Asn-127.
842259	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1406 as residues: Pro-16 to Gly-23, Glu-37 to Pro-45, Gly-52 to Ser-57.
842463	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1407 as residues: Cys-74 to Tyr-79.
842595	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1408 as residues: Pro-93 to Ala-105, Ser-133 to Ser-142, Arg-150 to Glu-155, Lys-220 to Trp-

	226, Glu-257 to Lys-271, Gln-280 to Leu-289.
842722	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1409 as residues: Glu-9 to Arg-20, Ser-48 to Lys-56, Ile-69 to Glu-81, Pro-83 to Lys-89, Lys-94 to Ile-99, Pro-104 to Gly-110, Glu-116 to Asp-133, Ile-140 to Ser-154, Gln-206 to His-217, Pro-219 to Leu-231, Arg-237 to Lys-243, Gln-247 to Pro-256, Leu-271 to Thr-283, Lys-289 to Lys-294, Ser-338 to Lys-355, Gly-375 to Thr-381, Ser-428 to Pro-454, Gly-460 to Gln-467, Lys-480 to Lys-488.
842818	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1411 as residues: Ala-25 to Ala-30, Lys-32 to Ala-51, Gln-61 to Ala-68, Glu-83 to Lys-91, Phe-99 to Glu-105, Glu-123 to Gly-129.
843251	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1412 as residues: Pro-30 to Ser-40, Lys-47 to Thr-52, Val-59 to Pro-64, Lys-129 to Arg-134, Leu-169 to Asp-177.
843422	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1413 as residues: Thr-9 to Lys-20, Lys-25 to Cys-31, Pro-33 to Tyr-42, Asn-76 to Lys-84, Leu-102 to Trp-112.
843784	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1414 as residues: Leu-16 to Thr-24, Glu-41 to Gln-47, Lys-64 to Cys-72, Thr-87 to Ser-100, Pro-130 to Asn-143, Thr-163 to Asp-170.
844017	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1415 as residues: Leu-11 to Ile-17, Leu-30 to Met-45.
844138	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1416 as residues: Lys-19 to Thr-28, Arg-47 to Gln-52, Leu-73 to Leu-81, Asp-122 to Phe-131, Ala-135 to Ser-148, Pro-155 to Asp-163, Ser-184 to His-191, Leu-219 to Asn-225, Asp-238 to Thr-248, Pro-253 to Cys-259, Cys-356 to His-368, Ser-426 to Gly-435, Pro-467 to Cys-478, Glu-504 to Cys-509, His-553 to Gly-568, Ala-581 to Cys-586, Ala-595 to Cys-600, Arg-602 to Trp-608.
844194	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1418 as residues: Pro-23 to Arg-31, Gln-79 to Gln-85, Cys-93 to Cys-107, Pro-216 to Leu-222.
844394	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1419 as residues: Arg-1 to Phe-11.
844450	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1420 as residues: Ser-37 to Trp-43, Pro-47 to Thr-55, Arg-60 to Lys-69, Tyr-125 to His-131, Pro-187 to Lys-195, Gly-346 to Lys-351.
844535	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1422 as residues: Asp-8 to Ala-18, Ser-47 to Ala-52, Thr-62 to Arg-69, Pro-119 to Asp-126, Trp-164 to Thr-170, Ala-206 to Ala-213, Pro-230 to Gly-235, Lys-304 to Lys-314, Lys-341 to Val-347, Tyr-387 to Thr-398.
844644	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1423 as residues: Ala-9 to Asp-16, Asn-78 to Tyr-86.
844653	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1424 as residues: Arg-1 to Gly-8, Ala-30 to Gln-36.
844796	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1426 as residues: His-12 to His-22.
844812	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1427 as residues: Gly-281 to Arg-290, Ala-349 to Ser-355, Glu-378 to Asp-388.
844894	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1428 as residues: Pro-2 to Phe-8, Ser-13 to Ala-34, Pro-37 to Phe-43, Lys-63 to Gly-73, Cys-88 to Asp-93, Gly-98 to Trp-103, Cys-273 to Ile-287, Ile-290 to Ser-296.
845361	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1429 as residues: Met-10 to Ile-21, Glu-108 to Lys-122, Lys-272 to Gly-280, Gly-298 to Lys-304, Trp-364 to Lys-369.
845620	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1430 as residues: Thr-62 to Ala-67, Leu-96 to Glu-101, Cys-184 to Trp-190.
845639	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1431 as residues: Arg-41 to Arg-48, Met-72 to Val-79, Gln-81 to Trp-89, Ala-96 to Asp-101,

	Arg-110 to Gly-118, Asn-126 to Arg-135, Ala-144 to Asp-149, Leu-199 to Lys-213, Gln-245 to Glu-256, Arg-261 to Thr-267.
845660	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1432 as residues: Gly-5 to Leu-17, Arg-19 to Arg-29, Pro-36 to Arg-50, Arg-60 to Pro-67, Gln-133 to Leu-150, Gln-168 to Phe-187, Pro-189 to Gln-194, Asp-240 to Gly-251, Thr-308 to Cys-317, Val-325 to Glu-331, Leu-354 to Pro-369, Lys-381 to Cys-388, Arg-410 to Phe-417.
845720	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1433 as residues: Thr-1 to Glu-11, Arg-21 to Pro-27, Pro-44 to His-49, Glu-56 to Leu-69, Ala-74 to Gly-80, Phe-82 to Pro-87.
845897	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1435 as residues: Gly-1 to Ser-9, Gly-31 to Ser-38, Arg-52 to Val-68, Leu-71 to Glu-84.
845922	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1436 as residues: Asn-1 to Pro-6, Pro-29 to Gln-36, Glu-95 to Arg-100, Pro-150 to Met-157, Ser-272 to Tyr-278, Gly-289 to Arg-294, Lys-397 to Ser-403.
846040	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1438 as residues: Cys-6 to Ser-16, Glu-52 to Tyr-58, Asn-144 to Lys-153.
846073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1439 as residues: Arg-6 to Thr-16, Ile-43 to Gln-48, Leu-131 to Gly-139, Gly-147 to Asp-155, Asp-191 to Asp-198, Gly-204 to Thr-214.
846257	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1440 as residues: Lys-24 to Phe-44, Arg-58 to Gly-64, Ser-69 to Val-75, Lys-83 to Leu-90, Lys-93 to Glu-106.
HTXPN06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1441 as residues: Gly-1 to His-8.
HWAFU16R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1443 as residues: Ile-29 to Lys-34.
HOEMT44R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1445 as residues: Asp-73 to Lys-79.
HE2OW04R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1446 as residues: Cys-1 to Asn-6, Met-41 to Thr-51, Lys-77 to Thr-82.
HFCFG25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1447 as residues: Lys-29 to Ile-37, Arg-42 to Lys-47.
HAPQP94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1448 as residues: Pro-18 to Arg-23, Ala-43 to Ser-48.
H2CBI37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1449 as residues: Gly-5 to Lys-19, Phe-26 to Trp-31.
HCRNC25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1451 as residues: Leu-2 to Asn-8.
H2LAY26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1453 as residues: Pro-20 to His-36.
HAPQA06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1454 as residues: Tyr-15 to Ala-22, Ser-68 to Gly-74.
HBGOK18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1456 as residues: Gly-1 to Tyr-6, Asp-40 to Thr-47, Lys-91 to Glu-97.
HTWKF26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1458 as residues: Gly-31 to Gly-39.
HTAHR89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1459 as residues: Asp-73 to Gly-78.
HOELC27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1461 as residues: Asn-19 to Gln-25, Arg-33 to Ala-42, Pro-92 to Lys-99.
HWLVW62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1463 as residues: Lys-6 to Phe-13, His-25 to Ser-30, Glu-35 to Ala-41, Pro-57 to Gly-62.
HFKHD94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1465 as residues: Leu-1 to Gly-6, Pro-29 to Gly-42, Lys-52 to Gly-62.
HOFOA89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1467 as

	residues: Ala-20 to Lys-29, Arg-48 to Ile-56.
HCROL58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1470 as residues: Lys-1 to Ser-16.
HCHMV24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1473 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41.
HCHPT49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1474 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-70.
HCHPF59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1477 as residues: Arg-10 to Lys-22.
HS2IA81R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1478 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76.
HCRNC17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1479 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76, Lys-107 to Pro-112.
HISDJ39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1480 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76.
HASCG71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1482 as residues: Lys-6 to Ile-13.
HOEMO43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1483 as residues: Lys-31 to Gln-43.
HSYDG18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1486 as residues: Pro-1 to Glu-7, Asp-42 to Gly-47, Leu-61 to Glu-69, Lys-97 to Ile-107, Asp-115 to Gly-120.
HACAC47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1490 as residues: Ala-18 to Asp-26.
HLQFY41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1491 as residues: Val-11 to Asp-16, Glu-46 to Arg-51, Pro-55 to Lys-61, Lys-82 to Val-87.
HOFMO83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1492 as residues: Thr-31 to Asp-39, Thr-52 to Gly-60.
HFTDR22R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1493 as residues: Glu-1 to Trp-13.
HOEKC39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1495 as residues: Tyr-25 to Phe-32.
HOSNR06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1498 as residues: Thr-1 to Tyr-7.
HCQDL20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1499 as residues: Ser-12 to His-21.
HFKHD49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1503 as residues: Ala-42 to Glu-68.
H6EAQ15R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1506 as residues: Ala-1 to Leu-9.
HCFLM34R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1507 as residues: Lys-7 to Thr-13, Asp-24 to Thr-30, Gly-39 to Glu-52, Leu-70 to Ile-78.
HKIXL19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1510 as residues: Thr-2 to Asn-12, Gly-14 to Arg-24.
HAJRB09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1512 as residues: Pro-1 to Glu-8, Ala-10 to Gly-26.
HAPNI86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1513 as residues: Glu-53 to Ser-59, His-121 to Gln-130.
HAPRJ22R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1515 as residues: Gly-49 to Glu-64, Phe-76 to Thr-81.
HADGE45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1518 as residues: Arg-1 to Gln-26, Phe-59 to Lys-68.
HTXPN11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1519 as residues: Asp-1 to Lys-8, Asp-35 to Glu-41.
HCDBN37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1520 as residues: Cys-1 to Leu-15.

HABGF46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1527 as residues: Arg-11 to Arg-20, Asn-42 to Pro-57, Arg-64 to Ser-81.
HOELC15R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1528 as residues: His-8 to Gly-18, Gln-56 to Arg-61.
H2LAR26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1529 as residues: Glu-11 to Asn-16, Lys-38 to Glu-43, Ala-62 to Asp-67, Asp-80 to Ser-101.
H2LA V85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1530 as residues: Pro-14 to Thr-25, Asp-89 to Gln-102, Ile-121 to Thr-131.
HBSDC92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1531 as residues: Arg-1 to Leu-11.
HUTHN01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1532 as residues: Pro-34 to Ser-42, Cys-82 to Lys-89.
H2LAW03R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1533 as residues: Arg-120 to Arg-127.
HOEMO60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1534 as residues: Pro-6 to Arg-11, Phe-18 to Asn-23, Leu-36 to Thr-41.
HOELF72R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1537 as residues: Arg-1 to Pro-14, Gln-47 to Cys-52.
HAPNX59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1538 as residues: Cys-19 to Ser-25, Asp-28 to Trp-34, Lys-71 to Trp-76, Glu-112 to Lys-120.
HBJS17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1539 as residues: His-14 to Glu-26.
H2CBN02R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1542 as residues: Ala-1 to Pro-9, Arg-20 to Val-25.
H2CBV68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1543 as residues: Pro-41 to Asp-46, Leu-56 to Lys-61, Ala-72 to Thr-83, Lys-100 to Asn-106, Leu-125 to Thr-133.
H6EDK07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1544 as residues: Glu-32 to Glu-40, Val-45 to Thr-51, Pro-61 to Arg-67.
H2CBN54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1547 as residues: Cys-36 to Tyr-44, Glu-55 to Asp-61, Arg-79 to Pro-84, Asp-89 to Pro-105, Cys-108 to Ala-118, Lys-126 to Gly-142.
HWHPX50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1549 as residues: Pro-35 to Tyr-41.
HAPQD84R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1550 as residues: Lys-32 to Glu-39.
HAMGQ78 R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1554 as residues: Arg-46 to Arg-60, Glu-69 to Gly-78.
HODEV64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1555 as residues: Glu-1 to Gly-27, Asn-34 to Phe-48, Gly-63 to Gly-68.
HOEMK78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1558 as residues: Asp-27 to Gly-34, Ser-41 to Glu-49, Val-55 to Gln-62.
H2CBD13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1559 as residues: Ile-17 to His-22, Ser-24 to Arg-29.
HCFMU61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1560 as residues: Ser-10 to Asp-20, Leu-22 to Pro-36, Ser-42 to Lys-57, Gln-102 to Glu-110.
HOSNE94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1561 as residues: Arg-1 to Glu-6, Asp-74 to Ser-79, Asp-122 to Thr-127.
HHBEF47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1563 as residues: Arg-25 to His-31, Ala-50 to Ala-55.
HOSNR67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1566 as residues: Val-56 to Cys-61, Thr-108 to Gln-122, Gln-125 to Lys-131, Glu-140 to Leu-146.
H2LA V92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1567 as residues: Leu-3 to Ala-10, Pro-12 to Gly-21, Pro-32 to Pro-38, Ala-58 to Lys-64, Lys-67 to Val-75, Asp-92 to Leu-103.

HCLBZ27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1570 as residues: Asp-12 to Glu-18, Ala-22 to Ile-28, Ala-48 to Gly-60.
H2LAV11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1571 as residues: Thr-5 to Thr-14, Arg-20 to His-25, Arg-35 to Gly-40, Lys-58 to Arg-66, His-101 to Ser-107, Arg-111 to Lys-125.
HOEMJ56R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1573 as residues: Lys-27 to Tyr-48.
HDPLP40R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1576 as residues: Gly-1 to Cys-24, Cys-27 to Gly-43, Ala-46 to Trp-54, Ala-56 to Arg-68, Phe-83 to Arg-93.
HABAD57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1578 as residues: Gly-3 to Gln-16, Pro-36 to Ala-41.
H2CBL68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1581 as residues: Pro-19 to Val-24, Thr-31 to Gln-38, His-103 to Lys-114, Arg-129 to Leu-137, Pro-139 to Ser-146.
HNTNE17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1582 as residues: Val-8 to Lys-15, Tyr-25 to Asn-35, Lys-48 to Lys-53, Leu-77 to Asn-87, Asp-103 to Glu-108.
HBJLR37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1583 as residues: Asn-1 to His-11, Pro-82 to Glu-89, Pro-91 to Asp-96, Arg-103 to Met-109.
HOSNG20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1584 as residues: Thr-50 to Lys-55.
HBGNY11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1586 as residues: Thr-10 to Trp-15, Leu-24 to Ala-30, Leu-32 to Glu-38, Asn-41 to Ala-59, Arg-81 to Asp-89, Lys-104 to Lys-111.
HOEKC80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1587 as residues: Pro-49 to Phe-55, Gly-82 to Gly-88.
HFCESS3R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1589 as residues: Thr-12 to Leu-18.
HWAFE36R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1592 as residues: Glu-2 to Ile-9, Glu-34 to Lys-42.
HTXPF20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1594 as residues: Gly-4 to Thr-13.
HCRMD09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1595 as residues: Thr-2 to Asn-10, Glu-22 to Gln-30, Ser-58 to Gln-80, Gln-88 to Phe-96, Thr-99 to Tyr-104, Lys-110 to Asp-115.
HAJRB47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1596 as residues: Trp-18 to Ser-26, Asp-91 to Trp-99.
HAHCR61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1603 as residues: Ser-17 to Cys-25.
HAPQK19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1609 as residues: Arg-1 to Lys-10, Ser-15 to Tyr-22, Gly-25 to Leu-31.
HBGOK25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1615 as residues: Thr-38 to Trp-45, Pro-63 to Gln-70, Pro-78 to Gln-85.
HBJK105R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1619 as residues: Pro-43 to Trp-50.
HBLGD42R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1621 as residues: Pro-17 to Pro-27, Pro-32 to Tyr-38, Ala-44 to Pro-49.
HCHAK80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1627 as residues: Gln-3 to His-13, Gly-48 to Gly-55.
HCHMW79R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1628 as residues: Ser-16 to His-21, Ala-29 to Thr-35.
HCHOB92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1629 as residues: Lys-20 to Lys-28, Ser-53 to Leu-60.
HCLBO01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1630 as residues: Leu-1 to Leu-18.

HCRPC63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1633 as residues: Glu-1 to Arg-28.
HCUDC51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1634 as residues: Pro-22 to Gly-32, Trp-67 to Lys-81.
HDPFI40R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1635 as residues: Tyr-1 to Phe-6, Pro-9 to Asn-22, Arg-30 to Ala-38, Pro-47 to Lys-69.
HDPRZ54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1637 as residues: Gly-1 to Ala-8.
HFAUO64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1640 as residues: Asn-7 to Lys-29.
HJMAU64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1645 as residues: Leu-58 to Tyr-69.
HKBAC48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1647 as residues: Ser-16 to His-46, Arg-49 to Thr-58.
HKBAD57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1648 as residues: Thr-23 to Ser-30.
HODAY16R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1653 as residues: Pro-15 to Thr-20.
HOEMO27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1655 as residues: Ala-7 to Ser-12.
HOEMO62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1656 as residues: Ile-3 to Lys-11.
HOENU53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1658 as residues: Lys-37 to Asn-44.
HOGAP33R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1659 as residues: Gln-29 to Asp-35, Gln-43 to Thr-49.
HOSNF25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1661 as residues: Pro-29 to Arg-36.
HPIAC23R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1663 as residues: Thr-62 to Thr-69.
HRAAD31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1664 as residues: Val-1 to Thr-6, Arg-64 to Arg-69.
HRADJ57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1666 as residues: Val-11 to Gln-16.
HROAX48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1667 as residues: Gly-7 to Thr-20.
HTWDH05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1670 as residues: Ala-5 to Lys-11, Arg-29 to Ser-36.
HUTHF75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1673 as residues: Lys-40 to Gly-47.
HWAFW07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1674 as residues: Phe-44 to Arg-49.
HWLLX91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1676 as residues: Gly-29 to Asp-34.
HMIAI78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1678 as residues: Lys-24 to Arg-29, Cys-34 to Ala-41.
HBGFJ39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1679 as residues: Leu-21 to Asp-38.
HAMHH32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1680 as residues: Ala-1 to Cys-10, Glu-15 to Gln-21.
HOSNE37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1683 as residues: Lys-17 to Thr-23.
HWAFE41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1684 as residues: Ser-3 to Lys-8, Trp-92 to Leu-97.

The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of the polypeptide sequence shown in SEQ ID NO:Y, or an epitope of the polypeptide sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or encoded by a polynucleotide that hybridizes to the complement of an epitope encoding sequence of SEQ ID NO:X, or an epitope encoding sequence contained in the deposited cDNA clone under stringent hybridization conditions, or alternatively, under lower stringency hybridization conditions, as defined supra. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to this complementary strand under stringent hybridization conditions or alternatively, under lower stringency hybridization conditions, as defined supra.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described infra. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross-reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at
5 least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100
10 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more
15 of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe
20 et al., supra; Wilson et al., supra; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for
25 eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very
30 least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g., Sutcliffe et al., supra; Wilson et al., supra, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl- N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention, and immunogenic and/or antigenic epitope fragments thereof can be fused to other polypeptide sequences. For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light

- chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion disulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 270:3958-3964 (1995).
- 10 Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively,
- 15 deleting the Fc part after the fusion protein has been expressed, detected, and purified, may be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See,
- 20 D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue,

25 Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope

derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

5 Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., Proc. Natl. Acad. Sci. USA 10 88:8972- 897 (1991)). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni²⁺ nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing 15 buffers.

Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to 20 modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. 25 Biol. 287:265-76 (1999); and Lorenzo and Blasco, Biotechniques 24(2):308- 13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA 30 segments by homologous or site-specific recombination to generate variation in the

polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

As discussed herein, any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, polypeptides of the present invention which are shown to be secreted can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

In certain preferred embodiments, proteins of the invention comprise fusion proteins wherein the polypeptides are N and/or C- terminal deletion mutants. In preferred embodiments, the application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences encoding polypeptides having the amino acid sequence of the specific N- and C-terminal deletions mutants. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell

or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

5

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral
10 vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced
15 in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac
20 promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a
25 translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin
30 resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples

of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris* (ATCC Accession No. 201178)); insect cells such as *Drosophila* S2 and *Spodoptera Sf9* cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlsbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., *Basic Methods In Molecular Biology* (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most

preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether
5 directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition,
10 polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed
15 in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express polypeptides of the invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast
20 which can metabolize methanol as its sole carbon source. A main step in the methanol metabolism pathway is the oxidation of methanol to formaldehyde using O₂. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for O₂.
25 Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase genes (*AOX1*) is highly active. In the presence of methanol, alcohol oxidase produced from the *AOX1* gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. See, Ellis, S.B., *et al.*, *Mol. Cell. Biol.* 5:1111-21 (1985); Koutz, P.J., *et al.*, *Yeast*

5:167-77 (1989); Tschopp, J.F., *et al.*, *Nucl. Acids Res.* 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the *AOX1* regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

10 In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a polypeptide of the invention by virtue of the strong *AOX1* promoter linked to the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

15 Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

20 In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

25 In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and

which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

10 In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller et al., Nature, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized by use of a peptide synthesizer. Furthermore, if
15 desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid,
20 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β -methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L
25 (levorotary).

Non-naturally occurring variants may be produced using art-known mutagenesis techniques, which include, but are not limited to oligonucleotide mediated mutagenesis, alanine scanning, PCR mutagenesis, site directed mutagenesis (see, e.g., Carter et al., Nucl. Acids Res. 13:4331 (1986); and Zoller et al., Nucl. Acids
30 Res. 10:6487 (1982)), cassette mutagenesis (see, e.g., Wells et al., Gene 34:315

(1985)), restriction selection mutagenesis (*see, e.g., Wells et al., Philos. Trans. R. Soc. London SerA 317:415 (1986)*).

The invention additionally, encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between

about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release
5 desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200; 500; 1000; 1500; 2000; 2500; 3000; 3500; 4000; 4500; 5000; 5500; 6000; 6500; 7000; 7500; 8000; 8500; 9000; 9500; 10,000;
10 10,500; 11,000; 11,500; 12,000; 12,500; 13,000; 13,500; 14,000; 14,500; 15,000; 15,500; 16,000; 16,500; 17,000; 17,500; 18,000; 18,500; 19,000; 19,500; 20,000; 25,000; 30,000; 35,000; 40,000; 50,000; 55,000; 60,000; 65,000; 70,000; 75,000; 80,000; 85,000; 90,000; 95,000; or 100,000 kDa.

As noted above, the polyethylene glycol may have a branched structure.
15 Branched polyethylene glycols are described, for example, in U.S. Patent No. 5,643,575; Morpurgo *et al.*, *Appl. Biochem. Biotechnol.* 56:59-72 (1996); Vorobjev *et al.*, *Nucleosides Nucleotides* 18:2745-2750 (1999); and Caliceti *et al.*, *Bioconjug. Chem.* 10:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

20 The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik *et al.*, *Exp. Hematol.* 20:1028-1035 (1992) (reporting
25 pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues;
30 those having a free carboxyl group may include aspartic acid residues glutamic acid

residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

5 As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to a proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol to specific amino acid residues (e.g., lysine,
10 histidine, aspartic acid, glutamic acid, or cysteine) of the protein or to more than one type of amino acid residue (e.g., lysine, histidine, aspartic acid, glutamic acid, cysteine and combinations thereof) of the protein.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may
15 select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this
20 moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for
25 derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

As indicated above, pegylation of the proteins of the invention may be accomplished by any number of means. For example, polyethylene glycol may be
30 attached to the protein either directly or by an intervening linker. Linkerless systems

for attaching polyethylene glycol to proteins are described in Delgado *et al.*, *Crit. Rev. Thera. Drug Carrier Sys.* 9:249-304 (1992); Francis *et al.*, *Intern. J. of Hematol.* 68:1-18 (1998); U.S. Patent No. 4,002,531; U.S. Patent No. 5,349,052; WO 95/06058; and WO 98/32466, the disclosures of each of which are incorporated
5 herein by reference.

One system for attaching polyethylene glycol directly to amino acid residues of proteins without an intervening linker employs tresylated MPEG, which is produced by the modification of monmethoxy polyethylene glycol (MPEG) using tresylchloride ($\text{ClSO}_2\text{CH}_2\text{CF}_3$). Upon reaction of protein with tresylated MPEG,
10 polyethylene glycol is directly attached to amine groups of the protein. Thus, the invention includes protein-polyethylene glycol conjugates produced by reacting proteins of the invention with a polyethylene glycol molecule having a 2,2,2-trifluoroethane sulphonyl group.

Polyethylene glycol can also be attached to proteins using a number of
15 different intervening linkers. For example, U.S. Patent No. 5,612,460, the entire disclosure of which is incorporated herein by reference, discloses urethane linkers for connecting polyethylene glycol to proteins. Protein-polyethylene glycol conjugates wherein the polyethylene glycol is attached to the protein by a linker can also be produced by reaction of proteins with compounds such as MPEG-
20 succinimidylsuccinate, MPEG activated with 1,1'-carbonyldiimidazole, MPEG-2,4,5-trichloropenylcarbonate, MPEG-p-nitrophenolcarbonate, and various MPEG-succinate derivatives. A number additional polyethylene glycol derivatives and reaction chemistries for attaching polyethylene glycol to proteins are described in WO 98/32466, the entire disclosure of which is incorporated herein by reference.
25 Pegylated protein products produced using the reaction chemistries set out herein are included within the scope of the invention.

The number of polyethylene glycol moieties attached to each protein of the invention (*i.e.*, the degree of substitution) may also vary. For example, the pegylated proteins of the invention may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12,
30 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of

substitution within ranges such as 1-3, 2-4, 3-5, 4-6, 5-7, 6-8, 7-9, 8-10, 9-11, 10-12, 11-13, 12-14, 13-15, 14-16, 15-17, 16-18, 17-19, or 18-20 polyethylene glycol moieties per protein molecule. Methods for determining the degree of substitution are discussed, for example, in Delgado *et al.*, *Crit. Rev. Thera. Drug Carrier Sys.* 9:249-304 (1992).

The cancer antigen polypeptides of the invention may be in monomers or multimers (i.e., dimers, trimers, tetramers and higher multimers). Accordingly, the present invention relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, Therapeutics) containing them. In specific embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer, refers to a multimer containing only polypeptides corresponding to the amino acid sequence of SEQ ID NO:Y or an amino acid sequence encoded by SEQ ID NO:X, and/or an amino acid sequence encoded by the cDNA in a related cDNA clone contained in a deposited library (including fragments, variants, splice variants, and fusion proteins, corresponding to any one of these as described herein). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only polypeptides having an identical amino acid sequence. In another specific embodiment, a homomer of the invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (e.g., containing polypeptides having identical or different amino acid sequences) or a homotrimer (e.g., containing polypeptides having identical and/or different amino acid sequences). In additional embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (i.e., polypeptides of different proteins) in addition to

the polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer.

5 Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked, by for example, liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers
10 of the invention, such as, for example, heterotrimers or heterotetramers, are formed when polypeptides of the invention contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the invention are formed by covalent associations with and/or between the polypeptides
15 of the invention. Such covalent associations may involve one or more amino acid residues contained in the polypeptide sequence (e.g., that recited in SEQ ID NO:Y, or contained in a polypeptide encoded by SEQ ID NO:X, and/or by the cDNA in the related cDNA clone contained in a deposited library). In one instance, the covalent associations are cross-linking between cysteine residues located within the
20 polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide sequence in a fusion protein. In one example, covalent associations are between the
25 heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In a specific example, the covalent associations are between the heterologous sequence contained in a Fc fusion protein of the invention (as described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from
30 another protein that is capable of forming covalently associated multimers, such as for

example, osteoprotegerin (see, e.g., International Publication NO: WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another embodiment, two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper polypeptide sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science 240:1759, (1988)), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a polypeptide of the invention fused to a polypeptide sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric fusion protein is recovered from the culture supernatant using techniques known in the art.

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S. patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

In another example, proteins of the invention are associated by interactions between Flag® polypeptide sequence contained in fusion proteins of the invention

containing Flag® polypeptide sequence. In a further embodiment, associations of proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in Flag® fusion proteins of the invention and anti-Flag® antibody.

5 The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).
10 Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely
15 modified by the addition of cysteine or biotin to the C-terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the
20 polypeptide components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

 Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained
25 in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the
30 invention to a sequence encoding a linker polypeptide and then further to a synthetic

polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described
5 herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hydrophobic or signal peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

10

Antibodies

Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of SEQ ID NO:Y, and/or an epitope, of the present invention (as
15 determined by immunoassays well known in the art for assaying specific antibody-antigen binding). Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id
20 antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass
25 of immunoglobulin molecule.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')₂, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and
30 fragments comprising either a VL or VH domain. Antigen-binding antibody

fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region,
5 CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, sheep rabbit, goat, guinea pig, camel, horse, or chicken. As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from
10 human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described infra and, for example in, U.S. Patent No. 5,939,598 by Kucherlapati et al.

The antibodies of the present invention may be monospecific, bispecific, trispecific or of greater multispecificity. Multispecific antibodies may be specific for
15 different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol. 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920;
20 5,601,819; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, or by size
25 in contiguous amino acid residues. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that specifically bind polypeptides of the present invention, and allows for the exclusion of the same. □

Antibodies of the present invention may also be described or specified in
30 terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog,

or homolog of a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react with murine, rat and/or rabbit homologs of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under stringent hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or K_d less than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, or 10^{-15} M.

The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at least 95%, at least 90%, at least 85 %, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferably, antibodies of the present invention
5 bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor
10 activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described supra). In specific embodiments, antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at
15 least 50% of the activity in absence of the antibody.

The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the receptor-ligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing
20 antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of
25 the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Patent No.
30 5,811,097; Deng et al., Blood 92(6):1981-1988 (1998); Chen et al., Cancer Res.

58(16):3668-3678 (1998); Harrop et al., J. Immunol. 161(4):1786-1794 (1998); Zhu et al., Cancer Res. 58(15):3209-3214 (1998); Yoon et al., J. Immunol. 160(7):3170-3179 (1998); Prat et al., J. Cell. Sci. 111(Pt2):237-247 (1998); Pitard et al., J. Immunol. Methods 205(2):177-190 (1997); Liautard et al., Cytokine 9(4):233-241 (1997); Carlson et al., J. Biol. Chem. 272(17):11295-11301 (1997); Taryman et al., Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9):1153-1167 (1998); Bartunek et al., Cytokine 8(1):14-20 (1996) (which are all incorporated by reference herein in their entirety).

Antibodies of the present invention may be used, for example, but not limited to, to purify, detect, and target the polypeptides of the present invention, including both in vitro and in vivo diagnostic and therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) (incorporated by reference herein in its entirety).

As discussed in more detail below, the antibodies of the present invention may be used either alone or in combination with other compositions. The antibodies may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalently and non-covalently conjugations) to polypeptides or other compositions. For example, antibodies of the present invention may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, radionuclides, or toxins. See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Patent No. 5,314,995; and EP 396,387.

The antibodies of the invention include derivatives that are modified, i.e., by the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody from generating an anti-idiotypic response. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups,

proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more
5 non-classical amino acids.

The antibodies of the present invention may be generated by any suitable method known in the art. Polyclonal antibodies to an antigen-of- interest can be produced by various procedures well known in the art. For example, a polypeptide of the invention can be administered to various host animals including, but not limited
10 to, rabbits, mice, rats, etc. to induce the production of sera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols,
15 polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants are also well known in the art.

Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display
20 technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: Monoclonal Antibodies and T-Cell Hybridomas 563-681 (Elsevier, N.Y., 1981) (said references incorporated by
25 reference in their entirety). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art and are discussed in detail in the Examples. In a non-limiting example, mice can be immunized with a polypeptide of the invention or a cell expressing such peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP20 available from the ATCC. Hybridomas are selected and cloned by limited dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention. Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

Accordingly, the present invention provides methods of generating monoclonal antibodies as well as antibodies produced by the method comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably, the hybridoma is generated by fusing splenocytes isolated from a mouse immunized with an antigen of the invention with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind a polypeptide of the invention.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab')₂ fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). F(ab')₂ fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

For example, the antibodies of the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains expressed from a repertoire

or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods 182:41-50 (1995); Ames et al., J. Immunol. Methods 184:177-186 (1995); Kettleborough et al., Eur. J. Immunol. 24:952-958 (1994); Persic et al., Gene 187 9-18 (1997); Burton et al., Advances in Immunology 57:191-280 (1994); PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')₂ fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., BioTechniques 12(6):864-869 (1992); and Sawai et al., AJRI 34:26-34 (1995); and Better et al., Science 240:1041-1043 (1988) (said references incorporated by reference in their entireties).

Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Patents 4,946,778 and 5,258,498; Huston et al., Methods in Enzymology 203:46-88 (1991); Shu et al., PNAS 90:7995-7999

(1993); and Skerra et al., Science 240:1038-1040 (1988). For some uses, including in vivo use of antibodies in humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Gillies et al., (1989) J. Immunol. Methods 125:191-202; U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entirety. Humanized antibodies are antibody molecules from non-human species antibody that binds the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and a framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Patent No. 5,585,089; Riechmann et al., Nature 332:323 (1988), which are incorporated herein by reference in their entirety.) Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Patent Nos. 5,225,539; 5,530,101; and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Padlan, Molecular Immunology 28(4/5):489-498 (1991); Studnicka et al., Protein Engineering 7(6):805-814 (1994); Roguska. et al., PNAS 91:969-973 (1994)), and chain shuffling (U.S. Patent No. 5,565,332).

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody

libraries derived from human immunoglobulin sequences. See also, U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

5 Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes may be introduced randomly or by homologous recombination into mouse embryonic stem cells. Alternatively, the
10 human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes may be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous
15 deletion of the JH region prevents endogenous antibody production. The modified embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention.
20 Monoclonal antibodies directed against the antigen can be obtained from the immunized, transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG,
25 IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies; see Lonberg and Huszar, Int. Rev. Immunol. 13:65-93 (1995). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European
30 Patent No. 0 598 877; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825;

5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Freemont, CA) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., Bio/technology 12:899-903 (1988)).

Further, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotypic antibodies that "mimic" polypeptides of the invention using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, FASEB J. 7(5):437-444; (1989) and Nissinoff, J. Immunol. 147(8):2429-2438 (1991)). For example, antibodies which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to a ligand can be used to generate anti-idiotypes that "mimic" the polypeptide multimerization and/or binding domain and, as a consequence, bind to and neutralize polypeptide and/or its ligand. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize polypeptide ligand. For example, such anti-idiotypic antibodies can be used to bind a polypeptide of the invention and/or to bind its ligands/receptors, and thereby block its biological activity.

Polynucleotides Encoding Antibodies

The invention further provides polynucleotides comprising a nucleotide sequence encoding an antibody of the invention and fragments thereof. The invention also encompasses polynucleotides that hybridize under stringent or alternatively, under lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, that specifically binds to a

polypeptide of the invention, preferably, an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:Y.

The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, if the
5 nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody may be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., *BioTechniques* 17:242 (1994)), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligating of those oligonucleotides, and then amplification of
10 the ligated oligonucleotides by PCR.

Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the immunoglobulin may be chemically synthesized
15 or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe
20 specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence and corresponding amino acid sequence of the
25 antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, *Molecular Cloning, A Laboratory Manual*, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
30 and Ausubel et al., eds., 1998, *Current Protocols in Molecular Biology*, John Wiley &

Sons, NY, which are both incorporated by reference herein in their entireties), to generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

In a specific embodiment, the amino acid sequence of the heavy and/or light chain variable domains may be inspected to identify the sequences of the complementarity determining regions (CDRs) by methods that are well know in the art, e.g., by comparison to known amino acid sequences of other heavy and light chain variable regions to determine the regions of sequence hypervariability. Using routine recombinant DNA techniques, one or more of the CDRs may be inserted within framework regions, e.g., into human framework regions to humanize a non-human antibody, as described supra. The framework regions may be naturally occurring or consensus framework regions, and preferably human framework regions (see, e.g., Chothia et al., J. Mol. Biol. 278: 457-479 (1998) for a listing of human framework regions). Preferably, the polynucleotide generated by the combination of the framework regions and CDRs encodes an antibody that specifically binds a polypeptide of the invention. Preferably, as discussed supra, one or more amino acid substitutions may be made within the framework regions, and, preferably, the amino acid substitutions improve binding of the antibody to its antigen. Additionally, such methods may be used to make amino acid substitutions or deletions of one or more variable region cysteine residues participating in an intrachain disulfide bond to generate antibody molecules lacking one or more intrachain disulfide bonds. Other alterations to the polynucleotide are encompassed by the present invention and within the skill of the art.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., Proc. Natl. Acad. Sci. 81:851-855 (1984); Neuberger et al., Nature 312:604-608 (1984); Takeda et al., Nature 314:452-454 (1985)) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived

from a murine mAb and a human immunoglobulin constant region, e.g., humanized antibodies.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778; Bird, Science 242:423- 42 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature 334:544-54 (1989)) can be adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in E. coli may also be used (Skerra et al., Science 242:1038- 1041 (1988)).

Methods of Producing Antibodies

The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant expression techniques.

Recombinant expression of an antibody of the invention, or fragment, derivative or analog thereof, (e.g., a heavy or light chain of an antibody of the invention or a single chain antibody of the invention), requires construction of an expression vector containing a polynucleotide that encodes the antibody. Once a polynucleotide encoding an antibody molecule or a heavy or light chain of an antibody, or portion thereof (preferably containing the heavy or light chain variable domain), of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing a protein by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The invention, thus, provides replicable vectors comprising a

nucleotide sequence encoding an antibody molecule of the invention, or a heavy or light chain thereof, or a heavy or light chain variable domain, operably linked to a promoter. Such vectors may include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT
5 Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of the antibody may be cloned into such a vector for expression of the entire heavy or light chain.

The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an
10 antibody of the invention. Thus, the invention includes host cells containing a polynucleotide encoding an antibody of the invention, or a heavy or light chain thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the expression of double-chained antibodies, vectors encoding both the heavy and light chains may be co-expressed in the host cell
15 for expression of the entire immunoglobulin molecule, as detailed below.

A variety of host-expression vector systems may be utilized to express the antibody molecules of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with
20 the appropriate nucleotide coding sequences, express an antibody molecule of the invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast
25 expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid)
30 containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO,

BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *Escherichia coli*,
5 and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for
10 antibodies (Foecking et al., *Gene* 45:101 (1986); Cockett et al., *Bio/Technology* 8:2 (1990)).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the
15 generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., *EMBO J.* 2:1791 (1983)), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding
20 region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, *Nucleic Acids Res.* 13:3101-3109 (1985); Van Heeke & Schuster, *J. Biol. Chem.* 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by
25 adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhedrosis virus
30 (AcNPV) is used as a vector to express foreign genes. The virus grows in

Spodoptera frugiperda cells. The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

5 In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the antibody coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo
10 recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (e.g., see Logan & Shenk, Proc. Natl. Acad. Sci. USA 81:355-359 (1984)). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the
15 ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate
20 transcription enhancer elements, transcription terminators, etc. (see Bittner et al., Methods in Enzymol. 153:51-544 (1987)).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g.,
25 cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which
30 possess the cellular machinery for proper processing of the primary transcript,

glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERY, BHK, Hela, COS, MDCK, 293, 3T3, WI38, and in particular, breast cancer cell lines such as, for example, BT483, Hs578T, HTB2, BT20 and T47D, and normal mammary gland cell
5 line such as, for example, CRL7030 and Hs578Bst.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the antibody molecule may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by
10 appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection
15 and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the antibody molecule. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that interact directly or indirectly with the antibody molecule.

20 A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., Cell 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, Proc. Natl. Acad. Sci. USA 48:202 (1992)), and adenine phosphoribosyltransferase (Lowy et al., Cell 22:817 (1980)) genes can be employed in tk-, hgp^rt- or ap^rt- cells, respectively.
25 Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., Natl. Acad. Sci. USA 77:357 (1980); O'Hare et al., Proc. Natl. Acad. Sci. USA 78:1527 (1981)); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, Proc. Natl. Acad. Sci. USA 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-
30 418 Clinical Pharmacy 12:488-505; Wu and Wu, Biotherapy 3:87-95 (1991);

Tolstoshev. *Ann. Rev. Pharmacol. Toxicol.* 32:573-596 (1993); Mulligan, *Science* 260:926-932 (1993); and Morgan and Anderson, *Ann. Rev. Biochem.* 62:191-217 (1993); May, 1993, *TIB TECH* 11(5):155-215; and hygromycin, which confers resistance to hygromycin (Santerre et al., *Gene* 30:147 (1984)). Methods commonly known in the art of recombinant DNA technology may be routinely applied to select the desired recombinant clone, and such methods are described, for example, in Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, NY (1993); Kriegler, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY (1990); and in Chapters 12 and 13, Dracopoli et al. (eds), *Current Protocols in Human Genetics*, John Wiley & Sons, NY (1994); Colberre-Garapin et al., *J. Mol. Biol.* 150:1 (1981), which are incorporated by reference herein in their entireties.

The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, *The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning*, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., *Mol. Cell. Biol.* 3:257 (1983)).

The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, *Nature* 322:52 (1986); Kohler, *Proc. Natl. Acad. Sci. USA* 77:2197 (1980)). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once an antibody molecule of the invention has been produced by an animal, chemically synthesized, or recombinantly expressed, it may be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for
5 the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. In addition, the antibodies of the present invention or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art, to facilitate purification.

10 The present invention encompasses antibodies recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugations) to a polypeptide (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention to generate fusion proteins. The fusion does not necessarily need to be direct, but may occur through
15 linker sequences. The antibodies may be specific for antigens other than polypeptides (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention. For example, antibodies may be used to target the polypeptides of the present invention to particular cell types, either in vitro or in vivo, by fusing or conjugating the polypeptides of the present invention to antibodies specific for particular cell surface receptors. Antibodies fused or
20 conjugated to the polypeptides of the present invention may also be used in in vitro immunoassays and purification methods using methods known in the art. See e.g., Harbor et al., supra, and PCT publication WO 93/21232; EP 439,095; Naramura et al., Immunol. Lett. 39:91-99 (1994); U.S. Patent 5,474,981; Gillies et al., PNAS 89:1428-1432 (1992); Fell et al., J. Immunol. 146:2446-2452(1991), which are
25 incorporated by reference in their entireties.

The present invention further includes compositions comprising the polypeptides of the present invention fused or conjugated to antibody domains other than the variable regions. For example, the polypeptides of the present invention may
30 be fused or conjugated to an antibody Fc region, or portion thereof. The antibody

portion fused to a polypeptide of the present invention may comprise the constant region, hinge region, CH1 domain, CH2 domain, and CH3 domain or any combination of whole domains or portions thereof. The polypeptides may also be fused or conjugated to the above antibody portions to form multimers. For example, 5 Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present invention to antibody portions are known in the art. See, e.g., U.S. Patent Nos. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 10 5,447,851; 5,112,946; EP 307,434; EP 367,166; PCT publications WO 96/04388; WO 91/06570; Ashkenazi et al., Proc. Natl. Acad. Sci. USA 88:10535-10539 (1991); Zheng et al., J. Immunol. 154:5590-5600 (1995); and Vil et al., Proc. Natl. Acad. Sci. USA 89:11337-11341(1992) (said references incorporated by reference in their entireties).

15 As discussed, supra, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of SEQ ID NO:Y may be fused or conjugated to the above antibody portions to increase the in vivo half life of the polypeptides or for use in immunoassays using methods known in the art. Further, the polypeptides corresponding to SEQ ID NO:Y may be fused or conjugated to the above antibody 20 portions to facilitate purification. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP 394,827; Traunecker et al., Nature 331:84-86 (1988). The polypeptides of the present invention fused or conjugated to an antibody having 25 disulfide-linked dimeric structures (due to the IgG) may also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995)). In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP A 30 232,262). Alternatively, deleting the Fc part after the fusion protein has been

expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, Bennett et al., J. Molecular Recognition 8:52-58 (1995); Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).

Moreover, the antibodies or fragments thereof of the present invention can be fused to marker sequences, such as a peptide to facilitate purification. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., Cell 37:767 (1984)) and the "flag" tag.

The present invention further encompasses antibodies or fragments thereof conjugated to a diagnostic or therapeutic agent. The antibodies can be used diagnostically to, for example, monitor the development or progression of a tumor as part of a clinical testing procedure to, e.g., determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance may be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. See, for example, U.S. Patent No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Examples of suitable enzymes include horseradish

peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine
5 fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include ¹²⁵I, ¹³¹I, ¹¹¹In or ⁹⁹Tc.

Further, an antibody or fragment thereof may be conjugated to a therapeutic
10 moiety such as a cytotoxin, e.g., a cytostatic or cytocidal agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, ²¹³Bi. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include paclitaxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin,
15 dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine,
20 thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic
25 agents (e.g., vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the therapeutic agent or drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include,
30 for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria

toxin; a protein such as tumor necrosis factor, α -interferon, β -interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator, an apoptotic agent, e.g., TNF- α , TNF- β , AIM I (See, International Publication No. WO 97/33899), AIM II (See, International Publication No. WO 97/34911), Fas
5 Ligand (Takahashi *et al.*, *Int. Immunol.*, 6:1567-1574 (1994)), VEGF (See, International Publication No. WO 99/23105), a thrombotic agent or an anti-angiogenic agent, e.g., angiostatin or endostatin; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-
10 CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

15 Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon *et al.*, "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld *et al.* (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom *et al.*, "Antibodies For Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson *et al.* (eds.), pp.
20 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera *et al.* (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in *Monoclonal Antibodies For Cancer Detection And Therapy*,
25 Baldwin *et al.* (eds.), pp. 303-16 (Academic Press 1985), and Thorpe *et al.*, "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.* 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980, which
30 is incorporated herein by reference in its entirety.

An antibody, with or without a therapeutic moiety conjugated to it, administered alone or in combination with cytotoxic factor(s) and/or cytokine(s) can be used as a therapeutic.

5 *Immunophenotyping*

The antibodies of the invention may be utilized for immunophenotyping of cell lines and biological samples. The translation product of the gene of the present invention may be useful as a cell specific marker, or more specifically as a cellular marker that is differentially expressed at various stages of differentiation and/or
10 maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, will allow for the screening of cellular populations expressing the marker. Various techniques can be utilized using monoclonal antibodies to screen for cellular populations expressing the marker(s), and include magnetic separation using antibody-coated magnetic beads, "panning"
15 with antibody attached to a solid matrix (i.e., plate), and flow cytometry (See, e.g., U.S. Patent 5,985,660; and Morrison *et al.*, *Cell*, 96:737-49 (1999)).

These techniques allow for the screening of particular populations of cells, such as might be found with hematological malignancies (i.e. minimal residual disease (MRD) in acute leukemic patients) and "non-self" cells in transplantations to
20 prevent Graft-versus-Host Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might be found in human umbilical cord blood.

Assays For Antibody Binding

25 The antibodies of the invention may be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions,
30 gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays,

complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known in the art (see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by
5 reference herein in its entirety). Exemplary immunoassays are described briefly below (but are not intended by way of limitation).

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X- 100, 1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1%
10 Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSF, aprotinin, sodium vanadate), adding the antibody of interest to the cell lysate, incubating for a period of time (e.g., 1-4 hours) at 4° C, adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4° C, washing the beads in lysis buffer and resuspending the beads in
15 SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, e.g., western blot analysis. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding
20 immunoprecipitation protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.16.1.

Western blot analysis generally comprises preparing protein samples, electrophoresis of the protein samples in a polyacrylamide gel (e.g., 8%- 20% SDS-PAGE depending on the molecular weight of the antigen), transferring the protein
25 sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e.g., PBS with 3% BSA or non-fat milk), washing the membrane in washing buffer (e.g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer, washing the membrane in washing buffer, blocking the membrane with a
30 secondary antibody (which recognizes the primary antibody, e.g., an anti-human

antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e.g., ^{32}P or ^{125}I) diluted in blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding western blot protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.8.1.

ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected as well as other variations of ELISAs known in the art. For further discussion regarding ELISAs see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 11.2.1.

The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g., ^3H or ^{125}I) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by

scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e.g., ^3H or ^{125}I) in the presence of increasing amounts of an unlabeled second antibody.

5

Therapeutic Uses

The present invention is further directed to antibody-based therapies which involve administering antibodies of the invention to an animal, preferably a mammal, and most preferably a human, patient for treating one or more of the disclosed
10 diseases, disorders, or conditions. Therapeutic compounds of the invention include, but are not limited to, antibodies of the invention (including fragments, analogs and derivatives thereof as described herein) and nucleic acids encoding antibodies of the invention (including fragments, analogs and derivatives thereof and anti-idiotypic antibodies as described herein). The antibodies of the invention can be used to treat,
15 inhibit or prevent diseases, disorders or conditions associated with aberrant expression and/or activity of a polypeptide of the invention, including, but not limited to, any one or more of the diseases, disorders, or conditions described herein. The treatment and/or prevention of diseases, disorders, or conditions associated with aberrant expression and/or activity of a polypeptide of the invention includes, but is
20 not limited to, alleviating symptoms associated with those diseases, disorders or conditions. Antibodies of the invention may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the
25 present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes
30 without undue experimentation.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors (such as, e.g., IL-2, IL-3 and IL-7), for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

The antibodies of the invention may be administered alone or in combination with other types of treatments (e.g., radiation therapy, chemotherapy, hormonal therapy, immunotherapy and anti-tumor agents). Generally, administration of products of a species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, human antibodies, fragments derivatives, analogs, or nucleic acids, are administered to a human patient for therapy or prophylaxis.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides of the invention, including fragments thereof. Preferred binding affinities include those with a dissociation constant or K_d less than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, and 10^{-15} M.

25 *Gene Therapy*

In a specific embodiment, nucleic acids comprising sequences encoding antibodies or functional derivatives thereof, are administered to treat, inhibit or prevent a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention, by way of gene therapy. Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic

acid. In this embodiment of the invention, the nucleic acids produce their encoded protein that mediates a therapeutic effect.

Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

5 For general reviews of the methods of gene therapy, see Goldspiel et al., Clinical Pharmacy 12:488-505 (1993); Wu and Wu, Biotherapy 3:87-95 (1991); Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62:191-217 (1993); May, TIBTECH 11(5):155-215 (1993). Methods commonly known in the art
10 of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); and Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990).

In a preferred aspect, the compound comprises nucleic acid sequences
15 encoding an antibody, said nucleic acid sequences being part of expression vectors that express the antibody or fragments or chimeric proteins or heavy or light chains thereof in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the antibody coding region, said promoter being inducible or constitutive, and, optionally, tissue-specific. In another particular embodiment,
20 nucleic acid molecules are used in which the antibody coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the antibody encoding nucleic acids (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989). In
25 specific embodiments, the expressed antibody molecule is a single chain antibody; alternatively, the nucleic acid sequences include sequences encoding both the heavy and light chains, or fragments thereof, of the antibody.

Delivery of the nucleic acids into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid- carrying vectors, or
30 indirect, in which case, cells are first transformed with the nucleic acids in vitro, then

transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

In a specific embodiment, the nucleic acid sequences are directly administered in vivo, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing them as part of an appropriate nucleic acid expression vector and administering it so that they become intracellular, e.g., by infection using defective or attenuated retrovirals or other viral vectors (see U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, encapsulation in liposomes, microparticles, or microcapsules, or by administering them in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)) (which can be used to target cell types specifically expressing the receptors), etc. In another embodiment, nucleic acid-ligand complexes can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180; WO 92/22635; WO92/20316; WO93/14188, WO 93/20221). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989)).

In a specific embodiment, viral vectors that contains nucleic acid sequences encoding an antibody of the invention are used. For example, a retroviral vector can be used (see Miller et al., Meth. Enzymol. 217:581-599 (1993)). These retroviral vectors contain the components necessary for the correct packaging of the viral genome and integration into the host cell DNA. The nucleic acid sequences encoding the antibody to be used in gene therapy are cloned into one or more vectors, which

facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., *Biotherapy* 6:291-302 (1994), which describes the use of a retroviral vector to deliver the *mdrl* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., *J. Clin. Invest.* 93:644-651 (1994); Kiem et al., *Blood* 83:1467-1473 (1994); Salmons and Gunzberg, *Human Gene Therapy* 4:129-141 (1993); and Grossman and Wilson, *Curr. Opin. in Genetics and Devel.* 3:110-114 (1993).

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, *Current Opinion in Genetics and Development* 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout et al., *Human Gene Therapy* 5:3-10 (1994) demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., *Science* 252:431-434 (1991); Rosenfeld et al., *Cell* 68:143-155 (1992); Mastrangeli et al., *J. Clin. Invest.* 91:225-234 (1993); PCT Publication WO94/12649; and Wang, et al., *Gene Therapy* 2:775-783 (1995). In a preferred embodiment, adenovirus vectors are used.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., *Proc. Soc. Exp. Biol. Med.* 204:289-300 (1993); U.S. Patent No. 5,436,146).

Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection

to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method known in the art, including but not limited to transfection, electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, *Meth. Enzymol.* 217:599-618 (1993); Cohen et al., *Meth. Enzymol.* 217:618-644 (1993); Cline, *Pharmac. Ther.* 29:69-92m (1985) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes; blood cells such as Tlymphocytes, Blymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes; various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, nucleic acid sequences encoding an antibody are introduced into the cells such that they are expressible by the cells or their progeny, and the recombinant cells are then administered in vivo for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained in vitro can potentially be used in accordance with this embodiment of the present invention (see e.g. PCT Publication WO 94/08598; Stemple and Anderson, Cell 71:973-985 (1992); Rheinwald, Meth. Cell Bio. 21A:229 (1980); and Pittelkow and Scott, Mayo Clinic Proc. 61:771 (1986)).

10 In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription. Demonstration of Therapeutic or Prophylactic Activity

15 The compounds or pharmaceutical compositions of the invention are preferably tested in vitro, and then in vivo for the desired therapeutic or prophylactic activity, prior to use in humans. For example, in vitro assays to demonstrate the therapeutic or prophylactic utility of a compound or pharmaceutical composition include, the effect of a compound on a cell line or a patient tissue sample. The effect of the compound or composition on the cell line and/or tissue sample can be determined utilizing techniques known to those of skill in the art including, but not limited to, rosette formation assays and cell lysis assays. In accordance with the invention, in vitro assays which can be used to determine whether administration of a specific compound is indicated, include in vitro cell culture assays in which a patient tissue sample is grown in culture, and exposed to or otherwise administered a compound, and the effect of such compound upon the tissue sample is observed.

Therapeutic/Prophylactic Administration and Composition

30 The invention provides methods of treatment, inhibition and prophylaxis by administration to a subject of an effective amount of a compound or pharmaceutical

composition of the invention, preferably a polypeptide or antibody of the invention. In a preferred aspect, the compound is substantially purified (e.g., substantially free from substances that limit its effect or produce undesired side-effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human.

Formulations and methods of administration that can be employed when the compound comprises a nucleic acid or an immunoglobulin are described above; additional appropriate formulations and routes of administration can be selected from among those described herein below.

Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds or compositions may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compounds or compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compounds or compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after

surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. Preferably, when administering a protein, including an antibody, of the invention, care must be taken
5 to use materials to which the protein does not absorb.

In another embodiment, the compound or composition can be delivered in a vesicle, in particular a liposome (see Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353- 365 (1989); Lopez-Berestein, *ibid.*, pp.
10 317-327; see generally *ibid.*)

In yet another embodiment, the compound or composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.* 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)). In another
15 embodiment, polymeric materials can be used (see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, J., *Macromol. Sci. Rev. Macromol. Chem.* 23:61 (1983); see also Levy et al., *Science* 228:190 (1985); During et al., *Ann. Neurol.* 25:351 (1989); Howard et al., *J. Neurosurg.* 71:105 (1989)). In yet
20 another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in *Medical Applications of Controlled Release*, *supra*, vol. 2, pp. 115-138 (1984)).

25 Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered *in vivo* to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic
30 acid expression vector and administering it so that it becomes intracellular, e.g., by

use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection. or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox- like peptide which is known to enter the nucleus (see e.g.,
5 Joliot et al., Proc. Natl. Acad. Sci. USA 88:1864-1868 (1991)), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a compound, and a
10 pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the
15 therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as
20 liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH
25 buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate,
30 sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable

pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation
5 should suit the mode of administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the
10 composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the
15 composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The compounds of the invention can be formulated as neutral or salt forms.
20 Pharmaceutically acceptable salts include those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

25 The amount of the compound of the invention which will be effective in the treatment, inhibition and prevention of a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the
30 formulation will also depend on the route of administration, and the seriousness of

the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

For antibodies, the dosage administered to a patient is typically 0.1 mg/kg to 100 mg/kg of the patient's body weight. Preferably, the dosage administered to a patient is between 0.1 mg/kg and 20 mg/kg of the patient's body weight, more preferably 1 mg/kg to 10 mg/kg of the patient's body weight. Generally, human antibodies have a longer half-life within the human body than antibodies from other species due to the immune response to the foreign polypeptides. Thus, lower dosages of human antibodies and less frequent administration is often possible. Further, the dosage and frequency of administration of antibodies of the invention may be reduced by enhancing uptake and tissue penetration (e.g., into the brain) of the antibodies by modifications such as, for example, lipidation.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

Diagnosis and Imaging

Labeled antibodies, and derivatives and analogs thereof, which specifically bind to a polypeptide of interest can be used for diagnostic purposes to detect, diagnose, or monitor diseases, disorders, and/or conditions associated with the aberrant expression and/or activity of a polypeptide of the invention. The invention provides for the detection of aberrant expression of a polypeptide of interest, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level,

whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of aberrant expression.

The invention provides a diagnostic assay for diagnosing a disorder, comprising (a) assaying the expression of the polypeptide of interest in cells or body
5 fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a particular disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied
10 tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

15 Antibodies of the invention can be used to assay protein levels in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, et al., J. Cell . Biol. 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked
20 immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{112}In), and technetium (^{99}Tc); luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

25 One aspect of the invention is the detection and diagnosis of a disease or disorder associated with aberrant expression of a polypeptide of interest in an animal, preferably a mammal and most preferably a human. In one embodiment, diagnosis comprises: a) administering (for example, parenterally, subcutaneously, or intraperitoneally) to a subject an effective amount of a labeled molecule which
30 specifically binds to the polypeptide of interest; b) waiting for a time interval

following the administering for permitting the labeled molecule to preferentially concentrate at sites in the subject where the polypeptide is expressed (and for unbound labeled molecule to be cleared to background level); c) determining background level; and d) detecting the labeled molecule in the subject, such that
5 detection of labeled molecule above the background level indicates that the subject has a particular disease or disorder associated with aberrant expression of the polypeptide of interest. Background level can be determined by various methods including, comparing the amount of labeled molecule detected to a standard value previously determined for a particular system.

10 It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of ^{99m}Tc. The labeled antibody or antibody fragment will then preferentially
15 accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).

20 Depending on several variables, including the type of label used and the mode of administration, the time interval following the administration for permitting the labeled molecule to preferentially concentrate at sites in the subject and for unbound labeled molecule to be cleared to background level is 6 to 48 hours or 6 to 24 hours or 6 to 12 hours. In another embodiment the time interval following administration is 5
25 to 20 days or 5 to 10 days.

In an embodiment, monitoring of the disease or disorder is carried out by repeating the method for diagnosing the disease or disease, for example, one month after initial diagnosis, six months after initial diagnosis, one year after initial diagnosis, etc.

Presence of the labeled molecule can be detected in the patient using methods known in the art for in vivo scanning. These methods depend upon the type of label used. Skilled artisans will be able to determine the appropriate method for detecting a particular label. Methods and devices that may be used in the diagnostic methods of the invention include, but are not limited to, computed tomography (CT), whole body scan such as position emission tomography (PET), magnetic resonance imaging (MRI), and sonography.

In a specific embodiment, the molecule is labeled with a radioisotope and is detected in the patient using a radiation responsive surgical instrument (Thurston et al., U.S. Patent No. 5,441,050). In another embodiment, the molecule is labeled with a fluorescent compound and is detected in the patient using a fluorescence responsive scanning instrument. In another embodiment, the molecule is labeled with a positron emitting metal and is detected in the patient using positron emission-tomography. In yet another embodiment, the molecule is labeled with a paramagnetic label and is detected in a patient using magnetic resonance imaging (MRI).

Kits

The present invention provides kits that can be used in the above methods. In one embodiment, a kit comprises an antibody of the invention, preferably a purified antibody, in one or more containers. In a specific embodiment, the kits of the present invention contain a substantially isolated polypeptide comprising an epitope which is specifically immunoreactive with an antibody included in the kit. Preferably, the kits of the present invention further comprise a control antibody which does not react with the polypeptide of interest. In another specific embodiment, the kits of the present invention contain a means for detecting the binding of an antibody to a polypeptide of interest (e.g., the antibody may be conjugated to a detectable substrate such as a fluorescent compound, an enzymatic substrate, a radioactive compound or a luminescent compound, or a second antibody which recognizes the first antibody may be conjugated to a detectable substrate).

In another specific embodiment of the present invention, the kit is a diagnostic kit for use in screening serum containing antibodies specific against proliferative and/or cancerous polynucleotides and polypeptides. Such a kit may include a control antibody that does not react with the polypeptide of interest. Such a kit may include a substantially isolated polypeptide antigen comprising an epitope which is specifically immunoreactive with at least one anti-polypeptide antigen antibody. Further, such a kit includes means for detecting the binding of said antibody to the antigen (e.g., the antibody may be conjugated to a fluorescent compound such as fluorescein or rhodamine which can be detected by flow cytometry). In specific embodiments, the kit may include a recombinantly produced or chemically synthesized polypeptide antigen. The polypeptide antigen of the kit may also be attached to a solid support.

In a more specific embodiment the detecting means of the above-described kit includes a solid support to which said polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the polypeptide antigen can be detected by binding of the said reporter-labeled antibody.

In an additional embodiment, the invention includes a diagnostic kit for use in screening serum containing antigens of the polypeptide of the invention. The diagnostic kit includes a substantially isolated antibody specifically immunoreactive with polypeptide or polynucleotide antigens, and means for detecting the binding of the polynucleotide or polypeptide antigen to the antibody. In one embodiment, the antibody is attached to a solid support. In a specific embodiment, the antibody may be a monoclonal antibody. The detecting means of the kit may include a second, labeled monoclonal antibody. Alternatively, or in addition, the detecting means may include a labeled, competing antigen.

In one diagnostic configuration, test serum is reacted with a solid phase reagent having a surface-bound antigen obtained by the methods of the present invention. After binding with specific antigen antibody to the reagent and removing unbound serum components by washing, the reagent is reacted with reporter-labeled anti-human antibody to bind reporter to the reagent in proportion to the amount of

bound anti-antigen antibody on the solid support. The reagent is again washed to remove unbound labeled antibody, and the amount of reporter associated with the reagent is determined. Typically, the reporter is an enzyme which is detected by incubating the solid phase in the presence of a suitable fluorometric, luminescent or colorimetric substrate (Sigma, St. Louis, MO).

The solid surface reagent in the above assay is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plate or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

Thus, the invention provides an assay system or kit for carrying out this diagnostic method. The kit generally includes a support with surface-bound recombinant antigens, and a reporter-labeled anti-human antibody for detecting surface-bound anti-antigen antibody.

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The cancer antigen polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each sequence is specifically targeted to and can hybridize with a particular location on an individual human chromosome, thus each polynucleotide of the present invention can routinely be used as a chromosome marker using techniques known in the art.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably at least 15 bp (e.g., 15-25 bp) from the sequences shown in SEQ ID NO:X, or the complement thereto. Primers can optionally be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, preselection by hybridization to construct chromosome specific-cDNA libraries, and computer mapping techniques (See, e.g., Shuler, Trends Biotechnol 16:456-459 (1998) which is hereby incorporated by reference in its entirety).

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes).

Thus, the present invention also provides a method for chromosomal localization which involves (a) preparing PCR primers from the polynucleotide sequences in Table 3 and SEQ ID NO:X and (b) screening somatic cell hybrids containing individual chromosomes.

The polynucleotides of the present invention would likewise be useful for radiation hybrid mapping, HAPPY mapping, and long range restriction mapping. For a review of these techniques and others known in the art, see, e.g. Dear, "Genome Mapping: A Practical Approach," IRL Press at Oxford University Press, London (1997); Aydin, J. Mol. Med. 77:691-694 (1999); Hacia et al., Mol. Psychiatry 3:483-492 (1998); Herrick et al., Chromosome Res. 7:409-423 (1999); Hamilton et al., Methods Cell Biol. 62:265-280 (2000); and/or Ott, J. Hered. 90:68-70 (1999) each of which is hereby incorporated by reference in its entirety.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in a polynucleotide of the invention and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using the polynucleotides of the invention. Any of these alterations (altered expression,

chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention provides a method of detecting increased or decreased expression levels of the cancer polynucleotides in affected individuals as compared to
5 unaffected individuals using polynucleotides of the present invention and techniques known in the art, including but not limited to the method described in Example 11. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention also provides a diagnostic method useful during diagnosis
10 of a tissue specific disorder, including cancer, involving measuring the expression level of cancer polynucleotides in tissues or other cells or body fluid from an individual and comparing the measured gene expression level with a standard cancer polynucleotide expression level, whereby an increase or decrease in the gene expression level compared to the standard is indicative of a tissue specific disorder.

15 In still another embodiment, the invention includes a kit for analyzing samples for the presence of proliferative and/or cancerous polynucleotides derived from a test subject. In a general embodiment, the kit includes at least one polynucleotide probe containing a nucleotide sequence that will specifically hybridize with a polynucleotide of the invention and a suitable container. In a specific embodiment,
20 the kit includes two polynucleotide probes defining an internal region of the polynucleotide of the invention, where each probe has one strand containing a 31' mer-end internal to the region. In a further embodiment, the probes may be useful as primers for polymerase chain reaction amplification.

Where a diagnosis of a tissue specific disorder, including, for example,
25 diagnosis of a tumor, has already been made according to conventional methods, the present invention is useful as a prognostic indicator, whereby patients exhibiting enhanced or depressed cancer polynucleotide expression will experience a worse clinical outcome relative to patients expressing the gene at a level nearer the standard level.

By "measuring the expression level of cancer polynucleotides" is intended qualitatively or quantitatively measuring or estimating the level of the cancer polypeptide or the level of the mRNA encoding the cancer polypeptide in a first biological sample either directly (e.g., by determining or estimating absolute protein level or mRNA level) or relatively (e.g., by comparing to the cancer polypeptide level or mRNA level in a second biological sample). Preferably, the cancer polypeptide level or mRNA level in the first biological sample is measured or estimated and compared to a standard cancer polypeptide level or mRNA level, the standard being taken from a second biological sample obtained from an individual not having the tissue specific disorder or being determined by averaging levels from a population of individuals not having the tissue specific disorder. As will be appreciated in the art, once a standard cancer polypeptide level or mRNA level is known, it can be used repeatedly as a standard for comparison.

By "biological sample" is intended any biological sample obtained from an individual, body fluid, cell line, tissue culture, or other source which contains a cancer polypeptide or the corresponding mRNA. As indicated, biological samples include body fluids (such as sputum, breast milk, vaginal pool, bile, semen, lymph, sera, plasma, urine, synovial fluid and spinal fluid) which contain the cancer polypeptide, and other tissue sources found to express the cancer polypeptide. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art. Where the biological sample is to include mRNA, a tissue biopsy is the preferred source.

The method(s) provided above may preferably be applied in a diagnostic method and/or kits in which polynucleotides and/or polypeptides of the invention are attached to a solid support. In one exemplary method, the support may be a "gene chip" or a "biological chip" as described in US Patents 5,837,832, 5,874,219, and 5,856,174. Further, such a gene chip with cancer antigen polynucleotides attached may be used to identify polymorphisms between the cancer antigen polynucleotide sequences, with polynucleotides isolated from a test subject. The knowledge of such polymorphisms (i.e. their location, as well as, their existence) would be beneficial in

identifying disease loci for many disorders, such as for example, in neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions. Such a method is described in
5 US Patents 5,858,659 and 5,856,104. The US Patents referenced supra are hereby incorporated by reference in their entirety herein.

The present invention encompasses cancer polynucleotides that are chemically synthesized, or reproduced as peptide nucleic acids (PNA), or according to other methods known in the art. The use of PNAs would serve as the preferred form if the
10 polynucleotides of the invention are incorporated onto a solid support, or gene chip. For the purposes of the present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine, thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus oxides, or deoxyribose
15 derivatives, are not present in PNAs. As disclosed by P. E. Nielsen, M. Egholm, R. H. Berg and O. Buchardt, Science 254, 1497 (1991); and M. Egholm, O. Buchardt, L. Christensen, C. Behrens, S. M. Freier, D. A. Driver, R. H. Berg, S. K. Kim, B. Norden, and P. E. Nielsen, Nature 365, 666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact,
20 PNA binds more strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the strong
25 binding. In addition, it is more likely that single base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point ($T_{sub.m}$) by 8°-20° C, vs. 4°-16° C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce possible interference by salt during the
30 analysis.

The present invention have uses which include, but are not limited to, detecting cancer in mammals. In particular the invention is useful during diagnosis of pathological cell proliferative neoplasias which include, but are not limited to: acute myelogenous leukemias including acute monocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute erythroleukemia, acute megakaryocytic leukemia, and acute undifferentiated leukemia, etc.; and chronic myelogenous leukemias including chronic myelomonocytic leukemia, chronic granulocytic leukemia, etc. Preferred mammals include monkeys, apes, cats, dogs, cows, pigs, horses, rabbits and humans. Particularly preferred are humans.

Pathological cell proliferative disorders are often associated with inappropriate activation of proto-oncogenes. (Germann, E. P. et al., "The Etiology of Acute Leukemia: Molecular Genetics and Viral Oncology," in Neoplastic Diseases of the Blood, Vol 1., Wiernik, P. H. et al. eds., 161-182 (1985)). Neoplasias are now believed to result from the qualitative alteration of a normal cellular gene product, or from the quantitative modification of gene expression by insertion into the chromosome of a viral sequence, by chromosomal translocation of a gene to a more actively transcribed region, or by some other mechanism. (Germann et al., supra) It is likely that mutated or altered expression of specific genes is involved in the pathogenesis of some leukemias, among other tissues and cell types. (Germann et al., supra) Indeed, the human counterparts of the oncogenes involved in some animal neoplasias have been amplified or translocated in some cases of human leukemia and carcinoma. (Germann et al., supra)

For example, c-myc expression is highly amplified in the non-lymphocytic leukemia cell line HL-60. When HL-60 cells are chemically induced to stop proliferation, the level of c-myc is found to be downregulated. (International Publication Number WO 91/15580). However, it has been shown that exposure of HL-60 cells to a DNA construct that is complementary to the 5' end of c-myc or c-myb blocks translation of the corresponding mRNAs which downregulates expression of the c-myc or c-myb proteins and causes arrest of cell proliferation and

differentiation of the treated cells. (International Publication Number WO 91/15580; Wickstrom et al., Proc. Natl. Acad. Sci. 85:1028 (1988); Anfossi et al., Proc. Natl. Acad. Sci. 86:3379 (1989)). However, the skilled artisan would appreciate the present invention's usefulness is not limited to treatment of proliferative disorders of
5 hematopoietic cells and tissues, in light of the numerous cells and cell types of varying origins which are known to exhibit proliferative phenotypes.

In addition to the foregoing, a cancer antigen polynucleotide can be used to control gene expression through triple helix formation or through antisense DNA or RNA. Antisense techniques are discussed, for example, in Okano, J. Neurochem. 56:
10 560 (1991); "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance Lee et al., Nucleic Acids Research 6: 3073 (1979); Cooney et al., Science 241: 456 (1988); and Dervan et al., Science 251: 1360 (1991). Both methods rely on binding of the polynucleotide to a complementary DNA or RNA. For these
15 techniques, preferred polynucleotides are usually oligonucleotides 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as
20 Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. The oligonucleotide described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of
25 polypeptide of the present invention antigens. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease, and in particular, for the treatment of proliferative diseases and/or conditions.

Polynucleotides of the present invention are also useful in gene therapy. One
30 goal of gene therapy is to insert a normal gene into an organism having a defective

gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

5 The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for
10 identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

 The polynucleotides of the present invention can also be used as an alternative
15 to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an
20 individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

 Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen,
25 synovial fluid, amniotic fluid, breast milk, lymph, pulmonary sputum or surfactant, urine, fecal matter, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erichsen, PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are
30 digested with one or more restriction enzymes, yielding an identifying set of bands on

a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to cancer polynucleotides prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention are also useful as hybridization probes for differential identification of the tissue(s) or cell type(s) present in a biological sample. Similarly, polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of the tissue(s) (e.g., immunohistochemistry assays) or cell type(s) (e.g., immunocytochemistry assays). In addition, for a number of disorders of the above tissues or cells, significantly higher or lower levels of gene expression of the polynucleotides/polypeptides of the present invention may be detected in certain tissues (e.g., tissues expressing polypeptides and/or polynucleotides of the present invention, cancer tissues and/or cancerous and/or wounded tissues) or bodily fluids (e.g., semen, vaginal pool, breast milk, bile, lymph, serum, plasma, urine, synovial fluid or spinal fluid) taken from an individual having such a disorder, relative to a "standard" gene expression level, i.e., the expression level in healthy tissue from an individual not having the disorder.

Thus, the invention provides a diagnostic method of a disorder, which involves: (a) assaying gene expression level in cells or body fluid of an individual; (b) comparing the gene expression level with a standard gene expression level, whereby an increase or decrease in the assayed gene expression level compared to the standard expression level is indicative of a disorder.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making
5 oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

10 Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

Polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of the tissue(s) (e.g., immunohistochemistry assays such as, for example, ABC
15 immunoperoxidase (Hsu et al., J. Histochem. Cytochem. 29:577-580 (1981)) or cell type(s) (e.g., immunocytochemistry assays).

Antibodies can be used to assay levels of polypeptides encoded by polynucleotides of the invention in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, et al., J. Cell. Biol. 105:3087-3096
20 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine
25 (¹³¹I, ¹²⁵I, ¹²³I, ¹²¹I), carbon (¹⁴C), sulfur (³⁵S), tritium (³H), indium (^{115m}In, ^{113m}In, ¹¹²In, ¹¹¹In), and technetium (⁹⁹Tc, ^{99m}Tc), thallium (²⁰¹Tl), gallium (⁶⁸Ga, ⁶⁷Ga), palladium (¹⁰³Pd), molybdenum (⁹⁹Mo), xenon (¹³³Xe), fluorine (¹⁸F), ¹⁵³Sm, ¹⁷⁷Lu, ¹⁵⁹Gd, ¹⁴⁹Pm, ¹⁴⁰La, ¹⁷⁵Yb, ¹⁶⁶Ho, ⁹⁰Y, ⁴⁷Sc, ¹⁸⁶Re, ¹⁸⁸Re, ¹⁴²Pr, ¹⁰⁵Rh, ⁹⁷Ru; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and
30 rhodamine, and biotin.

In addition to assaying levels of polypeptide of the present invention in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I , ^{112}In , $^{99\text{m}}\text{Tc}$, (^{131}I , ^{125}I , ^{123}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium ($^{115\text{m}}\text{In}$, $^{113\text{m}}\text{In}$, ^{112}In , ^{111}In), and technetium (^{99}Tc , $^{99\text{m}}\text{Tc}$), thallium (^{201}Tl), gallium (^{68}Ga , ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F , ^{153}Sm , ^{177}Lu , ^{159}Gd , ^{149}Pm , ^{140}La , ^{175}Yb , ^{166}Ho , ^{90}Y , ^{47}Sc , ^{186}Re , ^{188}Re , ^{142}Pr , ^{105}Rh , ^{97}Ru), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously or intraperitoneally) into the mammal to be examined for immune system disorder. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of $^{99\text{m}}\text{Tc}$. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which express the polypeptide encoded by a polynucleotide of the invention. *In vivo* tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments" (Chapter 13 in *Tumor Imaging: The Radiochemical Detection of Cancer*, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982)).

In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (e.g., polypeptides encoded by polynucleotides of the invention and/or

antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate
5 episomally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention in association with toxins or cytotoxic prodrugs.

10 By "toxin" is meant one or more compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not
15 limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin.
20 "Toxin" also includes a cytostatic or cytotoxic agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, ^{213}Bi , or other radioisotopes such as, for example, ^{103}Pd , ^{133}Xe , ^{131}I , ^{68}Ge , ^{57}Co , ^{65}Zn , ^{85}Sr , ^{32}P , ^{35}S , ^{90}Y , ^{153}Sm , ^{153}Gd , ^{169}Yb , ^{51}Cr , ^{54}Mn , ^{75}Se , ^{113}Sn , $^{90}\text{Yttrium}$, ^{117}Tin , $^{186}\text{Rhenium}$, $^{166}\text{Holmium}$, and $^{188}\text{Rhenium}$; luminescent labels, such as luminol; and fluorescent
25 labels, such as fluorescein and rhodamine, and biotin.

Techniques known in the art may be applied to label polypeptides of the invention (including antibodies). Such techniques include, but are not limited to, the use of bifunctional conjugating agents (see e.g., U.S. Patent Nos. 5,756,065; 5,714,631; 5,696,239; 5,652,361; 5,505,931; 5,489,425; 5,435,990; 5,428,139;

5,342,604; 5,274,119; 4,994,560; and 5,808,003; the contents of each of which are hereby incorporated by reference in its entirety).

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression level of a cancer polypeptide of the present invention in cells or body fluid of an individual; and (b) comparing the assayed polypeptide expression level with a standard polypeptide expression level, whereby an increase or decrease in the assayed polypeptide expression level compared to the standard expression level is indicative of a disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Moreover, cancer antigen polypeptides of the present invention can be used to treat or prevent diseases or conditions such as, for example, neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B, SOD, catalase, DNA repair proteins), to inhibit the activity of a polypeptide (e.g., an oncogene or tumor suppressor), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth inhibition, enhancement of the immune response to proliferative cells or tissues).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease (as described supra, and elsewhere herein). For example,

administration of an antibody directed to a polypeptide of the present invention can bind, and/or neutralize the polypeptide, and/or reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

5 At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover,
10 the polypeptides of the present invention can be used to test the following biological activities.

Gene Therapy Methods

Another aspect of the present invention is to gene therapy methods for treating
15 or preventing disorders, diseases and conditions. The gene therapy methods relate to the introduction of nucleic acid (DNA, RNA and antisense DNA or RNA) sequences into an animal to achieve expression of the polypeptide of the present invention. This method requires a polynucleotide which codes for a polypeptide of the present invention operatively linked to a promoter and any other genetic elements necessary
20 for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques are known in the art, see, for example, WO90/11092, which is herein incorporated by reference.

Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) comprising a promoter operably linked to a
25 polynucleotide of the present invention ex vivo, with the engineered cells then being provided to a patient to be treated with the polypeptide of the present invention. Such methods are well-known in the art. For example, see Belldgrun, A., et al., J. Natl. Cancer Inst. 85: 207-216 (1993); Ferrantini, M. et al., Cancer Research 53: 1107-1112 (1993); Ferrantini, M. et al., J. Immunology 153: 4604-4615 (1994); Kaido, T., et al.,
30 Int. J. Cancer 60: 221-229 (1995); Ogura, H., et al., Cancer Research 50: 5102-5106

(1990); Santodonato, L., et al., Human Gene Therapy 7:1-10 (1996); Santodonato, L., et al., Gene Therapy 4:1246-1255 (1997); and Zhang, J.-F. et al., Cancer Gene Therapy 3: 31-38 (1996)), which are herein incorporated by reference. In one embodiment, the cells which are engineered are arterial cells. The arterial cells may be reintroduced into the patient through direct injection to the artery, the tissues surrounding the artery, or through catheter injection.

As discussed in more detail below, the polynucleotide constructs can be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, and the like). The polynucleotide constructs may be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

In one embodiment, the polynucleotide of the present invention is delivered as a naked polynucleotide. The term "naked" polynucleotide, DNA or RNA refers to sequences that are free from any delivery vehicle that acts to assist, promote or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotide of the present invention can also be delivered in liposome formulations and lipofectin formulations and the like can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in U.S. Patent Nos. 5,593,972, 5,589,466, and 5,580,859, which are herein incorporated by reference.

The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Appropriate vectors include pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; pSVK3, pBPV, pMSG and pSVL available from Pharmacia; and pEF1/V5, pcDNA3.1, and pRc/CMV2 available from Invitrogen. Other suitable vectors will be readily apparent to the skilled artisan.

Any strong promoter known to those skilled in the art can be used for driving the expression of the polynucleotide sequence. Suitable promoters include adenoviral

promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus (CMV) promoter; the respiratory syncytial virus (RSV) promoter; inducible promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoA1 promoter; human
5 globin promoters; viral thymidine kinase promoters, such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs; the b-actin promoter; and human growth hormone promoters. The promoter also may be the native promoter for the polynucleotide of the present invention.

Unlike other gene therapy techniques, one major advantage of introducing
10 naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct can be delivered to the interstitial space of tissues
15 within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular, fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in
20 the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the
25 tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. In vivo muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked nucleic acid sequence injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 mg/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration.

The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked DNA constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The naked polynucleotides are delivered by any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, and so-called "gene guns". These delivery methods are known in the art.

The constructs may also be delivered with delivery vehicles such as viral sequences, viral particles, liposome formulations, lipofectin, precipitating agents, etc. Such methods of delivery are known in the art.

In certain embodiments, the polynucleotide constructs are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner et al., Proc. Natl. Acad. Sci. USA (1987) 84:7413-7416, which is herein incorporated by reference); mRNA (Malone et al., Proc. Natl. Acad. Sci. USA (1989) 86:6077-6081, which is herein incorporated by reference); and purified

transcription factors (Debs et al., J. Biol. Chem. (1990) 265:10189-10192, which is herein incorporated by reference), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO
5 BRL, Grand Island, N.Y. (See, also, Felgner et al., Proc. Natl Acad. Sci. USA (1987) 84:7413-7416, which is herein incorporated by reference). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).

10 Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication No. WO 90/11092 (which is herein incorporated by reference) for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., P. Felgner et al., Proc.
15 Natl. Acad. Sci. USA 84:7413-7417, which is herein incorporated by reference. Similar methods can be used to prepare liposomes from other cationic lipid materials.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol,
20 phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

25 For example, commercially dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen
30 gas into a sonication vial. The sample is placed under a vacuum pump overnight and

is hydrated the following day with deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged vesicles can be prepared without sonication
5 to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred.
10 The various liposome-nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger et al., *Methods of Immunology* (1983), 101:512-527, which is herein incorporated by reference. For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated.
15 SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and
20 then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include Ca^{2+} -EDTA chelation (Papahadjopoulos et al., *Biochim. Biophys. Acta*
25 (1975) 394:483; Wilson et al., *Cell* (1979) 17:77); ether injection (Deamer, D. and Bangham, A., *Biochim. Biophys. Acta* (1976) 443:629; Ostro et al., *Biochem. Biophys. Res. Commun.* (1977) 76:836; Fraley et al., *Proc. Natl. Acad. Sci. USA* (1979) 76:3348); detergent dialysis (Enoch, H. and Strittmatter, P., *Proc. Natl. Acad. Sci. USA* (1979) 76:145); and reverse-phase evaporation (REV) (Fraley et al., *J. Biol.*
30 *Chem.* (1980) 255:10431; Szoka, F. and Papahadjopoulos, D., *Proc. Natl. Acad. Sci.*

USA (1978) 75:145; Schaefer-Ridder et al., Science (1982) 215:166), which are herein incorporated by reference.

Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ration will be from about 5:1 to about 1:5. More preferably, the
5 ration will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

U.S. Patent No. 5,676,954 (which is herein incorporated by reference) reports on the injection of genetic material, complexed with cationic liposomes carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469
10 (which are herein incorporated by reference) provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 (which are herein incorporated by reference) provide methods for delivering DNA-cationic lipid complexes to mammals.

15 In certain embodiments, cells are engineered, ex vivo or in vivo, using a retroviral particle containing RNA which comprises a sequence encoding a polypeptide of the present invention. Retroviruses from which the retroviral plasmid vectors may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, Rous sarcoma Virus, Harvey Sarcoma Virus, avian
20 leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PE501, PA317, R-2, R-AM, PA12, T19-14X, VT-
25 19-17-H2, RCRE, RCRIP, GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human Gene Therapy 1:5-14 (1990), which is incorporated herein by reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO₄ precipitation. In one alternative, the retroviral

plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include polynucleotide encoding a polypeptide of the present invention. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either
5 in vitro or in vivo. The transduced eukaryotic cells will express a polypeptide of the present invention.

In certain other embodiments, cells are engineered, ex vivo or in vivo, with polynucleotide contained in an adenovirus vector. Adenovirus can be manipulated
10 such that it encodes and expresses a polypeptide of the present invention, and at the same time is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. Adenovirus expression is achieved without integration of the viral DNA into the host cell chromosome, thereby alleviating concerns about insertional mutagenesis. Furthermore, adenoviruses have been used as live enteric vaccines for many years
15 with an excellent safety profile (Schwartz, A. R. et al. (1974) Am. Rev. Respir. Dis.109:233-238). Finally, adenovirus mediated gene transfer has been demonstrated in a number of instances including transfer of alpha-1-antitrypsin and CFTR to the lungs of cotton rats (Rosenfeld, M. A. et al. (1991) Science 252:431-434; Rosenfeld et al., (1992) Cell 68:143-155). Furthermore, extensive studies to attempt to establish
20 adenovirus as a causative agent in human cancer were uniformly negative (Green, M. et al. (1979) Proc. Natl. Acad. Sci. USA 76:6606).

Suitable adenoviral vectors useful in the present invention are described, for example, in Kozarsky and Wilson, Curr. Opin. Genet. Devel. 3:499-503 (1993); Rosenfeld et al., Cell 68:143-155 (1992); Engelhardt et al., Human Genet. Ther.
25 4:759-769 (1993); Yang et al., Nature Genet. 7:362-369 (1994); Wilson et al., Nature 365:691-692 (1993); and U.S. Patent No. 5,652,224, which are herein incorporated by reference. For example, the adenovirus vector Ad2 is useful and can be grown in human 293 cells. These cells contain the E1 region of adenovirus and constitutively express Ela and Elb, which complement the defective adenoviruses by providing the

products of the genes deleted from the vector. In addition to Ad2, other varieties of adenovirus (e.g., Ad3, Ad5, and Ad7) are also useful in the present invention.

Preferably, the adenoviruses used in the present invention are replication deficient. Replication deficient adenoviruses require the aid of a helper virus and/or packaging cell line to form infectious particles. The resulting virus is capable of infecting cells and can express a polynucleotide of interest which is operably linked to a promoter, but cannot replicate in most cells. Replication deficient adenoviruses may be deleted in one or more of all or a portion of the following genes: E1a, E1b, E3, E4, E2a, or L1 through L5.

In certain other embodiments, the cells are engineered, ex vivo or in vivo, using an adeno-associated virus (AAV). AAVs are naturally occurring defective viruses that require helper viruses to produce infectious particles (Muzyczka, N., Curr. Topics in Microbiol. Immunol. 158:97 (1992)). It is also one of the few viruses that may integrate its DNA into non-dividing cells. Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate, but space for exogenous DNA is limited to about 4.5 kb. Methods for producing and using such AAVs are known in the art. See, for example, U.S. Patent Nos. 5,139,941, 5,173,414, 5,354,678, 5,436,146, 5,474,935, 5,478,745, and 5,589,377.

For example, an appropriate AAV vector for use in the present invention will include all the sequences necessary for DNA replication, encapsidation, and host-cell integration. The polynucleotide construct is inserted into the AAV vector using standard cloning methods, such as those found in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (1989). The recombinant AAV vector is then transfected into packaging cells which are infected with a helper virus, using any standard technique, including lipofection, electroporation, calcium phosphate precipitation, etc. Appropriate helper viruses include adenoviruses, cytomegaloviruses, vaccinia viruses, or herpes viruses. Once the packaging cells are transfected and infected, they will produce infectious AAV viral particles which contain the polynucleotide construct. These viral particles are then used to transduce eukaryotic cells, either ex vivo or in vivo. The transduced cells will contain the

polynucleotide construct integrated into its genome, and will express a polypeptide of the invention.

Another method of gene therapy involves operably associating heterologous control regions and endogenous polynucleotide sequences (e.g. encoding a polypeptide of the present invention) via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not normally expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made, using standard techniques known in the art, which contain the promoter with targeting sequences flanking the promoter. Suitable promoters are described herein. The targeting sequence is sufficiently complementary to an endogenous sequence to permit homologous recombination of the promoter-targeting sequence with the endogenous sequence. The targeting sequence will be sufficiently near the 5' end of the desired endogenous polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination.

The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter. The amplified promoter and targeting sequences are digested and ligated together.

The promoter-targeting sequence construct is delivered to the cells, either as naked polynucleotide, or in conjunction with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, whole viruses, lipofection, precipitating agents, etc., described in more detail above. The P promoter-targeting sequence can

be delivered by any method, included direct needle injection, intravenous injection, topical administration, catheter infusion, particle accelerators, etc. The methods are described in more detail below.

5 The promoter-targeting sequence construct is taken up by cells. Homologous recombination between the construct and the endogenous sequence takes place, such that an endogenous sequence is placed under the control of the promoter. The promoter then drives the expression of the endogenous sequence.

10 Preferably, the polynucleotide encoding a polypeptide of the present invention contains a secretory signal sequence that facilitates secretion of the protein. Typically, the signal sequence is positioned in the coding region of the polynucleotide to be expressed towards or at the 5' end of the coding region. The signal sequence may be homologous or heterologous to the polynucleotide of interest and may be homologous or heterologous to the cells to be transfected. Additionally, the signal sequence may be chemically synthesized using methods known in the art.

15 Any mode of administration of any of the above-described polynucleotides constructs can be used so long as the mode results in the expression of one or more molecules in an amount sufficient to provide a therapeutic effect. This includes direct needle injection, systemic injection, catheter infusion, biolistic injectors, particle accelerators (i.e., "gene guns"), gelfoam sponge depots, other commercially available depot materials, osmotic pumps (e.g., Alza minipumps), oral or suppositorial solid (tablet or pill) pharmaceutical formulations, and decanting or topical applications during surgery. For example, direct injection of naked calcium phosphate-precipitated plasmid into rat liver and rat spleen or a protein-coated plasmid into the portal vein has resulted in gene expression of the foreign gene in the rat livers (Kaneda et al., Science 243:375 (1989)).

25 A preferred method of local administration is by direct injection. Preferably, a recombinant molecule of the present invention complexed with a delivery vehicle is administered by direct injection into or locally within the area of arteries. Administration of a composition locally within the area of arteries refers to injecting the composition centimeters and preferably, millimeters within arteries.

30

Another method of local administration is to contact a polynucleotide construct of the present invention in or around a surgical wound. For example, a patient can undergo surgery and the polynucleotide construct can be coated on the surface of tissue inside the wound or the construct can be injected into areas of tissue
5 inside the wound.

Therapeutic compositions useful in systemic administration, include recombinant molecules of the present invention complexed to a targeted delivery vehicle of the present invention. Suitable delivery vehicles for use with systemic administration comprise liposomes comprising ligands for targeting the vehicle to a
10 particular site.

Preferred methods of systemic administration, include intravenous injection, aerosol, oral and percutaneous (topical) delivery. Intravenous injections can be performed using methods standard in the art. Aerosol delivery can also be performed using methods standard in the art (see, for example, Stribling et al., Proc. Natl. Acad.
15 Sci. USA 189:11277-11281, 1992, which is incorporated herein by reference). Oral delivery can be performed by complexing a polynucleotide construct of the present invention to a carrier capable of withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers, include plastic capsules or tablets, such as those known in the art. Topical delivery can be performed by mixing a
20 polynucleotide construct of the present invention with a lipophilic reagent (e.g., DMSO) that is capable of passing into the skin.

Determining an effective amount of substance to be delivered can depend upon a number of factors including, for example, the chemical structure and biological activity of the substance, the age and weight of the animal, the precise
25 condition requiring treatment and its severity, and the route of administration. The frequency of treatments depends upon a number of factors, such as the amount of polynucleotide constructs administered per dose, as well as the health and history of the subject. The precise amount, number of doses, and timing of doses will be determined by the attending physician or veterinarian.

Therapeutic compositions of the present invention can be administered to any animal, preferably to mammals and birds. Preferred mammals include humans, dogs, cats, mice, rats, rabbits sheep, cattle, horses and pigs, with humans being particularly preferred.

5

Biological Activities

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, can be used in assays to test for one or more biological activities. If these polynucleotides or polypeptides, or agonists or antagonists of the present invention,
10 do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides, and agonists or antagonists could be used to treat the associated disease.

15 Immune Activity

A polypeptide or polynucleotide, or agonists or antagonists of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called
20 hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, polynucleotides or polypeptides, or agonists or antagonists
25 of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. Polynucleotides or polypeptides, or agonists or antagonists of the
30 present invention could be used to increase differentiation and proliferation of

hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia
5 telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

10 Moreover, polynucleotides or polypeptides, or agonists or antagonists of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, polynucleotides or polypeptides, or agonists or antagonists of the present invention could be used to treat blood coagulation disorders
15 (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, polynucleotides or polypeptides, or agonists or antagonists of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of
20 heart attacks (infarction), strokes, or scarring.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response
25 leading to the destruction of the host tissue. Therefore, the administration of polynucleotides or polypeptides, or agonists or antagonists of the present invention that can inhibit an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitis, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by polynucleotides or polypeptides, or agonists or antagonists of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of polynucleotides or polypeptides, or agonists or antagonists of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to modulate inflammation. For example, polynucleotides or polypeptides, or agonists or antagonists of the present invention may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including chronic prostatitis, granulomatous prostatitis and malacoplakia, inflammation associated with infection (e.g., septic shock, sepsis, or

systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

5

Hyperproliferative Disorders

Polynucleotides or polypeptides, or agonists or antagonists of the present invention can be used to treat or detect hyperproliferative disorders, including neoplasms. Polynucleotides or polypeptides, or agonists or antagonists of the present
10 invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, Polynucleotides or polypeptides, or agonists or antagonists of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing
15 antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such
20 as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by Polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to neoplasms located in the: colon, abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid,
25 pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by polynucleotides or polypeptides, or agonists or antagonists of the present invention.
30 Examples of such hyperproliferative disorders include, but are not limited to:

hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

- 5 One preferred embodiment utilizes polynucleotides of the present invention to inhibit aberrant cellular division, by gene therapy using the present invention, and/or protein fusions or fragments thereof.

 Thus, the present invention provides a method for treating cell proliferative disorders by inserting into an abnormally proliferating cell a polynucleotide of the present invention, wherein said polynucleotide represses said expression.

- 10 Another embodiment of the present invention provides a method of treating cell-proliferative disorders in individuals comprising administration of one or more active gene copies of the present invention to an abnormally proliferating cell or cells. In a preferred embodiment, polynucleotides of the present invention is a DNA construct comprising a recombinant expression vector effective in expressing a DNA sequence encoding said polynucleotides. In another preferred embodiment of the present invention, the DNA construct encoding the poynucleotides of the present invention is inserted into cells to be treated utilizing a retrovirus, or more preferrably an adenoviral vector (See G J. Nabel, et. al., PNAS 1999 96: 324-326, which is hereby incorporated by reference). In a most preferred embodiment, the viral vector is defective and will not transform non-proliferating cells, only proliferating cells. Moreover, in a preferred embodiment, the polynucleotides of the present invention inserted into proliferating cells either alone, or in combination with or fused to other polynucleotides, can then be modulated via an external stimulus (i.e. magnetic, specific small molecule, chemical, or drug administration, etc.), which acts upon the promoter upstream of said polynucleotides to induce expression of the encoded protein product. As such the beneficial therapeutic affect of the present invention may be expressly modulated (i.e. to increase, decrease, or inhibit expression of the present invention) based upon said external stimulus.

Polynucleotides of the present invention may be useful in repressing expression of oncogenic genes or antigens. By "repressing expression of the oncogenic genes " is intended the suppression of the transcription of the gene, the degradation of the gene transcript (pre-message RNA), the inhibition of splicing, the
5 destruction of the messenger RNA, the prevention of the post-translational modifications of the protein, the destruction of the protein, or the inhibition of the normal function of the protein.

For local administration to abnormally proliferating cells, polynucleotides of the present invention may be administered by any method known to those of skill in
10 the art including, but not limited to transfection, electroporation, microinjection of cells, or in vehicles such as liposomes, lipofectin, or as naked polynucleotides, or any other method described throughout the specification. The polynucleotide of the present invention may be delivered by known gene delivery systems such as, but not limited to, retroviral vectors (Gilboa, J. Virology 44:845 (1982); Hocke, Nature
15 320:275 (1986); Wilson, et al., Proc. Natl. Acad. Sci. U.S.A. 85:3014), vaccinia virus system (Chakrabarty et al., Mol. Cell Biol. 5:3403 (1985) or other efficient DNA delivery systems (Yates et al., Nature 313:812 (1985)) known to those skilled in the art. These references are exemplary only and are hereby incorporated by reference. In order to specifically deliver or transfect cells which are abnormally proliferating
20 and spare non-dividing cells, it is preferable to utilize a retrovirus, or adenoviral (as described in the art and elsewhere herein) delivery system known to those of skill in the art. Since host DNA replication is required for retroviral DNA to integrate and the retrovirus will be unable to self replicate due to the lack of the retrovirus genes needed for its life cycle. Utilizing such a retroviral delivery system for
25 polynucleotides of the present invention will target said gene and constructs to abnormally proliferating cells and will spare the non-dividing normal cells.

The polynucleotides of the present invention may be delivered directly to cell proliferative disorder/disease sites in internal organs, body cavities and the like by use of imaging devices used to guide an injecting needle directly to the disease site. The

polynucleotides of the present invention may also be administered to disease sites at the time of surgical intervention.

By "cell proliferative disease" is meant any human or animal disease or disorder, affecting any one or any combination of organs, cavities, or body parts, which is characterized by single or multiple local abnormal proliferations of cells, groups of cells, or tissues, whether benign or malignant.

Any amount of the polynucleotides of the present invention may be administered as long as it has a biologically inhibiting effect on the proliferation of the treated cells. Moreover, it is possible to administer more than one of the polynucleotide of the present invention simultaneously to the same site. By "biologically inhibiting" is meant partial or total growth inhibition as well as decreases in the rate of proliferation or growth of the cells. The biologically inhibitory dose may be determined by assessing the effects of the polynucleotides of the present invention on target malignant or abnormally proliferating cell growth in tissue culture, tumor growth in animals and cell cultures, or any other method known to one of ordinary skill in the art.

The present invention is further directed to antibody-based therapies which involve administering of anti-polypeptides and anti-polynucleotide antibodies to a mammalian, preferably human, patient for treating one or more of the described disorders. Methods for producing anti-polypeptides and anti-polynucleotide antibodies polyclonal and monoclonal antibodies are described in detail elsewhere herein. Such antibodies may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of

the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

In particular, the antibodies, fragments and derivatives of the present invention are useful for treating a subject having or developing cell proliferative and/or differentiation disorders as described herein. Such treatment comprises administering
5 a single or multiple doses of the antibody, or a fragment, derivative, or a conjugate thereof.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or
10 hematopoietic growth factors, for example., which serve to increase the number or activity of effector cells which interact with the antibodies.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and
15 therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides, including fragments thereof. Preferred binding affinities include those with a dissociation constant or Kd
20 less than $5 \times 10^{-6} \text{M}$, 10^{-6}M , $5 \times 10^{-7} \text{M}$, 10^{-7}M , $5 \times 10^{-8} \text{M}$, 10^{-8}M , $5 \times 10^{-9} \text{M}$, 10^{-9}M , $5 \times 10^{-10} \text{M}$, 10^{-10}M , $5 \times 10^{-11} \text{M}$, 10^{-11}M , $5 \times 10^{-12} \text{M}$, 10^{-12}M , $5 \times 10^{-13} \text{M}$, 10^{-13}M , $5 \times 10^{-14} \text{M}$, 10^{-14}M , $5 \times 10^{-15} \text{M}$, and 10^{-15}M .

Moreover, polypeptides of the present invention are useful in inhibiting the angiogenesis of proliferative cells or tissues, either alone, as a protein fusion, or in combination with other polypeptides directly or indirectly, as described elsewhere
25 herein. In a most preferred embodiment, said anti-angiogenesis effect may be achieved indirectly, for example, through the inhibition of hematopoietic, tumor-specific cells, such as tumor-associated macrophages (See Joseph IB, et al. J Natl Cancer Inst, 90(21):1648-53 (1998), which is hereby incorporated by reference). Antibodies directed to polypeptides or polynucleotides of the present invention may
30 also result in inhibition of angiogenesis directly, or indirectly (See Witte L, et al.,

Cancer Metastasis Rev. 17(2):155-61 (1998), which is hereby incorporated by reference)).

Polypeptides, including protein fusions, of the present invention, or fragments thereof may be useful in inhibiting proliferative cells or tissues through the induction of apoptosis. Said polypeptides may act either directly, or indirectly to induce apoptosis of proliferative cells and tissues, for example in the activation of a death-domain receptor, such as tumor necrosis factor (TNF) receptor-1, CD95 (Fas/APO-1), TNF-receptor-related apoptosis-mediated protein (TRAMP) and TNF-related apoptosis-inducing ligand (TRAIL) receptor-1 and -2 (See Schulze-Osthoff K, et.al., Eur J Biochem 254(3):439-59 (1998), which is hereby incorporated by reference). Moreover, in another preferred embodiment of the present invention, said polypeptides may induce apoptosis through other mechanisms, such as in the activation of other proteins which will activate apoptosis, or through stimulating the expression of said proteins, either alone or in combination with small molecule drugs or adjuvants, such as apoptonin, galectins, thioredoxins, antiinflammatory proteins (See for example, Mutat Res 400(1-2):447-55 (1998), Med Hypotheses.50(5):423-33 (1998), Chem Biol Interact. Apr 24;111-112:23-34 (1998), J Mol Med.76(6):402-12 (1998), Int J Tissue React;20(1):3-15 (1998), which are all hereby incorporated by reference).

Polypeptides, including protein fusions to, or fragments thereof, of the present invention are useful in inhibiting the metastasis of proliferative cells or tissues. Inhibition may occur as a direct result of administering polypeptides, or antibodies directed to said polypeptides as described elsewhere herein, or indirectly, such as activating the expression of proteins known to inhibit metastasis, for example alpha 4 integrins, (See, e.g., Curr Top Microbiol Immunol 1998;231:125-41, which is hereby incorporated by reference). Such therapeutic affects of the present invention may be achieved either alone, or in combination with small molecule drugs or adjuvants.

In another embodiment, the invention provides a method of delivering compositions containing the polypeptides of the invention (e.g., compositions containing polypeptides or polypeptide antibodies associated with heterologous

polypeptides, heterologous nucleic acids, toxins, or prodrugs) to targeted cells expressing the polypeptide of the present invention. Polypeptides or polypeptide antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. Polypeptides, protein fusions to, or fragments thereof, of the present invention are useful in enhancing the immunogenicity and/or antigenicity of proliferating cells or tissues, either directly, such as would occur if the polypeptides of the present invention 'vaccinated' the immune response to respond to proliferative antigens and immunogens, or indirectly, such as in activating the expression of proteins known to enhance the immune response (e.g. chemokines), to said antigens and immunogens.

Cardiovascular Disorders

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, may be used to treat cardiovascular disorders, including peripheral artery disease, such as limb ischemia.

Cardiovascular disorders include cardiovascular abnormalities, such as arterio-arterial fistula, arteriovenous fistula, cerebral arteriovenous malformations, congenital heart defects, pulmonary atresia, and Scimitar Syndrome. Congenital heart defects include aortic coarctation, cor triatriatum, coronary vessel anomalies, crisscross heart, dextrocardia, patent ductus arteriosus, Ebstein's anomaly, Eisenmenger complex, hypoplastic left heart syndrome, levocardia, tetralogy of fallot, transposition of great vessels, double outlet right ventricle, tricuspid atresia, persistent truncus arteriosus, and heart septal defects, such as aortopulmonary septal defect, endocardial cushion defects, Lutembacher's Syndrome, trilog of Fallot, ventricular heart septal defects.

Cardiovascular disorders also include heart disease, such as arrhythmias, carcinoid heart disease, high cardiac output, low cardiac output, cardiac tamponade, endocarditis (including bacterial), heart aneurysm, cardiac arrest, congestive heart failure, congestive cardiomyopathy, paroxysmal dyspnea, cardiac edema, heart hypertrophy, congestive cardiomyopathy, left ventricular hypertrophy, right

ventricular hypertrophy, post-infarction heart rupture, ventricular septal rupture, heart valve diseases, myocardial diseases, myocardial ischemia, pericardial effusion, pericarditis (including constrictive and tuberculous), pneumopericardium, postpericardiotomy syndrome, pulmonary heart disease, rheumatic heart disease,
5 ventricular dysfunction, hyperemia, cardiovascular pregnancy complications, Scimitar Syndrome, cardiovascular syphilis, and cardiovascular tuberculosis.

Arrhythmias include sinus arrhythmia, atrial fibrillation, atrial flutter, bradycardia, extrasystole, Adams-Stokes Syndrome, bundle-branch block, sinoatrial block, long QT syndrome, parasystole, Lown-Ganong-Levine Syndrome, Mahaim-type pre-excitation syndrome, Wolff-Parkinson-White syndrome, sick sinus
10 syndrome, tachycardias, and ventricular fibrillation. Tachycardias include paroxysmal tachycardia, supraventricular tachycardia, accelerated idioventricular rhythm, atrioventricular nodal reentry tachycardia, ectopic atrial tachycardia, ectopic junctional tachycardia, sinoatrial nodal reentry tachycardia, sinus tachycardia,
15 Torsades de Pointes, and ventricular tachycardia.

Heart valve disease include aortic valve insufficiency, aortic valve stenosis, hear murmurs, aortic valve prolapse, mitral valve prolapse, tricuspid valve prolapse, mitral valve insufficiency, mitral valve stenosis, pulmonary atresia, pulmonary valve insufficiency, pulmonary valve stenosis, tricuspid atresia, tricuspid valve
20 insufficiency, and tricuspid valve stenosis.

Myocardial diseases include alcoholic cardiomyopathy, congestive cardiomyopathy, hypertrophic cardiomyopathy, aortic subvalvular stenosis, pulmonary subvalvular stenosis, restrictive cardiomyopathy, Chagas cardiomyopathy, endocardial fibroelastosis, endomyocardial fibrosis, Kearns Syndrome, myocardial
25 reperfusion injury, and myocarditis.

Myocardial ischemias include coronary disease, such as angina pectoris, coronary aneurysm, coronary arteriosclerosis, coronary thrombosis, coronary vasospasm, myocardial infarction and myocardial stunning.

Cardiovascular diseases also include vascular diseases such as aneurysms,
30 angiodyplasia, angiomatosis, bacillary angiomatosis, Hippel-Lindau Disease,

Klippel-Trenaunay-Weber Syndrome. Sturge-Weber Syndrome, angioneurotic edema, aortic diseases, Takayasu's Arteritis, aortitis, Leriche's Syndrome, arterial occlusive diseases, arteritis, enarteritis, polyarteritis nodosa, cerebrovascular disorders, diabetic angiopathies, diabetic retinopathy, embolisms, thrombosis, erythromelalgia, hemorrhoids, hepatic veno-occlusive disease, hypertension, hypotension, ischemia, peripheral vascular diseases, phlebitis, pulmonary veno-occlusive disease, Raynaud's disease, CREST syndrome, retinal vein occlusion, Scimitar syndrome, superior vena cava syndrome, telangiectasia, atacia telangiectasia, hereditary hemorrhagic telangiectasia, varicocele, varicose veins, varicose ulcer, vasculitis, and venous insufficiency.

Aneurysms include dissecting aneurysms, false aneurysms, infected aneurysms, ruptured aneurysms, aortic aneurysms, cerebral aneurysms, coronary aneurysms, heart aneurysms, and iliac aneurysms.

Arterial occlusive diseases include arteriosclerosis, intermittent claudication, carotid stenosis, fibromuscular dysplasias, mesenteric vascular occlusion, Moyamoya disease, renal artery obstruction, retinal artery occlusion, and thromboangiitis obliterans.

Cerebrovascular disorders include carotid artery diseases, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformation, cerebral artery diseases, cerebral embolism and thrombosis, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, cerebral hemorrhage, epidural hematoma, subdural hematoma, subarachnoid hemorrhage, cerebral infarction, cerebral ischemia (including transient), subclavian steal syndrome, periventricular leukomalacia, vascular headache, cluster headache, migraine, and vertebrobasilar insufficiency.

Embolisms include air embolisms, amniotic fluid embolisms, cholesterol embolisms, blue toe syndrome, fat embolisms, pulmonary embolisms, and thromboembolisms. Thrombosis include coronary thrombosis, hepatic vein thrombosis, retinal vein occlusion, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, and thrombophlebitis.

Ischemia includes cerebral ischemia, ischemic colitis, compartment syndromes, anterior compartment syndrome, myocardial ischemia, reperfusion injuries, and peripheral limb ischemia. Vasculitis includes aortitis, arteritis, Behcet's Syndrome, Churg-Strauss Syndrome, mucocutaneous lymph node syndrome, 5 thromboangiitis obliterans, hypersensitivity vasculitis, Schoenlein-Henoch purpura, allergic cutaneous vasculitis, and Wegener's granulomatosis.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, are especially effective for the treatment of critical limb ischemia and coronary disease.

10 Polypeptides may be administered using any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, biolistic injectors, particle accelerators, gelfoam sponge depots, other commercially available depot materials, osmotic pumps, oral or suppository solid pharmaceutical formulations, decanting or 15 topical applications during surgery, aerosol delivery. Such methods are known in the art. Polypeptides may be administered as part of a Therapeutic, described in more detail below. Methods of delivering polynucleotides are described in more detail herein.

20 Anti-Angiogenesis Activity

The naturally occurring balance between endogenous stimulators and inhibitors of angiogenesis is one in which inhibitory influences predominate. Rastinejad *et al.*, *Cell* 56:345-355 (1989). In those rare instances in which neovascularization occurs under normal physiological conditions, such as wound 25 healing, organ regeneration, embryonic development, and female reproductive processes, angiogenesis is stringently regulated and spatially and temporally delimited. Under conditions of pathological angiogenesis such as that characterizing solid tumor growth, these regulatory controls fail. Unregulated angiogenesis becomes pathologic and sustains progression of many neoplastic and non-neoplastic diseases. 30 A number of serious diseases are dominated by abnormal neovascularization

including solid tumor growth and metastases, arthritis, some types of eye disorders, and psoriasis. See, e.g., reviews by Moses *et al.*, *Biotech.* 9:630-634 (1991); Folkman *et al.*, *N. Engl. J. Med.*, 333:1757-1763 (1995); Auerbach *et al.*, *J. Microvasc. Res.* 29:401-411 (1985); Folkman, *Advances in Cancer Research*, eds. Klein and Weinhouse, Academic Press, New York, pp. 175-203 (1985); Patz, *Am. J. Ophthalmol.* 94:715-743 (1982); and Folkman *et al.*, *Science* 221:719-725 (1983). In a number of pathological conditions, the process of angiogenesis contributes to the disease state. For example, significant data have accumulated which suggest that the growth of solid tumors is dependent on angiogenesis. Folkman and Klagsbrun, *Science* 235:442-447 (1987).

The polynucleotides encoding a polypeptide of the present invention may be administered along with other polynucleotides encoding an angiogenic protein. Examples of angiogenic proteins include, but are not limited to, acidic and basic fibroblast growth factors, VEGF-1, VEGF-2, VEGF-3, epidermal growth factor alpha and beta, platelet-derived endothelial cell growth factor, platelet-derived growth factor, tumor necrosis factor alpha, hepatocyte growth factor, insulin like growth factor, colony stimulating factor, macrophage colony stimulating factor, granulocyte/macrophage colony stimulating factor, and nitric oxide synthase.

The present invention provides for treatment of diseases or disorders associated with neovascularization by administration of the polynucleotides and/or polypeptides of the invention, as well as agonists or antagonists of the present invention. Malignant and metastatic conditions which can be treated with the polynucleotides and polypeptides, or agonists or antagonists of the invention include, but are not limited to, malignancies, solid tumors, and cancers described herein and otherwise known in the art (for a review of such disorders, see Fishman *et al.*, *Medicine*, 2d Ed., J. B. Lippincott Co., Philadelphia (1985)). Thus, the present invention provides a method of treating an angiogenesis-related disease and/or disorder, comprising administering to an individual in need thereof a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist of the invention. For example, polynucleotides, polypeptides, antagonists and/or agonists

may be utilized in a variety of additional methods in order to therapeutically treat a cancer or tumor. Cancers which may be treated with polynucleotides, polypeptides, antagonists and/or agonists include, but are not limited to solid tumors, including prostate, lung, breast, ovarian, stomach, pancreas, larynx, esophagus, testes, liver, parotid, biliary tract, colon, rectum, cervix, uterus, endometrium, kidney, bladder, thyroid cancer; primary tumors and metastases; melanomas; glioblastoma; Kaposi's sarcoma; leiomyosarcoma; non-small cell lung cancer; colorectal cancer; advanced malignancies; and blood born tumors such as leukemias. For example, polynucleotides, polypeptides, antagonists and/or agonists may be delivered topically, in order to treat cancers such as skin cancer, head and neck tumors, breast tumors, and Kaposi's sarcoma.

Within yet other aspects, polynucleotides, polypeptides, antagonists and/or agonists may be utilized to treat superficial forms of bladder cancer by, for example, intravesical administration. Polynucleotides, polypeptides, antagonists and/or agonists may be delivered directly into the tumor, or near the tumor site, via injection or a catheter. Of course, as the artisan of ordinary skill will appreciate, the appropriate mode of administration will vary according to the cancer to be treated. Other modes of delivery are discussed herein.

Polynucleotides, polypeptides, antagonists and/or agonists may be useful in treating other disorders, besides cancers, which involve angiogenesis. These disorders include, but are not limited to: benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; arteriosclerotic plaques; ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, uveitis and Pterygia (abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization;

telangiectasia; hemophiliac joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis.

For example, within one aspect of the present invention methods are provided for treating hypertrophic scars and keloids, comprising the step of administering a polynucleotide, polypeptide, antagonist and/or agonist of the invention to a hypertrophic scar or keloid.

Within one embodiment of the present invention polynucleotides, polypeptides, antagonists and/or agonists are directly injected into a hypertrophic scar or keloid, in order to prevent the progression of these lesions. This therapy is of particular value in the prophylactic treatment of conditions which are known to result in the development of hypertrophic scars and keloids (e.g., burns), and is preferably initiated after the proliferative phase has had time to progress (approximately 14 days after the initial injury), but before hypertrophic scar or keloid development. As noted above, the present invention also provides methods for treating neovascular diseases of the eye, including for example, corneal neovascularization, neovascular glaucoma, proliferative diabetic retinopathy, retrolental fibroplasia and macular degeneration.

Moreover, Ocular disorders associated with neovascularization which can be treated with the polynucleotides and polypeptides of the present invention (including agonists and/or antagonists) include, but are not limited to: neovascular glaucoma, diabetic retinopathy, retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of prematurity macular degeneration, corneal graft neovascularization, as well as other eye inflammatory diseases, ocular tumors and diseases associated with choroidal or iris neovascularization. See, e.g., reviews by Waltman *et al.*, *Am. J. Ophthalmol.* 85:704-710 (1978) and Gartner *et al.*, *Surv. Ophthalmol.* 22:291-312 (1978).

Thus, within one aspect of the present invention methods are provided for treating neovascular diseases of the eye such as corneal neovascularization (including corneal graft neovascularization), comprising the step of administering to a patient a therapeutically effective amount of a compound (as described above) to the cornea, such that the formation of blood vessels is inhibited. Briefly, the cornea is a tissue which normally lacks blood vessels. In certain pathological conditions however,

capillaries may extend into the cornea from the pericorneal vascular plexus of the limbus. When the cornea becomes vascularized, it also becomes clouded, resulting in a decline in the patient's visual acuity. Visual loss may become complete if the cornea completely opacitates. A wide variety of disorders can result in corneal
5 neovascularization, including for example, corneal infections (e.g., trachoma, herpes simplex keratitis, leishmaniasis and onchocerciasis), immunological processes (e.g., graft rejection and Stevens-Johnson's syndrome), alkali burns, trauma, inflammation (of any cause), toxic and nutritional deficiency states, and as a complication of wearing contact lenses.

10 Within particularly preferred embodiments of the invention, may be prepared for topical administration in saline (combined with any of the preservatives and antimicrobial agents commonly used in ocular preparations), and administered in eyedrop form. The solution or suspension may be prepared in its pure form and administered several times daily. Alternatively, anti-angiogenic compositions,
15 prepared as described above, may also be administered directly to the cornea. Within preferred embodiments, the anti-angiogenic composition is prepared with a muco-adhesive polymer which binds to cornea. Within further embodiments, the anti-angiogenic factors or anti-angiogenic compositions may be utilized as an adjunct to conventional steroid therapy. Topical therapy may also be useful prophylactically in
20 corneal lesions which are known to have a high probability of inducing an angiogenic response (such as chemical burns). In these instances the treatment, likely in combination with steroids, may be instituted immediately to help prevent subsequent complications.

Within other embodiments, the compounds described above may be injected
25 directly into the corneal stroma by an ophthalmologist under microscopic guidance. The preferred site of injection may vary with the morphology of the individual lesion, but the goal of the administration would be to place the composition at the advancing front of the vasculature (i.e., interspersed between the blood vessels and the normal cornea). In most cases this would involve perilimbic corneal injection to "protect" the
30 cornea from the advancing blood vessels. This method may also be utilized shortly

after a corneal insult in order to prophylactically prevent corneal neovascularization. In this situation the material could be injected in the perilimbic cornea interspersed between the corneal lesion and its undesired potential limbic blood supply. Such methods may also be utilized in a similar fashion to prevent capillary invasion of transplanted corneas. In a sustained-release form injections might only be required 2-3 times per year. A steroid could also be added to the injection solution to reduce inflammation resulting from the injection itself.

Within another aspect of the present invention, methods are provided for treating neovascular glaucoma, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. In one embodiment, the compound may be administered topically to the eye in order to treat early forms of neovascular glaucoma. Within other embodiments, the compound may be implanted by injection into the region of the anterior chamber angle. Within other embodiments, the compound may also be placed in any location such that the compound is continuously released into the aqueous humor. Within another aspect of the present invention, methods are provided for treating proliferative diabetic retinopathy, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eyes, such that the formation of blood vessels is inhibited.

Within particularly preferred embodiments of the invention, proliferative diabetic retinopathy may be treated by injection into the aqueous humor or the vitreous, in order to increase the local concentration of the polynucleotide, polypeptide, antagonist and/or agonist in the retina. Preferably, this treatment should be initiated prior to the acquisition of severe disease requiring photocoagulation.

Within another aspect of the present invention, methods are provided for treating retrolental fibroplasia, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. The

compound may be administered topically, via intravitreal injection and/or via intraocular implants.

Additionally, disorders which can be treated with the polynucleotides, polypeptides, agonists and/or antagonists include, but are not limited to, hemangioma, arthritis, psoriasis, angiofibroma, atherosclerotic plaques, delayed wound healing,
5 granulations, hemophilic joints, hypertrophic scars, nonunion fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma, trachoma, and vascular adhesions.

Moreover, disorders and/or states, which can be treated with the polynucleotides, polypeptides, agonists and/or antagonists include, but are not limited to, solid tumors, blood born tumors such as leukemias, tumor metastasis,
10 Kaposi's sarcoma, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, and uveitis, delayed wound healing,
15 endometriosis, vasculogenesis, granulations, hypertrophic scars (keloids), nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, Osler-Webber Syndrome, plaque neovascularization, telangiectasia, hemophilic joints, angiofibroma fibromuscular dysplasia, wound granulation,
20 Crohn's disease, atherosclerosis, birth control agent by preventing vascularization required for embryo implantation controlling menstruation, diseases that have angiogenesis as a pathologic consequence such as cat scratch disease (Rochelomina quintosa), ulcers (Helicobacter pylori), Bartonellosis and bacillary
25 angiomatosis.

In one aspect of the birth control method, an amount of the compound sufficient to block embryo implantation is administered before or after intercourse and fertilization have occurred, thus providing an effective method of birth control, possibly a "morning after" method. Polynucleotides, polypeptides, agonists and/or
30 antagonists may also be used in controlling menstruation or administered as either a

peritoneal lavage fluid or for peritoneal implantation in the treatment of endometriosis.

Polynucleotides, polypeptides, agonists and/or agonists of the present invention may be incorporated into surgical sutures in order to prevent stitch
5 granulomas.

Polynucleotides, polypeptides, agonists and/or agonists may be utilized in a wide variety of surgical procedures. For example, within one aspect of the present invention a compositions (in the form of, for example, a spray or film) may be utilized to coat or spray an area prior to removal of a tumor, in order to isolate normal
10 surrounding tissues from malignant tissue, and/or to prevent the spread of disease to surrounding tissues. Within other aspects of the present invention, compositions (e.g., in the form of a spray) may be delivered via endoscopic procedures in order to coat tumors, or inhibit angiogenesis in a desired locale. Within yet other aspects of the present invention, surgical meshes which have been coated with anti- angiogenic
15 compositions of the present invention may be utilized in any procedure wherein a surgical mesh might be utilized. For example, within one embodiment of the invention a surgical mesh laden with an anti-angiogenic composition may be utilized during abdominal cancer resection surgery (e.g., subsequent to colon resection) in order to provide support to the structure, and to release an amount of the anti-
20 angiogenic factor.

Within further aspects of the present invention, methods are provided for treating tumor excision sites, comprising administering a polynucleotide, polypeptide, agonist and/or agonist to the resection margins of a tumor subsequent to excision, such that the local recurrence of cancer and the formation of new blood vessels at the
25 site is inhibited. Within one embodiment of the invention, the anti-angiogenic compound is administered directly to the tumor excision site (e.g., applied by swabbing, brushing or otherwise coating the resection margins of the tumor with the anti-angiogenic compound). Alternatively, the anti-angiogenic compounds may be incorporated into known surgical pastes prior to administration. Within particularly

preferred embodiments of the invention, the anti-angiogenic compounds are applied after hepatic resections for malignancy, and after neurosurgical operations.

Within one aspect of the present invention, polynucleotides, polypeptides, agonists and/or agonists may be administered to the resection margin of a wide variety of tumors, including for example, breast, colon, brain and hepatic tumors. For example, within one embodiment of the invention, anti-angiogenic compounds may be administered to the site of a neurological tumor subsequent to excision, such that the formation of new blood vessels at the site are inhibited.

The polynucleotides, polypeptides, agonists and/or agonists of the present invention may also be administered along with other anti-angiogenic factors. Representative examples of other anti-angiogenic factors include: Anti-Invasive Factor, retinoic acid and derivatives thereof, paclitaxel, Suramin, Tissue Inhibitor of Metalloproteinase-1, Tissue Inhibitor of Metalloproteinase-2, Plasminogen Activator Inhibitor-1, Plasminogen Activator Inhibitor-2, and various forms of the lighter "d group" transition metals.

Lighter "d group" transition metals include, for example, vanadium, molybdenum, tungsten, titanium, niobium, and tantalum species. Such transition metal species may form transition metal complexes. Suitable complexes of the above-mentioned transition metal species include oxo transition metal complexes.

Representative examples of vanadium complexes include oxo vanadium complexes such as vanadate and vanadyl complexes. Suitable vanadate complexes include metavanadate and orthovanadate complexes such as, for example, ammonium metavanadate, sodium metavanadate, and sodium orthovanadate. Suitable vanadyl complexes include, for example, vanadyl acetylacetonate and vanadyl sulfate including vanadyl sulfate hydrates such as vanadyl sulfate mono- and trihydrates.

Representative examples of tungsten and molybdenum complexes also include oxo complexes. Suitable oxo tungsten complexes include tungstate and tungsten oxide complexes. Suitable tungstate complexes include ammonium tungstate, calcium tungstate, sodium tungstate dihydrate, and tungstic acid. Suitable tungsten oxides include tungsten (IV) oxide and tungsten (VI) oxide. Suitable oxo

molybdenum complexes include molybdate, molybdenum oxide, and molybdenyl complexes. Suitable molybdate complexes include ammonium molybdate and its hydrates, sodium molybdate and its hydrates, and potassium molybdate and its hydrates. Suitable molybdenum oxides include molybdenum (VI) oxide, molybdenum (VI) oxide, and molybdic acid. Suitable molybdenyl complexes include, for example, molybdenyl acetylacetonate. Other suitable tungsten and molybdenum complexes include hydroxo derivatives derived from, for example, glycerol, tartaric acid, and sugars.

A wide variety of other anti-angiogenic factors may also be utilized within the context of the present invention. Representative examples include platelet factor 4; protamine sulphate; sulphated chitin derivatives (prepared from queen crab shells), (Murata et al., Cancer Res. 51:22-26, 1991); Sulphated Polysaccharide Peptidoglycan Complex (SP- PG) (the function of this compound may be enhanced by the presence of steroids such as estrogen, and tamoxifen citrate); Staurosporine; modulators of matrix metabolism, including for example, proline analogs, cishydroxyproline, d,L-3,4-dehydroproline, Thiaproline, alpha,alpha-dipyridyl, aminopropionitrile fumarate; 4-propyl-5-(4-pyridinyl)-2(3H)-oxazolone; Methotrexate; Mitoxantrone; Heparin; Interferons; 2 Macroglobulin-serum; ChIMP-3 (Pavloff et al., J. Bio. Chem. 267:17321-17326, 1992); Chymostatin (Tomkinson et al., Biochem J. 286:475-480, 1992); Cyclodextrin Tetradecasulfate; Eponemycin; Camptothecin; Fumagillin (Ingber et al., Nature 348:555-557, 1990); Gold Sodium Thiomalate ("GST"; Matsubara and Ziff, J. Clin. Invest. 79:1440-1446, 1987); anticollagenase-serum; alpha2-antiplasmin (Holmes et al., J. Biol. Chem. 262(4):1659-1664, 1987); Bisantrone (National Cancer Institute); Lobenzarit disodium (N-(2)-carboxyphenyl-4-chloroanthronilic acid disodium or "CCA"; Takeuchi et al., Agents Actions 36:312-316, 1992); Thalidomide; Angostatic steroid; AGM-1470; carboxynaminimidazole; and metalloproteinase inhibitors such as BB94.

Diseases at the Cellular Level

Diseases associated with increased cell survival or the inhibition of apoptosis that could be treated or detected by polynucleotides or polypeptides, as well as antagonists or agonists of the present invention, include cancers (such as follicular
5 lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, including, but not limited to colon cancer, cardiac tumors, pancreatic cancer, melanoma, retinoblastoma, glioblastoma, lung cancer, intestinal cancer, testicular cancer, stomach cancer, neuroblastoma, myxoma, myoma, lymphoma, endothelioma, osteoblastoma, osteoclastoma, osteosarcoma, chondrosarcoma, adenoma, breast
10 cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation,
15 graft v. host disease, acute graft rejection, and chronic graft rejection. In preferred embodiments, polynucleotides, polypeptides, and/or antagonists of the invention are used to inhibit growth, progression, and/or metasis of cancers, in particular those listed above.

Additional diseases or conditions associated with increased cell survival that
20 could be treated or detected by polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to, progression, and/or metastases of malignancies and related disorders such as leukemia (including acute leukemias (e.g., acute lymphocytic leukemia, acute myelocytic leukemia (including myeloblastic, promyelocytic, myelomonocytic, monocytic, and erythroleukemia)) and
25 chronic leukemias (e.g., chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia)), polycythemia vera, lymphomas (e.g., Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors including, but not limited to, sarcomas and carcinomas such as fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma,
30 osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma,

lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, 5 papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, 10 craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, melanoma, neuroblastoma, and retinoblastoma.

Diseases associated with increased apoptosis that could be treated or detected by polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, include AIDS; neurodegenerative disorders (such as Alzheimer's disease, 15 Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration and brain tumor or prior associated disease); autoimmune disorders (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) 20 myelodysplastic syndromes (such as aplastic anemia), graft v. host disease, ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion injury), liver injury (e.g., hepatitis related liver injury, ischemia/reperfusion injury, cholestasis (bile duct injury) and liver cancer); toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia.

25

Wound Healing and Epithelial Cell Proliferation

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, for therapeutic purposes, for example, to 30 stimulate epithelial cell proliferation and basal keratinocytes for the purpose of wound

healing, and to stimulate hair follicle production and healing of dermal wounds. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may be clinically useful in stimulating wound healing including surgical wounds, excisional wounds, deep wounds involving damage of the dermis and epidermis, eye tissue wounds, dental tissue wounds, oral cavity wounds, diabetic
5 ulcers, dermal ulcers, cubitus ulcers, arterial ulcers, venous stasis ulcers, burns resulting from heat exposure or chemicals, and other abnormal wound healing conditions such as uremia, malnutrition, vitamin deficiencies and complications associated with systemic treatment with steroids, radiation therapy and antineoplastic
10 drugs and antimetabolites. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to promote dermal reestablishment subsequent to dermal loss

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to increase the adherence of skin grafts to a wound
15 bed and to stimulate re-epithelialization from the wound bed. The following are types of grafts that polynucleotides or polypeptides, agonists or antagonists of the present invention, could be used to increase adherence to a wound bed: autografts, artificial skin, allografts, autodermic graft, autoepdermic grafts, avacular grafts, Blair-Brown grafts, bone graft, brephoplastic grafts, cutis graft, delayed graft, dermic graft,
20 epidermic graft, fascia graft, full thickness graft, heterologous graft, xenograft, homologous graft, hyperplastic graft, lamellar graft, mesh graft, mucosal graft, Ollier-Thiersch graft, omenpal graft, patch graft, pedicle graft, penetrating graft, split skin graft, thick split graft. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, can be used to promote skin strength and to
25 improve the appearance of aged skin.

It is believed that polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, will also produce changes in hepatocyte proliferation, and epithelial cell proliferation in the lung, breast, pancreas, stomach, small intesting, and large intestine. Polynucleotides or polypeptides, as well as
30 agonists or antagonists of the present invention, could promote proliferation of

epithelial cells such as sebocytes, hair follicles, hepatocytes, type II pneumocytes, mucin-producing goblet cells, and other epithelial cells and their progenitors contained within the skin, lung, liver, and gastrointestinal tract. Polynucleotides or polypeptides, agonists or antagonists of the present invention, may promote
5 proliferation of endothelial cells, keratinocytes, and basal keratinocytes.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could also be used to reduce the side effects of gut toxicity that result from radiation, chemotherapy treatments or viral infections. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may have a
10 cytoprotective effect on the small intestine mucosa. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may also stimulate healing of mucositis (mouth ulcers) that result from chemotherapy and viral infections.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could further be used in full regeneration of skin in full and partial
15 thickness skin defects, including burns, (i.e., repopulation of hair follicles, sweat glands, and sebaceous glands), treatment of other skin defects such as psoriasis. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to treat epidermolysis bullosa, a defect in adherence of the epidermis to the underlying dermis which results in frequent, open and painful blisters
20 by accelerating reepithelialization of these lesions. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could also be used to treat gastric and duodenal ulcers and help heal by scar formation of the mucosal lining and regeneration of glandular mucosa and duodenal mucosal lining more rapidly. Inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis, are
25 diseases which result in destruction of the mucosal surface of the small or large intestine, respectively. Thus, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to promote the resurfacing of the mucosal surface to aid more rapid healing and to prevent progression of inflammatory bowel disease. Treatment with polynucleotides or polypeptides, agonists or
30 antagonists of the present invention, is expected to have a significant effect on the

production of mucus throughout the gastrointestinal tract and could be used to protect the intestinal mucosa from injurious substances that are ingested or following surgery. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to treat diseases associate with the under expression.

5 Moreover, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to prevent and heal damage to the lungs due to various pathological states. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, which could stimulate proliferation and differentiation and promote the repair of alveoli and brochiolar epithelium to prevent
10 or treat acute or chronic lung damage. For example, emphysema, which results in the progressive loss of aveoli, and inhalation injuries, i.e., resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli could be effectively treated using polynucleotides or polypeptides, agonists or antagonists of the present invention. Also, polynucleotides or polypeptides, as well as
15 agonists or antagonists of the present invention, could be used to stimulate the proliferation of and differentiation of type II pneumocytes, which may help treat or prevent disease such as hyaline membrane diseases, such as infant respiratory distress syndrome and bronchopulmonary displasia, in premature infants.

 Polynucleotides or polypeptides, as well as agonists or antagonists of the
20 present invention, could stimulate the proliferation and differentiation of hepatocytes and, thus, could be used to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances (i.e., acetaminophen, carbon tetraholoride and other hepatotoxins known in the art).

25 In addition, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used treat or prevent the onset of diabetes mellitus. In patients with newly diagnosed Types I and II diabetes, where some islet cell function remains, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to maintain the islet function so as to alleviate,
30 delay or prevent permanent manifestation of the disease. Also, polynucleotides or

polypeptides, as well as agonists or antagonists of the present invention, could be used as an auxiliary in islet cell transplantation to improve or promote islet cell function.

5 Neurological Diseases

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, for therapeutic purposes, for example, to
10 stimulate neurological cell proliferation and/or differentiation. Therefore, polynucleotides, polypeptides, agonists and/or antagonists of the invention may be used to treat and/or detect neurologic diseases. Moreover, polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used as a marker or detector of a particular nervous system disease or disorder.

15 Examples of neurologic diseases which can be treated or detected with polynucleotides, polypeptides, agonists, and/or antagonists of the present invention include brain diseases, such as metabolic brain diseases which includes phenylketonuria such as maternal phenylketonuria, pyruvate carboxylase deficiency, pyruvate dehydrogenase complex deficiency, Wernicke's Encephalopathy, brain
20 edema, brain neoplasms such as cerebellar neoplasms which include infratentorial neoplasms, cerebral ventricle neoplasms such as choroid plexus neoplasms, hypothalamic neoplasms, supratentorial neoplasms, canavan disease, cerebellar diseases such as cerebellar ataxia which include spinocerebellar degeneration such as ataxia telangiectasia, cerebellar dyssynergia, Friederich's Ataxia, Machado-Joseph
25 Disease, olivopontocerebellar atrophy, cerebellar neoplasms such as infratentorial neoplasms, diffuse cerebral sclerosis such as encephalitis periaxialis, globoid cell leukodystrophy, metachromatic leukodystrophy and subacute sclerosing panencephalitis, cerebrovascular disorders (such as carotid artery diseases which include carotid artery thrombosis, carotid stenosis and Moyamoya Disease, cerebral
30 amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformations, cerebral artery diseases, cerebral embolism and

thrombosis such as carotid artery thrombosis, sinus thrombosis and Wallenberg's Syndrome, cerebral hemorrhage such as epidural hematoma, subdural hematoma and subarachnoid hemorrhage, cerebral infarction, cerebral ischemia such as transient cerebral ischemia, Subclavian Steal Syndrome and vertebrobasilar insufficiency,

5 vascular dementia such as multi-infarct dementia, periventricular leukomalacia, vascular headache such as cluster headache, migraine, dementia such as AIDS Dementia Complex, presenile dementia such as Alzheimer's Disease and Creutzfeldt-Jakob Syndrome, senile dementia such as Alzheimer's Disease and progressive supranuclear palsy, vascular dementia such as multi-infarct dementia, encephalitis

10 which include encephalitis periaxialis, viral encephalitis such as epidemic encephalitis, Japanese Encephalitis, St. Louis Encephalitis, tick-borne encephalitis and West Nile Fever, acute disseminated encephalomyelitis, meningoencephalitis such as uveomeningoencephalitic syndrome, Postencephalitic Parkinson Disease and subacute sclerosing panencephalitis, encephalomalacia such as periventricular

15 leukomalacia, epilepsy such as generalized epilepsy which includes infantile spasms, absence epilepsy, myoclonic epilepsy which includes MERRF Syndrome, tonic-clonic epilepsy, partial epilepsy such as complex partial epilepsy, frontal lobe epilepsy and temporal lobe epilepsy, post-traumatic epilepsy, status epilepticus such as Epilepsia Partialis Continua, Hallervorden-Spatz Syndrome, hydrocephalus such as

20 Dandy-Walker Syndrome and normal pressure hydrocephalus, hypothalamic diseases such as hypothalamic neoplasms, cerebral malaria, narcolepsy which includes cataplexy, bulbar poliomyelitis, cerebri pseudotumor, Rett Syndrome, Reye's Syndrome, thalamic diseases, cerebral toxoplasmosis, intracranial tuberculoma and Zellweger Syndrome, central nervous system infections such as AIDS Dementia

25 Complex, Brain Abscess, subdural empyema, encephalomyelitis such as Equine Encephalomyelitis, Venezuelan Equine Encephalomyelitis, Necrotizing Hemorrhagic Encephalomyelitis, Visna, cerebral malaria, meningitis such as arachnoiditis, aseptic meningitis such as viral meningitis which includes lymphocytic choriomeningitis. Bacterial meningitis which includes Haemophilus Meningitis, Listeria Meningitis,

30 Meningococcal Meningitis such as Waterhouse-Friderichsen Syndrome,

Pneumococcal Meningitis and meningeal tuberculosis, fungal meningitis such as Cryptococcal Meningitis, subdural effusion, meningoencephalitis such as uvemeningoencephalitic syndrome, myelitis such as transverse myelitis, neurosyphilis such as tabes dorsalis, poliomyelitis which includes bulbar poliomyelitis and postpoliomyelitis syndrome, prion diseases (such as Creutzfeldt-Jakob Syndrome, Bovine Spongiform Encephalopathy, Gerstmann-Straussler Syndrome, Kuru, Scrapie) cerebral toxoplasmosis, central nervous system neoplasms such as brain neoplasms that include cerebellar neoplasms such as infratentorial neoplasms, cerebral ventricle neoplasms such as choroid plexus neoplasms, hypothalamic neoplasms and supratentorial neoplasms, meningeal neoplasms, spinal cord neoplasms which include epidural neoplasms, demyelinating diseases such as Canavan Diseases, diffuse cerebral sclerolosis which includes adrenoleukodystrophy, encephalitis periaxialis, globoid cell leukodystrophy, diffuse cerebral sclerosis such as metachromatic leukodystrophy, allergic encephalomyelitis, necrotizing hemorrhagic encephalomyelitis, progressive multifocal leukoencephalopathy, multiple sclerosis, central pontine myelinolysis, transverse myelitis, neuromyelitis optica, Scrapie, Swayback, Chronic Fatigue Syndrome, Visna, High Pressure Nervous Syndrome, Meningism, spinal cord diseases such as amyotonia congenita, amyotrophic lateral sclerosis, spinal muscular atrophy such as Werdnig-Hoffmann Disease, spinal cord compression, spinal cord neoplasms such as epidural neoplasms, syringomyelia, Tabes Dorsalis, Stiff-Man Syndrome, mental retardation such as Angelman Syndrome, Cri-du-Chat Syndrome, De Lange's Syndrome, Down Syndrome, Gangliosidoses such as gangliosidoses G(M1), Sandhoff Disease, Tay-Sachs Disease, Hartnup Disease, homocystinuria, Laurence-Moon- Biedl Syndrome, Lesch-Nyhan Syndrome, Maple Syrup Urine Disease, mucopolipidosis such as fucosidosis, neuronal ceroid-lipofuscinosis, oculocerebrorenal syndrome, phenylketonuria such as maternal phenylketonuria, Prader-Willi Syndrome, Rett Syndrome, Rubinstein-Taybi Syndrome, Tuberous Sclerosis, WAGR Syndrome, nervous system abnormalities such as holoprosencephaly, neural tube defects such as anencephaly which includes hydrangencephaly, Arnold-Chairi Deformity, encephalocele, meningocele,

meningomyelocele, spinal dysraphism such as spina bifida cystica and spina bifida occulta, hereditary motor and sensory neuropathies which include Charcot-Marie Disease, Hereditary optic atrophy, Refsum's Disease, hereditary spastic paraplegia, Werdnig-Hoffmann Disease, Hereditary Sensory and Autonomic Neuropathies such as Congenital Analgesia and Familial Dysautonomia, Neurologic manifestations (such as agnosia that include Gerstmann's Syndrome, Amnesia such as retrograde amnesia, apraxia, neurogenic bladder, cataplexy, communicative disorders such as hearing disorders that includes deafness, partial hearing loss, loudness recruitment and tinnitus, language disorders such as aphasia which include agraphia, anomia, broca aphasia, and Wernicke Aphasia, Dyslexia such as Acquired Dyslexia, language development disorders, speech disorders such as aphasia which includes anomia, broca aphasia and Wernicke Aphasia, articulation disorders, communicative disorders such as speech disorders which include dysarthria, echolalia, mutism and stuttering, voice disorders such as aphonia and hoarseness, decerebrate state, delirium, fasciculation, hallucinations, meningism, movement disorders such as angelman syndrome, ataxia, athetosis, chorea, dystonia, hypokinesia, muscle hypotonia, myoclonus, tic, torticollis and tremor, muscle hypertonia such as muscle rigidity such as stiff-man syndrome, muscle spasticity, paralysis such as facial paralysis which includes Herpes Zoster Oticus, Gastroparesis, Hemiplegia, ophthalmoplegia such as diplopia, Duane's Syndrome, Horner's Syndrome, Chronic progressive external ophthalmoplegia such as Kearns Syndrome, Bulbar Paralysis, Tropical Spastic Paraparesis, Paraplegia such as Brown-Sequard Syndrome, quadriplegia, respiratory paralysis and vocal cord paralysis, paresis, phantom limb, taste disorders such as ageusia and dysgeusia, vision disorders such as amblyopia, blindness, color vision defects, diplopia, hemianopsia, scotoma and subnormal vision, sleep disorders such as hypersomnia which includes Kleine-Levin Syndrome, insomnia, and somnambulism, spasm such as trismus, unconsciousness such as coma, persistent vegetative state and syncope and vertigo, neuromuscular diseases such as amyotonia congenita, amyotrophic lateral sclerosis, Lambert-Eaton Myasthenic Syndrome, motor neuron disease, muscular atrophy such as spinal muscular atrophy, Charcot-Marie Disease

- and Werdnig-Hoffmann Disease, Postpoliomyelitis Syndrome, Muscular Dystrophy, Myasthenia Gravis, Myotonia Atrophica, Myotonia Confenita, Nemaline Myopathy, Familial Periodic Paralysis, Multiplex Paramyoclonus, Tropical Spastic Paraparesis and Stiff-Man Syndrome, peripheral nervous system diseases such as acrodynia, amyloid neuropathies, autonomic nervous system diseases such as Adie's Syndrome, Barre-Lieou Syndrome, Familial Dysautonomia, Horner's Syndrome, Reflex Sympathetic Dystrophy and Shy-Drager Syndrome, Cranial Nerve Diseases such as Acoustic Nerve Diseases such as Acoustic Neuroma which includes Neurofibromatosis 2, Facial Nerve Diseases such as Facial Neuralgia, Melkersson-Rosenthal Syndrome, ocular motility disorders which includes amblyopia, nystagmus, oculomotor nerve paralysis, ophthalmoplegia such as Duane's Syndrome, Horner's Syndrome, Chronic Progressive External Ophthalmoplegia which includes Kearns Syndrome, Strabismus such as Esotropia and Exotropia, Oculomotor Nerve Paralysis, Optic Nerve Diseases such as Optic Atrophy which includes Hereditary Optic Atrophy, Optic Disk Drusen, Optic Neuritis such as Neuromyelitis Optica, Papilledema, Trigeminal Neuralgia, Vocal Cord Paralysis, Demyelinating Diseases such as Neuromyelitis Optica and Swayback, Diabetic neuropathies such as diabetic foot, nerve compression syndromes such as carpal tunnel syndrome, tarsal tunnel syndrome, thoracic outlet syndrome such as cervical rib syndrome, ulnar nerve compression syndrome, neuralgia such as causalgia, cervico-brachial neuralgia, facial neuralgia and trigeminal neuralgia, neuritis such as experimental allergic neuritis, optic neuritis, polyneuritis, polyradiculoneuritis and radiculities such as polyradiculitis, hereditary motor and sensory neuropathies such as Charcot-Marie Disease, Hereditary Optic Atrophy, Refsum's Disease, Hereditary Spastic Paraplegia and Werdnig-Hoffmann Disease, Hereditary Sensory and Autonomic Neuropathies which include Congenital Analgesia and Familial Dysautonomia, POEMS Syndrome, Sciatica, Gustatory Sweating and Tetany).

Infectious Disease

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention. Examples of viruses, include, but are not limited to Examples of viruses, include, but are not limited to the following DNA and RNA viruses and viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Bimaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Dengue, EBV, HIV, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza A, Influenza B, and parainfluenza), Papiloma virus, Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, respiratory syncytial virus, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), Japanese B encephalitis, Junin, Chikungunya, Rift Valley fever, yellow fever, meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific

embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat: meningitis, Dengue, EBV, and/or hepatitis (e.g., hepatitis B). In an additional specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat patients nonresponsive to one or more
5 other commercially available hepatitis vaccines. In a further specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat AIDS.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide and/or agonist or
10 antagonist of the present invention include, but not limited to, include, but not limited to, the following Gram-Negative and Gram-positive bacteria and bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Cryptococcus neoformans, Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia (e.g., Borrelia burgdorferi,
15 Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, E. coli (e.g., Enterotoxigenic E. coli and Enterohemorrhagic E. coli), Enterobacteriaceae (Klebsiella, Salmonella (e.g., Salmonella typhi, and Salmonella paratyphi), Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Mycobacterium leprae,
20 Vibrio cholerae, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Meisseria meningitidis, Pasteurellacea Infections (e.g., Actinobacillus, Heamophilus (e.g., Heamophilus influenza type B), Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, Shigella spp., Staphylococcal, Meningiococcal, Pneumococcal and Streptococcal (e.g., Streptococcus pneumoniae and Group B
25 Streptococcus). These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme
30 Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning,

Typhoid, pneumonia, Gonorrhea, meningitis (e.g., meningitis types A and B), Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. Polynucleotides or polypeptides, agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, Polynucleotides, polypeptides, agonists or antagonists of the invention are used to treat: tetanus, Diphtheria, botulism, and/or meningitis type B.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, the following families or class: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas and Sporozoans (e.g., Plasmodium virax, Plasmodium falciparum, Plasmodium malariae and Plasmodium ovale). These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), malaria, pregnancy complications, and toxoplasmosis. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

30

Regeneration

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of
5 tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs
10 (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vasculature (including vascular and lymphatics), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, polynucleotides or polypeptides, as well as agonists or antagonists
15 of the present invention, may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome,
20 and other tendon or ligament defects. A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using
25 polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or
30 other medical therapies), localized neuropathies, and central nervous system diseases

(e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotides or polypeptides, as well as agonists or antagonists of the present invention.

5

Chemotaxis

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

Additionally, the receptor to which the polypeptide of the present invention binds can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting (Coligan, et al., Current Protocols in Immun., 1(2), Chapter 5, (1991)). For example, expression cloning is employed
5 wherein polyadenylated RNA is prepared from a cell responsive to the polypeptides, for example, NIH3T3 cells which are known to contain multiple receptors for the FGF family proteins, and SC-3 cells, and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are
10 exposed to the polypeptide of the present invention, after they have been labelled. The polypeptides can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase.

Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and
15 re-transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clones that encodes the putative receptor.

As an alternative approach for receptor identification, the labeled polypeptides can be photoaffinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE analysis and
20 exposed to X-ray film. The labeled complex containing the receptors of the polypeptides can be excised, resolved into peptide fragments, and subjected to protein microsequencing. The amino acid sequence obtained from microsequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the genes encoding the putative receptors.

25 Moreover, the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling") may be employed to modulate the activities of the polypeptide of the present invention thereby effectively generating agonists and antagonists of the polypeptide of the present invention. *See generally*, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721,
30 5,834,252, and 5,837,458, and Patten, P. A., *et al.*, *Curr. Opinion Biotechnol.* 8:724-

33 (1997); Harayama, S. *Trends Biotechnol.* 16(2):76-82 (1998); Hansson, L. O., *et al.*, *J. Mol. Biol.* 287:265-76 (1999); and Lorenzo, M. M. and Blasco, R. *Biotechniques* 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference). In one embodiment, alteration of polynucleotides and corresponding polypeptides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments into a desired molecule by homologous, or site-specific, recombination. In another embodiment, polynucleotides and corresponding polypeptides may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of the polypeptide of the present invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules. In preferred embodiments, the heterologous molecules are family members. In further preferred embodiments, the heterologous molecule is a growth factor such as, for example, platelet-derived growth factor (PDGF), insulin-like growth factor (IGF-I), transforming growth factor (TGF)-alpha, epidermal growth factor (EGF), fibroblast growth factor (FGF), TGF-beta, bone morphogenetic protein (BMP)-2, BMP-4, BMP-5, BMP-6, BMP-7, activins A and B, decapentaplegic(dpp), 60A, OP-2, dorsalin, growth differentiation factors (GDFs), nodal, MIS, inhibin-alpha, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta5, and glial-derived neurotrophic factor (GDNF).

Other preferred fragments are biologically active fragments of the polypeptide of the present invention. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Additionally, this invention provides a method of screening compounds to identify those which modulate the action of the polypeptide of the present invention. An example of such an assay comprises combining a mammalian fibroblast cell, a the polypeptide of the present invention, the compound to be screened and $^3\text{[H]}$

thymidine under cell culture conditions where the fibroblast cell would normally proliferate. A control assay may be performed in the absence of the compound to be screened and compared to the amount of fibroblast proliferation in the presence of the compound to determine if the compound stimulates proliferation by determining the uptake of $^3\text{[H]}$ thymidine in each case. The amount of fibroblast cell proliferation is measured by liquid scintillation chromatography which measures the incorporation of $^3\text{[H]}$ thymidine. Both agonist and antagonist compounds may be identified by this procedure.

In another method, a mammalian cell or membrane preparation expressing a receptor for a polypeptide of the present invention is incubated with a labeled polypeptide of the present invention in the presence of the compound. The ability of the compound to enhance or block this interaction could then be measured. Alternatively, the response of a known second messenger system following interaction of a compound to be screened and the receptor is measured and the ability of the compound to bind to the receptor and elicit a second messenger response is measured to determine if the compound is a potential agonist or antagonist. Such second messenger systems include but are not limited to, cAMP guanylate cyclase, ion channels or phosphoinositide hydrolysis.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptides of the invention from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the present invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the present invention, (b) assaying a biological

activity, and (b) determining if a biological activity of the polypeptide has been altered.

Targeted Delivery

5 In another embodiment, the invention provides a method of delivering compositions to targeted cells expressing a receptor for a polypeptide of the invention, or cells expressing a cell bound form of a polypeptide of the invention.

As discussed herein, polypeptides or antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or
10 prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (including antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic
15 protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific
20 destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention (e.g., polypeptides of the invention or antibodies of the invention) in association with toxins or cytotoxic prodrugs.

By "toxin" is meant compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of
25 toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced
30 endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha

toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. By "cytotoxic prodrug" is meant a non-toxic compound that is converted by an enzyme, normally present in the cell, into a cytotoxic compound. Cytotoxic prodrugs that may be used
5 according to the methods of the invention include, but are not limited to, glutamyl derivatives of benzoic acid mustard alkylating agent, phosphate derivatives of etoposide or mitomycin C, cytosine arabinoside, daunorubisin, and phenoxyacetamide derivatives of doxorubicin.

10 Drug Screening

Further contemplated is the use of the polypeptides of the present invention, or the polynucleotides encoding these polypeptides, to screen for molecules which modify the activities of the polypeptides of the present invention. Such a method would include contacting the polypeptide of the present invention with a selected
15 compound(s) suspected of having antagonist or agonist activity, and assaying the activity of these polypeptides following binding.

This invention is particularly useful for screening therapeutic compounds by using the polypeptides of the present invention, or binding fragments thereof, in any of a variety of drug screening techniques. The polypeptide or fragment employed in
20 such a test may be affixed to a solid support, expressed on a cell surface, free in solution, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. One may measure, for example, the formulation
25 of complexes between the agent being tested and a polypeptide of the present invention.

Thus, the present invention provides methods of screening for drugs or any other agents which affect activities mediated by the polypeptides of the present invention. These methods comprise contacting such an agent with a polypeptide of
30 the present invention or a fragment thereof and assaying for the presence of a

complex between the agent and the polypeptide or a fragment thereof, by methods well known in the art. In such a competitive binding assay, the agents to screen are typically labeled. Following incubation, free agent is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability
5 of a particular agent to bind to the polypeptides of the present invention.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the polypeptides of the present invention, and is described in great detail in European Patent Application 84/03564, published on September 13, 1984, which is incorporated herein by reference herein.
10 Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with polypeptides of the present invention and washed. Bound polypeptides are then detected by methods well known in the art. Purified polypeptides are coated directly onto plates for use in the aforementioned
15 drug screening techniques. In addition, non-neutralizing antibodies may be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding polypeptides of the present invention specifically compete with a test compound for binding to the polypeptides
20 or fragments thereof. In this manner, the antibodies are used to detect the presence of any peptide which shares one or more antigenic epitopes with a polypeptide of the invention.

Antisense And Ribozyme (Antagonists)

25 In specific embodiments, antagonists according to the present invention are nucleic acids corresponding to the sequences contained in SEQ ID NO:X, or the complementary strand thereof, and/or to nucleotide sequences contained in the cDNA contained in the related cDNA clone identified in Table 1. In one embodiment, antisense sequence is generated internally, by the organism, in another embodiment,
30 the antisense sequence is separately administered (see, for example, O'Connor, J.,

Neurochem. 56:560 (1991). Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Antisense technology can be used to control gene expression through antisense DNA or RNA, or through triple-helix formation. Antisense techniques are discussed for example, in Okano, J., Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance, Lee et al., Nucleic Acids Research 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1300 (1991). The methods are based on binding of a polynucleotide to a complementary DNA or RNA.

For example, the use of c-myc and c-myb antisense RNA constructs to inhibit the growth of the non-lymphocytic leukemia cell line HL-60 and other cell lines was previously described. (Wickstrom et al. (1988); Anfossi et al. (1989)). These experiments were performed in vitro by incubating cells with the oligoribonucleotide. A similar procedure for in vivo use is described in WO 91/15580. Briefly, a pair of oligonucleotides for a given antisense RNA is produced as follows: A sequence complimentary to the first 15 bases of the open reading frame is flanked by an EcoRI site on the 5' end and a HindIII site on the 3' end. Next, the pair of oligonucleotides is heated at 90°C for one minute and then annealed in 2X ligation buffer (20mM TRIS HCl pH 7.5, 10mM MgCl₂, 10mM dithiothreitol (DTT) and 0.2 mM ATP) and then ligated to the EcoRI/Hind III site of the retroviral vector PMV7 (WO 91/15580).

For example, the 5' coding portion of a polynucleotide that encodes the polypeptide of the present invention may be used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription thereby preventing transcription and the production of the receptor. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into receptor polypeptide.

In one embodiment, the antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector or a portion thereof, is transcribed, producing an antisense nucleic acid (RNA) of the

invention. Such a vector would contain a sequence encoding the antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors
5 can be plasmid, viral, or others known in the art, used for replication and expression in vertebrate cells. Expression of the sequence encoding the polypeptide of the present invention or fragments thereof, can be by any promoter known in the art to act in vertebrate, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter
10 region (Bernoist and Chambon, Nature 29:304-310 (1981), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., Cell 22:787-797 (1980), the herpes thymidine promoter (Wagner et al., Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445 (1981), the regulatory sequences of the metallothionein gene (Brinster, et al., Nature 296:39-42 (1982)), etc.

15 The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a gene of the present invention. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the
20 RNA, forming a stable duplex; in the case of double stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the larger the hybridizing nucleic acid, the more base mismatches with a RNA it may contain and still form a
25 stable duplex (or triplex as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the message, e.g., the
30 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the

3' untranslated sequences of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. See generally, Wagner, R., 1994, Nature 372:333-335. Thus, oligonucleotides complementary to either the 5'- or 3'- non- translated, non-coding regions of polynucleotide sequences described herein could be used in an antisense approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5'-, 3'- or coding region of mRNA of the present invention, antisense nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

The polynucleotides of the invention can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO88/09810, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including, but not limited to, 5-fluorouracil,

5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 5 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, 10 queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 15 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group including, but not limited to, a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a 20 phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an a-anomeric oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands 25 run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

Polynucleotides of the invention may be synthesized by standard methods 30 known in the art, e.g. by use of an automated DNA synthesizer (such as are

commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to the coding region sequence could be used, those complementary to the transcribed untranslated region are most preferred.

Potential antagonists according to the invention also include catalytic RNA, or a ribozyme (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al, Science 247:1222-1225 (1990). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, Nature 334:585-591 (1988). There are numerous potential hammerhead ribozyme cleavage sites within the nucleotide sequence of SEQ ID NO:X. Preferably, the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

As in the antisense approach, the ribozymes of the invention can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express in vivo. DNA constructs encoding the ribozyme may be introduced into the cell in the same manner as described above for the introduction of antisense encoding DNA. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive promoter, such as, for example, pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy

endogenous messages and inhibit translation. Since ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Antagonist/agonist compounds may be employed to inhibit the cell growth and proliferation effects of the polypeptides of the present invention on neoplastic
5 cells and tissues, i.e. stimulation of angiogenesis of tumors, and, therefore, retard or prevent abnormal cellular growth and proliferation, for example, in tumor formation or growth.

The antagonist/agonist may also be employed to prevent hyper-vascular diseases, and prevent the proliferation of epithelial lens cells after extracapsular
10 cataract surgery. Prevention of the mitogenic activity of the polypeptides of the present invention may also be desirable in cases such as restenosis after balloon angioplasty.

The antagonist/agonist may also be employed to prevent the growth of scar tissue during wound healing.

15 The antagonist/agonist may also be employed to treat the diseases described herein.

Thus, the invention provides a method of treating disorders or diseases, including but not limited to the disorders or diseases listed throughout this application, associated with overexpression of a polynucleotide of the present
20 invention by administering to a patient (a) an antisense molecule directed to the polynucleotide of the present invention, and/or (b) a ribozyme directed to the polynucleotide of the present invention.

Other Activities

25 A polypeptide, polynucleotide, agonist, or antagonist of the present invention, as a result of the ability to stimulate vascular endothelial cell growth, may be employed in treatment for stimulating re-vascularization of ischemic tissues due to various disease conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions. The polypeptide, polynucleotide, agonist, or antagonist of

the present invention may also be employed to stimulate angiogenesis and limb regeneration, as discussed above.

5 A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for treating wounds due to injuries, burns, post-operative tissue repair, and ulcers since they are mitogenic to various cells of different origins, such as fibroblast cells and skeletal muscle cells, and therefore, facilitate the repair or replacement of damaged or diseased tissue.

10 A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed stimulate neuronal growth and to treat and prevent neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions such as Alzheimer's disease, Parkinson's disease, and AIDS-related complex. A polypeptide, polynucleotide, agonist, or antagonist of the present invention may have the ability to stimulate chondrocyte growth, therefore, they may be employed to enhance bone and periodontal regeneration and aid in tissue transplants or bone
15 grafts.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may be also be employed to prevent skin aging due to sunburn by stimulating keratinocyte growth.

20 A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for preventing hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth. Along the same lines, a polypeptide, polynucleotide, agonist, or antagonist of the present invention may be employed to stimulate growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines.

25 A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed to maintain organs before transplantation or for supporting cell culture of primary tissues. A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for inducing tissue of mesodermal origin to differentiate in early embryos.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

5 A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide, polynucleotide, agonist, or antagonist of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of
10 energy.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, circadian rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or
15 Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals,
20 cofactors or other nutritional components.

The above-recited applications have uses in a wide variety of hosts. Such hosts include, but are not limited to, human, murine, rabbit, goat, guinea pig, camel, horse, mouse, rat, hamster, pig, micro-pig, chicken, goat, cow, sheep, dog, cat, non-human primate, and human. In specific embodiments, the host is a mouse, rabbit,
25 goat, guinea pig, chicken, rat, hamster, pig, sheep, dog or cat. In preferred embodiments, the host is a mammal. In most preferred embodiments, the host is a human.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions identified as "Start" and "End" in columns 7 and 8 as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X in the range of positions identified as "Start" and "End" in columns 7 and 8 as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in

the related cDNA clone contained in the deposit, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

5 Also preferred is a composition of matter comprising a DNA molecule which comprises a cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of the cDNA in the related cDNA clone
10 contained in the deposit.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of an open reading frame sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

15 Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is an isolated nucleic acid molecule
20 comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete
25 nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence
30 selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the

complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of
5 said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence
10 selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

15 A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the
20 complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample which comprises a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide
25 sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a nucleotide sequence of SEQ ID NO:X; or the cDNA in the related cDNA clone identified in Table 1 which encodes a
30 protein, wherein the method comprises a step of detecting in a biological sample

obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide
5 sequence of the cDNA in the related cDNA clone contained in the deposit.

Also preferred is the above method for diagnosing a pathological condition which comprises a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous
10 nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a
15 sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is a composition of matter comprising isolated nucleic acid
20 molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a DNA microarray or "chip" of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50, 100, 150, 200, 250, 300, 500, 1000, 2000, 3000 or 4000 nucleotide sequences, wherein at least one sequence in said DNA microarray or "chip" is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected
25 from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the cDNA clone referenced in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence
30 at least 90% identical to a sequence of at least about 10 contiguous amino acids in the

polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated polypeptide comprising an amino acid sequence
5 at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid
10 sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid
15 sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid
20 sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino
acids is included in the amino acid sequence of a portion of said polypeptide encoded by the cDNA clone referenced in Table 1; a polypeptide encoded by SEQ ID NO:X;
25 and/or the polypeptide sequence of SEQ ID NO:Y.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table I.

5 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table I.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a
10 sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is a method for detecting in a biological sample a
15 polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table I; which method comprises a step of comparing an amino acid
20 sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino
25 acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a
30 polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X;

and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a nucleic acid sequence identified in Table 1 encoding a polypeptide, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence
5 selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said
10 polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

15 Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

20 Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a human protein comprising an amino acid sequence selected from
25 the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an
30 increased level of a protein activity, which method comprises administering to such

an individual a Therapeutic comprising an amount of an isolated polypeptide, polynucleotide, immunogenic fragment or analogue thereof, binding agent, antibody, or antigen binding fragment of the claimed invention effective to increase the level of said protein activity in said individual.

- 5 Also preferred is a method of treatment of an individual in need of a decreased level of a protein activity, which method comprised administering to such an individual a Therapeutic comprising an amount of an isolated polypeptide, polynucleotide, immunogenic fragment or analogue thereof, binding agent, antibody, or antigen binding fragment of the claimed invention effective to decrease the level of
- 10 said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

*Examples**Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample*

5 Each deposited cDNA clone is contained in a plasmid vector. Table 5 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The following correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a
 10 particular clone is identified in Table 5 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
15	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
20	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are
 25 commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3
 30

primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the fl origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the fl ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 5, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited by reference to Table 2 and 5 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone referenced in Table 1.

TABLE 5

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HUKA HUKB HUKC HUKD HUKF HUKF HUKG	Human Uterine Cancer	Lambda ZAP II	LP01
HCNA HCNB	Human Colon	Lambda Zap II	LP01
HFFA	Human Fetal Brain, random primed	Lambda Zap II	LP01
HTWA	Resting T-Cell	Lambda ZAP II	LP01
HBQA	Early Stage Human Brain, random primed	Lambda ZAP II	LP01
HLMB HLMF HLMG HLMH HLMI HLMJ HLMM HLMN	breast lymph node CDNA library	Lambda ZAP II	LP01
HCQA HCQB	human colon cancer	Lambda ZAP II	LP01
HMEA HMEC HMEF HMEG HMEI HMEJ HMEK HMEI	Human Microvascular Endothelial Cells, fract. A	Lambda ZAP II	LP01
HUSA HUSC	Human Umbilical Vein Endothelial Cells, fract. A	Lambda ZAP II	LP01
HLQA HLQB	Hepatocellular Tumor	Lambda ZAP II	LP01
HHGA HHGB HHGC HHGD	Hemangiopericytoma	Lambda ZAP II	LP01
HSDM	Human Striatum Depression, re-rescue	Lambda ZAP II	LP01
HUSH	H Umbilical Vein Endothelial Cells, frac A, re-excision	Lambda ZAP II	LP01
HSGS	Salivary gland, subtracted	Lambda ZAP II	LP01
HFXA HFXB HFXC HFXD HFXE HFXF HFXG HFXH	Brain frontal cortex	Lambda ZAP II	LP01
HPQA HPQB HPQC	PERM TF274	Lambda ZAP II	LP01
HFXJ HFXK	Brain Frontal Cortex, re-excision	Lambda ZAP II	LP01
HCWA HCWB HCWC HCWD HCWE HCWF HCWG HCWH HCWI HCWJ HCWK	CD34 positive cells (Cord Blood)	ZAP Express	LP02
HCUA HCUB HCUC	CD34 depleted Buffy Coat (Cord Blood)	ZAP Express	LP02
HRSM	A-14 cell line	ZAP Express	LP02
HRSA	A1-CELL LINE	ZAP Express	LP02
HCUD HCUE HCUF HCUG HCUH HCUI	CD34 depleted Buffy Coat (Cord Blood), re-excision	ZAP Express	LP02
HBXE HBXF HBXG	H. Whole Brain #2, re-excision	ZAP Express	LP02
HRLM	L8 cell line	ZAP Express	LP02
HBXA HBXB HBXC HBXD	Human Whole Brain #2 - Oligo dT > 1.5Kb	ZAP Express	LP02
HUDA HUDB HUDC	Testes	ZAP Express	LP02
HHTM HHTN HHTO	H. hypothalamus, frac A; re-excision	ZAP Express	LP02
HHTL	H. hypothalamus, frac A	ZAP Express	LP02
HASA HASD	Human Adult Spleen	Uni-ZAP XR	LP03
HFKC HFKD HFKE HFKF HFKG	Human Fetal Kidney	Uni-ZAP XR	LP03
HE8A HE8B HE8C HE8D HE8E HE8F HE8M HE8N	Human 8 Week Whole Embryo	Uni-ZAP XR	LP03
HGBA HGBD HGBE HGBF HGBG HGBH HGBI	Human Gall Bladder	Uni-ZAP XR	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HLHA HLHB HLHC HLHD HLHE HLHF HLHG HLHH HLHQ	Human Fetal Lung III	Uni-ZAP XR	LP03
HPMA HPMB HPMC HPMD HPME HPMF HPMG HPMH	Human Placenta	Uni-ZAP XR	LP03
HPRA HPRB HPRC HPRD	Human Prostate	Uni-ZAP XR	LP03
HSIA HSIC HSID HSIE	Human Adult Small Intestine	Uni-ZAP XR	LP03
HTEA HTEB HTEC HTEd HTEE HTEF HTEG HTEH HTEI HTEJ HTEK	Human Testes	Uni-ZAP XR	LP03
HTPA HTPB HTPC HTPD HTPe	Human Pancreas Tumor	Uni-ZAP XR	LP03
HTTA HTTB HTTC HTTD HTTE HTTF	Human Testes Tumor	Uni-ZAP XR	LP03
HAPA HAPB HAPC HAPM	Human Adult Pulmonary	Uni-ZAP XR	LP03
HETA HETB HETC HETD HETE HETF HETG HETH HETI	Human Endometrial Tumor	Uni-ZAP XR	LP03
HHFB HHFC HHFD HHFE HHFF HHFG HHFH HHFI	Human Fetal Heart	Uni-ZAP XR	LP03
HHPB HHPC HHPD HHPE HHPF HHPG HHPH	Human Hippocampus	Uni-ZAP XR	LP03
HCE1 HCE2 HCE3 HCE4 HCE5 HCEB HCEC HCED HCEE HCEF HCEG	Human Cerebellum	Uni-ZAP XR	LP03
HUVB HUVc HUVD HUVE	Human Umbilical Vein, Endo. remake	Uni-ZAP XR	LP03
HSTA HSTB HSTC HSTD	Human Skin Tumor	Uni-ZAP XR	LP03
HTAA HTAB HTAC HTAD HTAE	Human Activated T-Cells	Uni-ZAP XR	LP03
HFEA HFEB HFEC	Human Fetal Epithelium (Skin)	Uni-ZAP XR	LP03
HJPA HJPB HJPC HJPD	HUMAN JURKAT MEMBRANE BOUND POLYSOMES	Uni-ZAP XR	LP03
HESA	Human epithelioid sarcoma	Uni-Zap XR	LP03
HLTA HLTB HLTC HLTD HLTE HLTF	Human T-Cell Lymphoma	Uni-ZAP XR	LP03
HFTA HFTB HFTC HFTD	Human Fetal Dura Mater	Uni-ZAP XR	LP03
HRDA HRDB HRDC HRDD HRDE HRDF	Human Rhabdomyosarcoma	Uni-ZAP XR	LP03
HCAA HCAB HCAC	Cem cells cyclohexamide treated	Uni-ZAP XR	LP03
HRGA HRGB HRGC HRGD	Raji Cells, cyclohexamide treated	Uni-ZAP XR	LP03
HSUA HSUB HSUC HSUM	Supt Cells, cyclohexamide treated	Uni-ZAP XR	LP03
HT4A HT4C HT4D	Activated T-Cells, 12 hrs.	Uni-ZAP XR	LP03
HE9A HE9B HE9C HE9D HE9E HE9F HE9G HE9H HE9M HE9N	Nine Week Old Early Stage Human	Uni-ZAP XR	LP03
HATA HATB HATC HATD HATE	Human Adrenal Gland Tumor	Uni-ZAP XR	LP03
HT5A	Activated T-Cells, 24 hrs.	Uni-ZAP XR	LP03
HFGA HFGM	Human Fetal Brain	Uni-ZAP XR	LP03
HNEA HNEB HNEC HNED HNEE	Human Neutrophil	Uni-ZAP XR	LP03
HBGB HBGD	Human Primary Breast Cancer	Uni-ZAP XR	LP03
HBNA HBNB	Human Normal Breast	Uni-ZAP XR	LP03
HCAS	Cem Cells, cyclohexamide treated, subtra	Uni-ZAP XR	LP03
HHPS	Human Hippocampus, subtracted	pBS	LP03
HKCS HKCU	Human Colon Cancer, subtracted	pBS	LP03
HRGS	Raji cells, cyclohexamide treated,	pBS	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
	subtracted		
HSUT	Supt cells. cyclohexamide treated. differentially expressed	pBS	LP03
HT4S	Activated T-Cells. 12 hrs. subtracted	Uni-ZAP XR	LP03
HCDA HCDB HCDC HCDD HCDE	Human Chondrosarcoma	Uni-ZAP XR	LP03
HOAA HOAB HOAC	Human Osteosarcoma	Uni-ZAP XR	LP03
HTLA HTLB HTLC HTLD HTLE HTLF	Human adult testis, large inserts	Uni-ZAP XR	LP03
HLMA HLMC HLMD	Breast Lymph node cDNA library	Uni-ZAP XR	LP03
H6EA H6EB H6EC	HL-60, PMA 4H	Uni-ZAP XR	LP03
HTXA HTXB HTXC HTXD HTXE HTXF HTXG HTXH	Activated T-Cell (12hs)/Thiouridine labelledEco	Uni-ZAP XR	LP03
HNFA HNFH HNFC HNFD HNFE HNFF HNFG HNFI HNFI	Human Neutrophil, Activated	Uni-ZAP XR	LP03
HTOB HTOC	HUMAN TONSILS. FRACTION 2	Uni-ZAP XR	LP03
HMGB	Human OB MG63 control fraction I	Uni-ZAP XR	LP03
HOPB	Human OB HOS control fraction I	Uni-ZAP XR	LP03
HORB	Human OB HOS treated (10 nM E2) fraction I	Uni-ZAP XR	LP03
HSVA HSVB HSVC	Human Chronic Synovitis	Uni-ZAP XR	LP03
HROA	HUMAN STOMACH	Uni-ZAP XR	LP03
HBJA HBJB HBJC HBJD HBJE HBJF HBJG HBJH HBJI HBJJ HBJK	HUMAN B CELL LYMPHOMA	Uni-ZAP XR	LP03
HCRA HCRB HCRC	human corpus colosum	Uni-ZAP XR	LP03
HODA HODB HODC HODD	human ovarian cancer	Uni-ZAP XR	LP03
HDSA	Dermatofibrosarcoma Protuberance	Uni-ZAP XR	LP03
HMWA HMWB HMWC HMWD HMWE HMWF HMWG HMWH HMWI HMWJ	Bone Marrow Cell Line (RS4;11)	Uni-ZAP XR	LP03
HSOA	stomach cancer (human)	Uni-ZAP XR	LP03
HERA	SKIN	Uni-ZAP XR	LP03
HMDA	Brain-medulloblastoma	Uni-ZAP XR	LP03
HGLA HGLB HGLD	Glioblastoma	Uni-ZAP XR	LP03
HEAA	H. Atrophic Endometrium	Uni-ZAP XR	LP03
HBCA HBCB	H. Lymph node breast Cancer	Uni-ZAP XR	LP03
HPWT	Human Prostate BPH, re-excision	Uni-ZAP XR	LP03
HFVG HFVH HFVI	Fetal Liver, subtraction II	pBS	LP03
HNFI	Human Neutrophils, Activated, re-excision	pBS	LP03
HBMB HBMC HBMD	Human Bone Marrow, re-excision	pBS	LP03
HKML HKMM HKMN	H. Kidney Medulla, re-excision	pBS	LP03
HKIX HKIY	H. Kidney Cortex, subtracted	pBS	LP03
HADT	H. Amygdala Depression, subtracted	pBS	LP03
H6AS	HL-60, untreated, subtracted	Uni-ZAP XR	LP03
H6ES	HL-60, PMA 4H. subtracted	Uni-ZAP XR	LP03
H6BS	HL-60, RA 4h. Subtracted	Uni-ZAP XR	LP03
H6CS	HL-60. PMA 1d. subtracted	Uni-ZAP XR	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HTXJ HTXK	Activated T-cell(12h)/Thiouridine-re-excision	Uni-ZAP XR	LP03
HMSA HMSB HMSC HMSE HMSE HMSF HMSG HMSH HMSI HMSJ HMSK	Monocyte activated	Uni-ZAP XR	LP03
HAGA HAGB HAGC HAGD HAGE HAGF	Human Amygdala	Uni-ZAP XR	LP03
HSRA HSRB HSRE	STROMAL -OSTEOCLASTOMA	Uni-ZAP XR	LP03
HSRD HSRF HSRG HSRH	Human Osteoclastoma Stromal Cells - unamplified	Uni-ZAP XR	LP03
HSQA HSQB HSQC HSQD HSQE HSQF HSQG	Stromal cell TF274	Uni-ZAP XR	LP03
HSKA HSKB HSKC HSKD HSKE HSKF HSKZ	Smooth muscle, serum treated	Uni-ZAP XR	LP03
HSLA HSLB HSLC HSLD HSLE HSLF HSLG	Smooth muscle, control	Uni-ZAP XR	LP03
HSDA HSDD HSDE HSDF HSDG HSDH	Spinal cord	Uni-ZAP XR	LP03
HPWS	Prostate-BPH subtracted II	pBS	LP03
HSKW HSKX HSKY	Smooth Muscle- HASTE normalized	pBS	LP03
HFPB HFPC HFPD	H. Frontal cortex, epileptic; re-excision	Uni-ZAP XR	LP03
HSDI HSDJ HSDK	Spinal Cord, re-excision	Uni-ZAP XR	LP03
HSKN HSKO	Smooth Muscle Serum Treated, Norm	pBS	LP03
HSKG HSKH HSKI	Smooth muscle, serum induced, re-exc	pBS	LP03
HFCA HFCB HFCC HFCD HFCE HFCF	Human Fetal Brain	Uni-ZAP XR	LP04
HPTA HPTB HPTD	Human Pituitary	Uni-ZAP XR	LP04
HTHB HTHC HTHD	Human Thymus	Uni-ZAP XR	LP04
HE6B HE6C HE6D HE6E HE6F HE6G HE6S	Human Whole Six Week Old Embryo	Uni-ZAP XR	LP04
HSSA HSSB HSSC HSSD HSSE HSSF HSSG HSSH HSSI HSSJ HSSK	Human Synovial Sarcoma	Uni-ZAP XR	LP04
HE7T	7 Week Old Early Stage Human, subtracted	Uni-ZAP XR	LP04
HEPA HEPB HEPC	Human Epididymus	Uni-ZAP XR	LP04
HSNA HSNB HSNB HSNM HSNM	Human Synovium	Uni-ZAP XR	LP04
HPFB HPFC HPFD HPFE	Human Prostate Cancer, Stage C fraction	Uni-ZAP XR	LP04
HE2A HE2D HE2E HE2H HE2I HE2M HE2N HE2O	12 Week Old Early Stage Human	Uni-ZAP XR	LP04
HE2B HE2C HE2F HE2G HE2P HE2Q	12 Week Old Early Stage Human, II	Uni-ZAP XR	LP04
HPTS HPTT HPTU	Human Pituitary, subtracted	Uni-ZAP XR	LP04
HAUA HAUB HAUC	Amniotic Cells - TNF induced	Uni-ZAP XR	LP04
HAQA HAQB HAQC HAQD	Amniotic Cells - Primary Culture	Uni-ZAP XR	LP04
HWTB HWTB HWTB	wilm's tumor	Uni-ZAP XR	LP04
HBSD	Bone Cancer, re-excision	Uni-ZAP XR	LP04
HSGB	Salivary gland, re-excision	Uni-ZAP XR	LP04
HSJA HSJB HSJC	Smooth muscle-ILb induced	Uni-ZAP XR	LP04
HSXA HSXB HSXC HSXD	Human Substantia Nigra	Uni-ZAP XR	LP04
HSJA HSHB HSHC	Smooth muscle, IL1b induced	Uni-ZAP XR	LP04

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HOUA HOUB HOUC HOUD HOUE	Adipocytes	Uni-ZAP XR	LP04
HPWA HPWB HPWC HPWD HPWE	Prostate BPH	Uni-ZAP XR	LP04
HELA HELB HELC HELD HELE HELF HELG HELH	Endothelial cells-control	Uni-ZAP XR	LP04
HEMA HEMB HEMC HEMD HEME HEMF HEMG HEMH	Endothelial-induced	Uni-ZAP XR	LP04
HBIA HBIB HBIC	Human Brain, Striatum	Uni-ZAP XR	LP04
HHSA HHSB HHSC HHSD HHSE	Human Hypothalamus.Schizophrenia	Uni-ZAP XR	LP04
HNGA HNGB HNGC HNGD HNGE HNGF HNGG HNGH HNGI HNGJ	neutrophils control	Uni-ZAP XR	LP04
HNHA HNHB HNHC HNHD HNHE HNHF HNHG HNHH HNHI HNHI	Neutrophils IL-1 and LPS induced	Uni-ZAP XR	LP04
HSDB HSDC	STRIATUM DEPRESSION	Uni-ZAP XR	LP04
HHPT	Hypothalamus	Uni-ZAP XR	LP04
HSAT HSAU HSAV HSAW HSAX HSAY HSAZ	Anergic T-cell	Uni-ZAP XR	LP04
HBMS HBMT HBMU HBMV HBMW HBMX	Bone marrow	Uni-ZAP XR	LP04
HOEA HOEB HOEC HOED HOEE HOEF HOEJ	Osteoblasts	Uni-ZAP XR	LP04
HAIA HAIB HAIC HAID HAIE HAIF	Epithelial-TNF α and INF induced	Uni-ZAP XR	LP04
HTGA HTGB HTGC HTGD	Apoptotic T-cell	Uni-ZAP XR	LP04
HMCA HMCB HMCC HMCD HMCE	Macrophage-oxLDL	Uni-ZAP XR	LP04
HMAA HMAB HMAG HMAD HMAE HMAF HMAG	Macrophage (GM-CSF treated)	Uni-ZAP XR	LP04
HPHA	Normal Prostate	Uni-ZAP XR	LP04
HPIA HPIB HPIC	LNCAP prostate cell line	Uni-ZAP XR	LP04
HPJA HPJB HPJC	PC3 Prostate cell line	Uni-ZAP XR	LP04
HOSE HOSF HOSG	Human Osteoclastoma, re-excision	Uni-ZAP XR	LP04
HTGE HTGF	Apoptotic T-cell, re-excision	Uni-ZAP XR	LP04
HMAJ HMAK	H Macrophage (GM-CSF treated), re-excision	Uni-ZAP XR	LP04
HACB HACC HACD	Human Adipose Tissue, re-excision	Uni-ZAP XR	LP04
HFPA	H. Frontal Cortex, Epileptic	Uni-ZAP XR	LP04
HFAA HFAB HFAC HFAD HFAE	Alzheimers, spongy change	Uni-ZAP XR	LP04
HFAM	Frontal Lobe, Dementia	Uni-ZAP XR	LP04
HMIA HMIB HMIC	Human Manic Depression Tissue	Uni-ZAP XR	LP04
HTSA HTSE HTSF HTSG HTSH	Human Thymus	pBS	LP05
HPBA HPBB HPBC HPBD HPBE	Human Pineal Gland	pBS	LP05
HSAA HSAB HSAC	HSA 172 Cells	pBS	LP05
HSBA HSBB HSBC HSBM	HSC172 cells	pBS	LP05
HJAA HJAB HJAC HJAD	Jurkat T-cell G1 phase	pBS	LP05
HJBA HJBB HJBC HJBD	Jurkat T-Cell, S phase	pBS	LP05
HAFA HAFB	Aorta endothelial cells + TNF- α	pBS	LP05
HAWA HAWB HAWC	Human White Adipose	pBS	LP05
HTNA HTNB	Human Thyroid	pBS	LP05
HONA	Normal Ovary, Premenopausal	pBS	LP05

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HARA HARB	Human Adult Retina	pBS	LP05
HLJA HLJB	Human Lung	pCMVSPORT 1	LP06
HOFM HOFN HOFO	H. Ovarian Tumor, II, OV5232	pCMVSPORT 2.0	LP07
HOGA HOGB HOGC	OV 10-3-95	pCMVSPORT 2.0	LP07
HCGL	CD34+cells, II	pCMVSPORT 2.0	LP07
HDLA	Hodgkin's Lymphoma I	pCMVSPORT 2.0	LP07
HDTA HDTB HDTC HDTD HDTE	Hodgkin's Lymphoma II	pCMVSPORT 2.0	LP07
HKAA HKAB HKAC HKAD HKAE HKAF HKAG HKAH	Keratinocyte	pCMVSPORT2.0	LP07
HCIM	CAPFINDER, Crohn's Disease, lib 2	pCMVSPORT 2.0	LP07
HKAL	Keratinocyte, lib 2	pCMVSPORT2.0	LP07
HKAT	Keratinocyte, lib 3	pCMVSPORT2.0	LP07
HNDA	Nasal polyps	pCMVSPORT2.0	LP07
HDRA	H. Primary Dendritic Cells.lib 3	pCMVSPORT2.0	LP07
HOHA HOHB HOHC	Human Osteoblasts II	pCMVSPORT2.0	LP07
HLDA HLDB HLDC	Liver, Hepatoma	pCMVSPORT3.0	LP08
HLDN HLDO HLDP	Human Liver, normal	pCMVSPORT3.0	LP08
HMTA	pBMC stimulated w/ poly I/C	pCMVSPORT3.0	LP08
HNTA	NTERA2, control	pCMVSPORT3.0	LP08
HDP A HDPB HDP C HDPD HDPF HDPG HDPH HDPI HDPJ HDPK HDP M HDPN HDPO HDPP	Primary Dendritic Cells, lib 1	pCMVSPORT3.0	LP08
HMUA HMUB HMUC	Primary Dendritic cells, frac 2	pCMVSPORT3.0	LP08
HHEA HHEB HHEC HHED	Myeloid Progenitor Cell Line	pCMVSPORT3.0	LP08
HHEM HHEN HHEO HHEP	T Cell helper I	pCMVSPORT3.0	LP08
HEQA HEQB HEQC	T cell helper II	pCMVSPORT3.0	LP08
HJMA HJMB	Human endometrial stromal cells	pCMVSPORT3.0	LP08
HSWA HSWB HSWC	Human endometrial stromal cells- treated with progesterone	pCMVSPORT3.0	LP08
HSYA HSYB HSYC	Human endometrial stromal cells- treated with estradiol	pCMVSPORT3.0	LP08
HLWA HLWB HLWC	Human Thymus Stromal Cells	pCMVSPORT3.0	LP08
HRAA HRAB HRAC	Human Placenta	pCMVSPORT3.0	LP08
HMTM	Rejected Kidney, lib 4	pCMVSPORT3.0	LP08
HMJA	PCR, pBMC I/C treated	PCRII	LP09
HMKA HMKB HMKC HMKD HMKE	H. Meningioma, M6	pSport 1	LP10
HUSG HUSI	H. Meningioma, M1	pSport 1	LP10
HUSX HUSY	Human umbilical vein endothelial cells, IL-4 induced	pSport 1	LP10
HOFA	Human Umbilical Vein Endothelial Cells, uninduced	pSport 1	LP10
HCFA HCFB HCFC HCFD	Ovarian Tumor I, OV5232	pSport 1	LP10
HCFL HCFM HCFN HCFO	T-Cell PHA 16 hrs	pSport 1	LP10
HADA HADC HADD HADE HADF HADG	T-Cell PHA 24 hrs	pSport 1	LP10
HOVA HOVB HOVC	Human Adipose	pSport 1	LP10
	Human Ovary	pSport 1	LP10

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HTWB HTWC HTWD HTWE HTWF	Resting T-Cell Library, II	pSport 1	LP10
HMMA	Spleen metastatic melanoma	pSport 1	LP10
HLYA HLYB HLYC HLYD HLYE	Spleen, Chronic lymphocytic leukemia	pSport 1	LP10
HCGA	CD34+ cell. I	pSport 1	LP10
HEOM HEON	Human Eosinophils	pSport 1	LP10
HTDA	Human Tonsil, Lib 3	pSport 1	LP10
HSPA	Salivary Gland, Lib 2	pSport 1	LP10
HCHA HCHB HCHC	Breast Cancer cell line, MDA 36	pSport 1	LP10
HCHM HCHN	Breast Cancer Cell line, angiogenic	pSport 1	LP10
HCIA	Crohn's Disease	pSport 1	LP10
HDAA HDAB HDAC	HEL cell line	pSport 1	LP10
HABA	Human Astrocyte	pSport 1	LP10
HUFA HUFB HUFC	Ulcerative Colitis	pSport 1	LP10
HNTM	NTERA2 + retinoic acid, 14 days	pSport 1	LP10
HDQA	Primary Dendritic cells, CapFinder2, frac 1	pSport 1	LP10
HDQM	Primary Dendritic Cells, CapFinder, frac 2	pSport 1	LP10
HLDX	Human Liver, normal, CapFinder	pSport 1	LP10
HULA HULB HULC	Human Dermal Endothelial Cells, untreated	pSport 1	LP10
HUMA	Human Dermal Endothelial cells, treated	pSport 1	LP10
HCJA	Human Stromal Endometrial fibroblasts, untreated	pSport 1	LP10
HCJM	Human Stromal endometrial fibroblasts, treated w/ estradiol	pSport 1	LP10
HEDA	Human Stromal endometrial fibroblasts, treated with progesterone	pSport 1	LP10
HFNA	Human ovary tumor cell OV350721	pSport 1	LP10
HKGA HKGB HKGC HKGD	Merkel Cells	pSport 1	LP10
HISA HISB HISC	Pancreas Islet Cell Tumor	pSport 1	LP10
HLSA	Skin, burned	pSport 1	LP10
HBZA	Prostate, BPH, Lib 2	pSport 1	LP10
HBZS	Prostate BPH, Lib 2, subtracted	pSport 1	LP10
HFIA HFIB HFIC	Synovial Fibroblasts (control)	pSport 1	LP10
HFII HFII HFII	Synovial hypoxia	pSport 1	LP10
HFIT HFIV HFIV	Synovial IL-1/TNF stimulated	pSport 1	LP10
HGCA	Mesangial cell, frac 1	pSport 1	LP10
HMVA HMVB HMVC	Bone Marrow Stromal Cell, untreated	pSport 1	LP10
HFIX HFII HFIZ	Synovial Fibroblasts (II1/TNF), sub1	pSport 1	LP10
HFOX HFOY HFOZ	Synovial hypoxia-RSF subtracted	pSport 1	LP10
HMQA HMQB HMQC HMQD	Human Activated Monocytes	Uni-ZAP XR	LP11
HLIA HLIB HLIC	Human Liver	pCMVSPORT 1	LP012
HHBA HHBB HHBC HHBD HHBE	Human Heart	pCMVSPORT 1	LP012
HBBA HBBB	Human Brain	pCMVSPORT 1	LP012
HLJA HLJB HLJC HLJD HLJE	Human Lung	pCMVSPORT 1	LP012

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HOGA HOGB HOGC	Ovarian Tumor	pCMVSPORT 2.0	LP012
HTJM	Human Tonsils. Lib 2	pCMVSPORT 2.0	LP012
HAMF HAMG	KMH2	pCMVSPORT 3.0	LP012
HAJA HAJB HAJC	L428	pCMVSPORT 3.0	LP012
HWBA HWBB HWBC HWBD HWBE	Dendritic cells, pooled	pCMVSPORT 3.0	LP012
HWAA HWAB HWAC HWAD HWAE	Human Bone Marrow. treated	pCMVSPORT 3.0	LP012
HYAA HYAB HYAC	B Cell lymphoma	pCMVSPORT 3.0	LP012
HWHG HWHH HWHI	Healing groin wound. 6.5 hours post incision	pCMVSPORT 3.0	LP012
HWHP HWHQ HWHR	Healing groin wound: 7.5 hours post incision	pCMVSPORT 3.0	LP012
HARM	Healing groin wound - zero hr post-incision (control)	pCMVSPORT 3.0	LP012
HBIM	Olfactory epithelium: nasalcavity	pCMVSPORT 3.0	LP012
HWDA	Healing Abdomen wound; 70&90 min post incision	pCMVSPORT 3.0	LP012
HWEA	Healing Abdomen Wound; 15 days post incision	pCMVSPORT 3.0	LP012
HWJA	Healing Abdomen Wound; 21&29 days	pCMVSPORT 3.0	LP012
HNAL	Human Tongue, frac 2	pSport1	LP012
HMJA	H. Meningima, M6	pSport1	LP012
HMKA HMKB HMKC HMKD HMKE	H. Meningima, M1	pSport1	LP012
HOFA	Ovarian Tumor I, OV5232	pSport1	LP012
HCFA HCFB HCFC HCFD	T-Cell PHA 16 hrs	pSport1	LP012
HCFL HCFM HCFN HCFO	T-Cell PHA 24 hrs	pSport1	LP012
HMMA HMMB HMMC	Spleen metastatic melanoma	pSport1	LP012
HTDA	Human Tonsil, Lib 3	pSport1	LP012
HDBA	Human Fetal Thymus	pSport1	LP012
HDUA	Pericardium	pSport1	LP012
HBZA	Prostate.BPH, Lib 2	pSport1	LP012
HWCA	Larynx tumor	pSport1	LP012
HWKA	Normal lung	pSport1	LP012
HSMB	Bone marrow stroma, treated	pSport1	LP012
HBHM	Normal trachea	pSport1	LP012
HLFC	Human Larynx	pSport1	LP012
HLRB	Siebben Polyposis	pSport1	LP012
HNIA	Mammary Gland	pSport1	LP012
HNJB	Palate carcinoma	pSport1	LP012
HNKA	Palate normal	pSport1	LP012
HMZA	Pharynx carcinoma	pSport1	LP012
HABG	Cheek Carcinoma	pSport1	LP012
HMZM	Pharynx Carcinoma	pSport1	LP012
HDRM	Larynx Carcinoma	pSport1	LP012
HVAA	Pancreas normal PCA4 No	pSport1	LP012
HICA	Tongue carcinoma	pSport1	LP012
HUKA HUKB HUKC HUKD HUKF	Human Uterine Cancer	Lambda ZAP II	LP013
HFFA	Human Fetal Brain, random primed	Lambda ZAP II	LP013
HTUA	Activated T-cell labeled with 4-thioluri	Lambda ZAP II	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HBQA	Early Stage Human Brain. random primed	Lambda ZAP II	LP013
HMEB	Human microvascular Endothelial cells, fract. B	Lambda ZAP II	LP013
HUSH	Human Umbilical Vein Endothelial cells, fract. A, re-excision	Lambda ZAP II	LP013
HLQC HLQD	Hepatocellular tumor. re-excision	Lambda ZAP II	LP013
HTWJ HTWK HTWL	Resting T-cell, re-excision	Lambda ZAP II	LP013
HF6S	Human Whole 6 week Old Embryo (II), subt	pBluescript	LP013
HHPS	Human Hippocampus, subtracted	pBluescript	LP013
HLIS	LNCAP. differential expression	pBluescript	LP013
HLHS HLHT	Early Stage Human Lung, Subtracted	pBluescript	LP013
HSUS	Supt cells, cyclohexamide treated, subtracted	pBluescript	LP013
HSUT	Supt cells, cyclohexamide treated, differentially expressed	pBluescript	LP013
HSDS	H. Striatum Depression, subtracted	pBluescript	LP013
HPTZ	Human Pituitary, Subtracted VII	pBluescript	LP013
HSDX	H. Striatum Depression. subt II	pBluescript	LP013
HSDZ	H. Striatum Depression, subt	pBluescript	LP013
HPBA HPBB HPBC HPBD HPBE	Human Pineal Gland	pBluescript SK-	LP013
HRTA	Colorectal Tumor	pBluescript SK-	LP013
HSBA HSBB HSBC HSBM	HSC172 cells	pBluescript SK-	LP013
HJAA HJAB HJAC HJAD	Jurkat T-cell G1 phase	pBluescript SK-	LP013
HJBA HJBB HJBC HJBD	Jurkat T-cell, S1 phase	pBluescript SK-	LP013
HTNA HTNB	Human Thyroid	pBluescript SK-	LP013
HAHA HAHB	Human Adult Heart	Uni-ZAP XR	LP013
HE6A	Whole 6 week Old Embryo	Uni-ZAP XR	LP013
HFCA HFCB HFCC HFCD HFCE	Human Fetal Brain	Uni-ZAP XR	LP013
HFKC HFKD HFKE HFKF HFKG	Human Fetal Kidney	Uni-ZAP XR	LP013
HGBA HGBD HGBE HGBF HGBG	Human Gall Bladder	Uni-ZAP XR	LP013
HPRA HPRB HPRC HPRD	Human Prostate	Uni-ZAP XR	LP013
HTEA HTEB HTEC HTED HTEE	Human Testes	Uni-ZAP XR	LP013
HTTA HTTB HTTC HTTD HTTE	Human Testes Tumor	Uni-ZAP XR	LP013
HYBA HYBB	Human Fetal Bone	Uni-ZAP XR	LP013
HFLA	Human Fetal Liver	Uni-ZAP XR	LP013
HHFB HHFC HHFD HHFE HHFF	Human Fetal Heart	Uni-ZAP XR	LP013
HUVB HUV C HUVD HUVE	Human Umbilical Vein, End. remake	Uni-ZAP XR	LP013
HTHB HTHC HTHD	Human Thymus	Uni-ZAP XR	LP013
HSTA HSTB HSTC HSTD	Human Skin Tumor	Uni-ZAP XR	LP013
HTAA HTAB HTAC HTAD HTAE	Human Activated T-cells	Uni-ZAP XR	LP013
HFEA HFEB HFEC	Human Fetal Epithelium (skin)	Uni-ZAP XR	LP013
HJPA HJPB HJPC HJPD	Human Jurkat Membrane Bound Polysomes	Uni-ZAP XR	LP013
HESA	Human Epithelioid Sarcoma	Uni-ZAP XR	LP013
HALS	Human Adult Liver, Subtracted	Uni-ZAP XR	LP013
HFTA HFTB HFTC HFTD	Human Fetal Dura Mater	Uni-ZAP XR	LP013
HCAA HCAB HCAC	Cern cells, cyclohexamide treated	Uni-ZAP XR	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HRGA HRGB HRGC HRGD	Raji Cells, cyclohexamide treated	Uni-ZAP XR	LP013
HE9A HE9B HE9C HE9D HE9E	Nine Week Old Early Stage Human	Uni-ZAP XR	LP013
HSFA	Human Fibrosarcoma	Uni-ZAP XR	LP013
HATA HATB HATC HATD HATE	Human Adrenal Gland Tumor	Uni-ZAP XR	LP013
HTRA	Human Trachea Tumor	Uni-ZAP XR	LP013
HE2A HE2D HE2E HE2H HE2I	12 Week Old Early Stage Human	Uni-ZAP XR	LP013
HE2B HE2C HE2F HE2G HE2P	12 Week Old Early Stage Human, II	Uni-ZAP XR	LP013
HNEA HNEB HNEC HNED HNEE	Human Neutrophil	Uni-ZAP XR	LP013
HBGA	Human Primary Breast Cancer	Uni-ZAP XR	LP013
HPTS HPTT HPTU	Human Pituitary, subtracted	Uni-ZAP XR	LP013
HMQA HMQB HMQC HMQD	Human Activated Monocytes	Uni-ZAP XR	LP013
HOAA HOAB HOAC	Human Osteosarcoma	Uni-ZAP XR	LP013
HTOA HTOD HTOE HTOF HTOG	human tonsils	Uni-ZAP XR	LP013
HMGB	Human OB MG63 control fraction I	Uni-ZAP XR	LP013
HOPB	Human OB HOS control fraction I	Uni-ZAP XR	LP013
HOQB	Human OB HOS treated (1 nM E2) fraction I	Uni-ZAP XR	LP013
HAUA HAUB HAUC	Amniotic Cells - TNF induced	Uni-ZAP XR	LP013
HAQA HAQB HAQC HAQD	Amniotic Cells - Primary Culture	Uni-ZAP XR	LP013
HROA HROC	HUMAN STOMACH	Uni-ZAP XR	LP013
HBJA HBJB HBJC HBJD HBJE	HUMAN B CELL LYMPHOMA	Uni-ZAP XR	LP013
HODA HODB HODC HODD	human ovarian cancer	Uni-ZAP XR	LP013
HCPA	Corpus Callosum	Uni-ZAP XR	LP013
HSOA	stomach cancer (human)	Uni-ZAP XR	LP013
HERA	SKIN	Uni-ZAP XR	LP013
HMDA	Brain-medulloblastoma	Uni-ZAP XR	LP013
HGLA HGLB HGLD	Glioblastoma	Uni-ZAP XR	LP013
HWTA HWTB HWTC	wilm's tumor	Uni-ZAP XR	LP013
HEAA	H. Atrophic Endometrium	Uni-ZAP XR	LP013
HAPN HAPO HAPR HAPQ HAPR	Human Adult Pulmonary;re-excision	Uni-ZAP XR	LP013
HLTG HLTH	Human T-cell lymphoma;re-excision	Uni-ZAP XR	LP013
HAHC HAHD HAHE	Human Adult Heart;re-excision	Uni-ZAP XR	LP013
HAGA HAGB HAGC HAGD HAGE	Human Amygdala	Uni-ZAP XR	LP013
HSJA HSJB HSJC	Smooth muscle-ILb induced	Uni-ZAP XR	LP013
HSJA HSHB HSHC	Smooth muscle, IL1b induced	Uni-ZAP XR	LP013
HPWA HPWB HPWC HPWD HPWE	Prostate BPH	Uni-ZAP XR	LP013
HPJA HPJB HPJC	LNCAP prostate cell line	Uni-ZAP XR	LP013
HPJA HPJB HPJC	PC3 Prostate cell line	Uni-ZAP XR	LP013
HBTA	Bone Marrow Stroma, TNF&LPS ind	Uni-ZAP XR	LP013
HMCF HMCG HMCH HMCI HMCJ	Macrophage-oxLDL; re-excision	Uni-ZAP XR	LP013
HAGG HAGH HAGI	Human Amygdala;re-excision	Uni-ZAP XR	LP013
HACA	H. Adipose Tissue	Uni-ZAP XR	LP013
HKFB	K562 + PMA (36 hrs);re-excision	ZAP Express	LP013
HCWT HCWU HCWV	CD34 positive cells (cord blood);re-ex	ZAP Express	LP013
HBWA	Whole brain	ZAP Express	LP013
HBXA HBXB HBXC HBXD	Human Whole Brain #2 - Oligo dT > 1.5Kb	ZAP Express	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HAVM	Temporal cortex-Alzheimer	pT-Adv	LP014
HAVT	Hippocampus, Alzheimer Subtracted	pT-Adv	LP014
HHAS	CHME Cell Line	Uni-ZAP XR	LP014
HAJR	Larynx normal	pSport 1	LP014
HWLE HWLF HWLG HWLH	Colon Normal	pSport 1	LP014
HCRM HCRN HCRO	Colon Carcinoma	pSport 1	LP014
HWLI HWLJ HWLK	Colon Normal	pSport 1	LP014
HWL HWLR HWLS HWLT	Colon Tumor	pSport 1	LP014
HBFM	Gastrocnemius Muscle	pSport 1	LP014
HBOD HBOE	Quadriceps Muscle	pSport 1	LP014
HBKD HBKE	Soleus Muscle	pSport 1	LP014
HCCM	Pancreatic Langerhans	pSport 1	LP014
HWGA	Larynx carcinoma	pSport 1	LP014
HWGM HWGN	Larynx carcinoma	pSport 1	LP014
HWLA HWLB HWLC	Normal colon	pSport 1	LP014
HWLM HWLN	Colon Tumor	pSport 1	LP014
HVAM HVAN HVAO	Pancreas Tumor	pSport 1	LP014
HWGQ	Larynx carcinoma	pSport 1	LP014
HAQM HAQN	Salivary Gland	pSport 1	LP014
HASM	Stomach; normal	pSport 1	LP014
HBCM	Uterus; normal	pSport 1	LP014
HCDM	Testis; normal	pSport 1	LP014
HDJM	Brain; normal	pSport 1	LP014
HEFM	Adrenal Gland, normal	pSport 1	LP014
HBAA	Rectum normal	pSport 1	LP014
HFDN	Rectum tumour	pSport 1	LP014
HGAM	Colon, normal	pSport 1	LP014
HHMM	Colon, tumour	pSport 1	LP014
HCLB HCLC	Human Lung Cancer	Lambda Zap II	LP015
HRLA	L1 Cell line	ZAP Express	LP015
HHAM	Hypothalamus, Alzheimer's	pCMVSPORT 3.0	LP015
HKBA	Ku 812F Basophils Line	pSport 1	LP015
HS2S	Saos2, Dexamethasone Treated	pSport 1	LP016
HASA	Lung Carcinoma A549 TNFalpha activated	pSport 1	LP016
HTFM	TF-1 Cell Line GM-CSF Treated	pSport 1	LP016
HYAS	Thyroid Tumour	pSport 1	LP016
HUTS	Larynx Normal	pSport 1	LP016
HXOA	Larynx Tumor	pSport 1	LP016
HEAH	Ea.hy.926 cell line	pSport 1	LP016
HINA	Adenocarcinoma Human	pSport 1	LP016
HRMA	Lung Mesothelium	pSport 1	LP016
HLCL	Human Pre-Differentiated Adipocytes	Uni-Zap XR	LP017
HS2A	Saos2 Cells	pSport 1	LP020
HS2I	Saos2 Cells; Vitamin D3 Treated	pSport 1	LP020
HUCM	CHME Cell Line, untreated	pSport 1	LP020
HEPN	Aryepiglottis Normal	pSport 1	LP020

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HPSN	Sinus Piniformis Tumour	pSport 1	LP020
HNSA	Stomach Normal	pSport 1	LP020
HNSM	Stomach Tumour	pSport 1	LP020
HNLA	Liver Normal Met5No	pSport 1	LP020
HUTA	Liver Tumour Met 5 Tu	pSport 1	LP020
HOCN	Colon Normal	pSport 1	LP020
HOCT	Colon Tumor	pSport 1	LP020
HTNT	Tongue Tumour	pSport 1	LP020
HLXN	Larynx Normal	pSport 1	LP020
HLXT	Larynx Tumour	pSport 1	LP020
HTYN	Thymus	pSport 1	LP020
HPLN	Placenta	pSport 1	LP020
HTNG	Tongue Normal	pSport 1	LP020
HZAA	Thyroid Normal (SDCA2 No)	pSport 1	LP020
HWES	Thyroid Thyroiditis	pSport 1	LP020
HFHD	Ficoll Human Stromal Cells, 5Fu treated	pTrip1Ex2	LP021
HFHM, HFHN	Ficoll Human Stromal Cells, Untreated	pTrip1Ex2	LP021
HPCI	Hep G2 Cells, lambda library	lambda Zap-CMV XR	LP021
HBCA, HBCB, HBCC	H. Lymph node breast Cancer	Uni-ZAP XR	LP021
HCOK	Chondrocytes	pSPORT1	LP022
HDCA, HDCB, HDCC	Dendritic Cells From CD34 Cells	pSPORT1	LP022
HDMA, HDMB	CD40 activated monocyte dendritic cells	pSPORT1	LP022
HDDM, HDDN, HDDO	LPS activated derived dendritic cells	pSPORT1	LP022
HPCR	Hep G2 Cells, PCR library	lambda Zap-CMV XR	LP022
HAAA, HAAB, HAAC	Lung, Cancer (4005313A3): Invasive Poorly Differentiated Lung Adenocarcinoma	pSPORT1	LP022
HIPA, HIPB, HIPC	Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma, Metastatic	pSPORT1	LP022
HOOH, HOOI	Ovary, Cancer: (4004562 B6) Papillary Serous Cystic Neoplasm, Low Malignant Pot	pSPORT1	LP022
HIDA	Lung, Normal: (4005313 B1)	pSPORT1	LP022
HUJA, HUJB, HUJC, HUJD, HUJE	B-Cells	pCMVSPORT 3.0	LP022
HNOA, HNOB, HNOC, HNOD	Ovary, Normal: (9805C040R)	pSPORT1	LP022
HNLM	Lung, Normal: (4005313 B1)	pSPORT1	LP022
HSCL	Stromal Cells	pSPORT1	LP022
HAAX	Lung, Cancer: (4005313 A3) Invasive Poorly-differentiated Metastatic lung adenocarcinoma	pSPORT1	LP022
HUUA, HUUB, HUUC, HUUD	B-cells (unstimulated)	pTrip1Ex2	LP022
HWWA, HWWB, HWWC, HWWD, HWE, HWWF, HWWG	B-cells (stimulated)	pSPORT1	LP022
HCCC	Colon, Cancer: (9808C064R)	pCMVSPORT 3.0	LP023
HPDO HPDP HPDQ HPDR HPD	Ovary, Cancer (9809C332): Poorly differentiated adenocarcinoma	pSport 1	LP023

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HPCO HPCP HPCQ HPCT	Ovary, Cancer (15395A1F): Grade II Papillary Carcinoma	pSport 1	LP023
HOCM HOCO HOCQ HOCQ	Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma	pSport 1	LP023
HCBM HCBN HCBO	Breast, Cancer: (4004943 A5)	pSport 1	LP023
HNBT HNBH HNBV	Breast, Normal: (4005522B2)	pSport 1	LP023
HBCP HBCQ	Breast, Cancer: (4005522 A2)	pSport 1	LP023
HBCJ	Breast, Cancer: (9806C012R)	pSport 1	LP023
HSAM HSAN	Stromal cells 3.88	pSport 1	LP023
HVCA HVCB HVCC HVCD	Ovary, Cancer: (4004332 A2)	pSport 1	LP023
HSCK HSEN HSEO	Stromal cells (HBM3.18)	pSport 1	LP023
HSCP HSCQ	stromal cell clone 2.5	pSport 1	LP023
HUXA	Breast Cancer: (4005385 A2)	pSport 1	LP023
HCOM HCON HCOO HCOP HCOQ	Ovary, Cancer (4004650 A3): Well-Differentiated Micropapillary Serous Carcinoma	pSport 1	LP023
HBNM	Breast, Cancer: (9802C020E)	pSport 1	LP023
HVVA HVVB HVVC HVVD HVVE	Human Bone Marrow, treated	pSport 1	LP023

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 5. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to the nucleotide sequence of SEQ ID NO:X.

5 Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid
10 mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using
15 Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

 Alternatively, two primers of 17-20 nucleotides derived from both ends of the
20 nucleotide sequence of SEQ ID NO:X are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 μg of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of
25 Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA
30 product.

 Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not

limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

5 Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full
10 length gene.

This above method starts with total RNA isolated from the desired source, although poly-A⁺ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the
15 RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis
20 using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

25

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the sequence corresponding to SEQ ID NO:X, according to the method
30 described in Example 1. (See also, Sambrook.)

Example 3: Tissue specific expression analysis

The Human Genome Sciences, Inc. (HGS) database is derived from sequencing tissue specific cDNA libraries. Libraries generated from a particular tissue are selected and the specific tissue expression pattern of EST groups or assembled contigs within these libraries is determined by comparison of the expression patterns of those groups or contigs within the entire database. ESTs which show tissue specific expression are selected.

The original clone from which the specific EST sequence was generated, is obtained from the catalogued library of clones and the insert amplified by PCR using methods known in the art. The PCR product is denatured then transferred in 96 well format to a nylon membrane (Schleicher and Scheull) generating an array filter of tissue specific clones. Housekeeping genes, maize genes, and known tissue specific genes are included on the filters. These targets can be used in signal normalization and to validate assay sensitivity. Additional targets are included to monitor probe length and specificity of hybridization.

Radioactively labeled hybridization probes are generated by first strand cDNA synthesis per the manufacturer's instructions (Life Technologies) from mRNA/RNA samples prepared from the specific tissue being analyzed. The hybridization probes are purified by gel exclusion chromatography, quantitated, and hybridized with the array filters in hybridization bottles at 65°C overnight. The filters are washed under stringent conditions and signals are captured using a Fuji phosphorimager.

Data is extracted using AIS software and following background subtraction, signal normalization is performed. This includes a normalization of filter-wide expression levels between different experimental runs. Genes that are differentially expressed in the tissue of interest are identified and the full length sequence of these clones is generated.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute

cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR
5 fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

A polynucleotide encoding a polypeptide of the present invention is amplified using
10 PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial
15 expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is
20 ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is
25 isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto
30 pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction

sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express
5 protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

The following alternative method can be used to purify a polypeptide expressed in *E*
10 *coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell
15 paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then
20 mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is
25 discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous
30 stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 μm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column
5 is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of
10 water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging
15 from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from
20 Commassie blue stained 16% SDS-PAGE gel when 5 μg of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

25 In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of
30 recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the

polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon, is amplified using the PCR protocol described in Example 1. If a naturally occurring signal sequence is used to produce the polypeptide of the present invention, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μ g of a plasmid containing the polynucleotide is co-transfected with 1.0 μ g of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc.

Natl. Acad. Sci. USA 84:7413-7417 (1987). One μg of BaculoGold™ virus DNA and 5 μg of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μl Lipofectin plus 90 μl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μCi of ^{35}S -methionine and 5 μCi ^{35}S -cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as DHFR, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 5 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction 10 enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If a naturally occurring signal sequence is used to produce the polypeptide of the present invention, the vector does not need a second signal peptide. 15 Alternatively, if a naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

20 The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

25 Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μ g of the expression plasmid pC6 or pC4 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM 30 supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones

are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

10

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the half-life time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without

a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the polypeptide of the present invention, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous
5 signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACCTCACACATGCCCACCGTGCCCAG
CACCTGAATTTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGA
10 CACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGTGGACGTAAGC
CACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT
AATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
AAGGTCTCCAACAAAGCCCTCCCAACCCCCATCGAGAAAACCATCTCCAAAGCC
15 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG
CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAAGC
GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGAC
CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACC
GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
20 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT
GAGTGCGACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1685)

Example 10: Production of an Antibody from a Polypeptide

25 a) Hybridoma Technology

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing polypeptide of the present invention are administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of polypeptide
30 of the present invention is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

Monoclonal antibodies specific for polypeptide of the present invention are prepared using hybridoma technology. (Kohler et al., Nature 256:495 (1975); Kohler et al., Eur. J. Immunol. 6:511 (1976); Kohler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981)). In
5 general, an animal (preferably a mouse) is immunized with polypeptide of the present invention or, more preferably, with a secreted polypeptide of the present invention-expressing cell. Such polypeptide-expressing cells are cultured in any suitable tissue culture medium, preferably in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino
10 acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in
15 HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981)). The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide of the present invention.

Alternatively, additional antibodies capable of binding to polypeptide of the present
20 invention can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma
25 cells are screened to identify clones which produce an antibody whose ability to bind to the polypeptide of the present invention-specific antibody can be blocked by polypeptide of the present invention. Such antibodies comprise anti-idiotypic antibodies to the polypeptide of the present invention-specific antibody and are used to immunize an animal to induce formation of further polypeptide of the present invention-specific antibodies.

30 For in vivo use of antibodies in humans, an antibody is "humanized". Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric and humanized

antibodies are known in the art and are discussed herein. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

b) Isolation Of Antibody Fragments Directed Against Polypeptide of the Present Invention From A Library Of scFvs

Naturally occurring V-genes isolated from human PBLs are constructed into a library of antibody fragments which contain reactivities against polypeptide of the present invention to which the donor may or may not have been exposed (see e.g., U.S. Patent 5,885,793 incorporated herein by reference in its entirety).

Rescue of the Library. A library of scFvs is constructed from the RNA of human PBLs as described in PCT publication WO 92/01047. To rescue phage displaying antibody fragments, approximately 10⁹ E. coli harboring the phagemid are used to inoculate 50 ml of 2xTY containing 1% glucose and 100 µg/ml of ampicillin (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to inoculate 50 ml of 2xTY-AMP-GLU, 2 x 10⁸ TU of delta gene 3 helper (M13 delta gene III, see PCT publication WO 92/01047) are added and the culture incubated at 37°C for 45 minutes without shaking and then at 37°C for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2xTY containing 100 µg/ml ampicillin and 50 µg/ml kanamycin and grown overnight. Phage are prepared as described in PCT publication WO 92/01047.

M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III particles are made by growing the helper phage in cells harboring a pUC19 derivative supplying the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at 37° C without shaking and then for a further hour at 37°C with shaking. Cells are spun down (IEC-Centra 8,400 r.p.m. for 10 min), resuspended in 300 ml 2xTY broth containing 100 µg ampicillin/ml and 25 µg kanamycin/ml (2xTY-AMP-KAN) and grown overnight, shaking at 37°C. Phage particles are purified and concentrated from the culture medium by two PEG-precipitations

(Sambrook et al., 1990), resuspended in 2 ml PBS and passed through a 0.45 μ m filter (Minisart NML; Sartorius) to give a final concentration of approximately 10¹³ transducing units/ml (ampicillin-resistant clones).

Panning of the Library. Immuntubes (Nunc) are coated overnight in PBS with 4 ml
5 of either 100 μ g/ml or 10 μ g/ml of a polypeptide of the present invention. Tubes are blocked
with 2% Marvel-PBS for 2 hours at 37°C and then washed 3 times in PBS. Approximately
10¹³ TU of phage is applied to the tube and incubated for 30 minutes at room temperature
tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes
are washed 10 times with PBS 0.1% Tween-20 and 10 times with PBS. Phage are eluted by
10 adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable
after which the solution is immediately neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4.
Phage are then used to infect 10 ml of mid-log E. coli TG1 by incubating eluted phage with
bacteria for 30 minutes at 37°C. The E. coli are then plated on TYE plates containing 1%
glucose and 100 μ g/ml ampicillin. The resulting bacterial library is then rescued with delta
15 gene 3 helper phage as described above to prepare phage for a subsequent round of selection.
This process is then repeated for a total of 4 rounds of affinity purification with tube-washing
increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

Characterization of Binders. Eluted phage from the 3rd and 4th rounds of selection
are used to infect E. coli HB 2151 and soluble scFv is produced (Marks, et al., 1991) from
20 single colonies for assay. ELISAs are performed with microtitre plates coated with either 10
 μ g/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones
positive in ELISA are further characterized by PCR fingerprinting (see, e.g., PCT publication
WO 92/01047) and then by sequencing. These ELISA positive clones may also be further
characterized by techniques known in the art, such as, for example, epitope mapping, binding
25 affinity, receptor signal transduction, ability to block or competitively inhibit
antibody/antigen binding, and competitive agonistic or antagonistic activity.

*Example 11: Method of Determining Alterations in a Gene Corresponding to a
Polynucleotide*

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X; and/or the nucleotide sequence of the related cDNA in the cDNA clone contained in a deposited library. Suggested PCR conditions consist of 35 cycles at 95 degrees C for 30 seconds; 60-120 seconds at 52-58 degrees C; and 60-120 seconds at 70 degrees C, using buffer solutions described in Sidransky et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton et al., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenin deoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an

associated disease.

Example 12: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

5 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

10 For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

15 The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

20 Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

25 Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 13: Formulation

30 The invention also provides methods of treatment and/or prevention of diseases or disorders (such as, for example, any one or more of the diseases or disorders disclosed

herein) by administration to a subject of an effective amount of a Therapeutic. By therapeutic is meant a polynucleotides or polypeptides of the invention (including fragments and variants), agonists or antagonists thereof, and/or antibodies thereto, in combination with a pharmaceutically acceptable carrier type (e.g., a sterile carrier).

5 The Therapeutic will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the Therapeutic alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such
10 considerations.

As a general proposition, the total pharmaceutically effective amount of the Therapeutic administered parenterally per dose will be in the range of about 1 ug/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most
15 preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the Therapeutic is typically administered at a dose rate of about 1 ug/kg/hour to about 50 ug/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following
20 treatment for responses to occur appears to vary depending on the desired effect.

Therapeutics can be are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material
25 or formulation auxiliary of any. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics are administered orally,
30 rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler,

diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release
5 systems. Suitable examples of sustained-release Therapeutics include suitable polymeric materials (such as, for example, semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules), suitable hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

10 Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al., *Biopolymers* 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (Langer et al., *J. Biomed. Mater. Res.* 15:167-277 (1981), and Langer, *Chem. Tech.* 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., *Id.*) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988).

15 Sustained-release Therapeutics also include liposomally entrapped Therapeutics of the invention (*see* generally, Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 317 -327 and 353-365 (1989)). Liposomes containing the Therapeutic are prepared by methods known per se: DE 3,218,121; Epstein et al., *Proc. Natl.*
20 *Acad. Sci. (USA)* 82:3688-3692 (1985); Hwang et al., *Proc. Natl. Acad. Sci.(USA)* 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being
25 adjusted for the optimal Therapeutic.

In yet an additional embodiment, the Therapeutics of the invention are delivered by way of a pump (*see* Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.* 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)).

Other controlled release systems are discussed in the review by Langer (*Science*
30 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Therapeutic is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form

(solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to the
5 Therapeutic.

Generally, the formulations are prepared by contacting the Therapeutic uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such
10 carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate,
15 succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including
20 cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The Therapeutic is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be
25 understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any pharmaceutical used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutics generally are placed into a container having a sterile access port,
30 for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Therapeutics ordinarily will be stored in unit or multi-dose containers, for example,

sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Therapeutic solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized Therapeutic
5 using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the Therapeutics of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products,
10 which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the Therapeutics may be employed in conjunction with other therapeutic compounds.

The Therapeutics of the invention may be administered alone or in combination with adjuvants. Adjuvants that may be administered with the Therapeutics of the invention
15 include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG, and MPL. In a specific embodiment, Therapeutics of the invention are administered in combination with alum. In another specific embodiment, Therapeutics of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the Therapeutics of the invention include,
20 but are not limited to, Monophosphoryl lipid immunomodulator, AdjuVax 100a, QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Virosomal adjuvant technology. Vaccines that may be administered with the Therapeutics of the invention include, but are not limited to, vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diphtheria, hepatitis A, hepatitis B, haemophilus influenzae B, whooping
25 cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined
30 agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

The Therapeutics of the invention may be administered alone or in combination with other therapeutic agents. Therapeutic agents that may be administered in combination with the Therapeutics of the invention, include but not limited to, other members of the TNF family, chemotherapeutic agents, antibiotics, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic agents, cytokines and/or growth factors. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

In one embodiment, the Therapeutics of the invention are administered in combination with members of the TNF family. TNF, TNF-related or TNF-like molecules that may be administered with the Therapeutics of the invention include, but are not limited to, soluble forms of TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), TR6 (International Publication No. WO 98/30694), OPG, and neutrokin-alpha (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-1BB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms CD154, CD70, and CD153.

In certain embodiments, Therapeutics of the invention are administered in combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors. Nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, RETROVIR™ (zidovudine/AZT), VIDEX™

(didanosine/ddI), HIVID™ (zalcitabine/ddC), ZERIT™ (stavudine/d4T), EPIVIR™ (lamivudine/3TC), and COMBIVIR™ (zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, VIRAMUNE™ (nevirapine), RESCRIPTOR™ (delavirdine), and SUSTIVA™ (efavirenz). Protease inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, CRIXIVAN™ (indinavir), NORVIR™ (ritonavir), INVIRASE™ (saquinavir), and VIRACEPT™ (nelfinavir). In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors may be used in any combination with Therapeutics of the invention to treat AIDS and/or to prevent or treat HIV infection.

In other embodiments, Therapeutics of the invention may be administered in combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, ATOVAQUONE™, ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, ETHAMBUTOL™, RIFABUTIN™, CLARITHROMYCIN™, AZITHROMYCIN™, GANCICLOVIR™, FOSCARNET™, CIDOFOVIR™, FLUCONAZOLE™, ITRACONAZOLE™, KETOCONAZOLE™, ACYCLOVIR™, FAMCICLOVIR™, PYRIMETHAMINE™, LEUCOVORIN™, NEUPOGEN™ (filgrastim/G-CSF), and LEUKINE™ (sargramostim/GM-CSF). In a specific embodiment, Therapeutics of the invention are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, and/or ATOVAQUONE™ to prophylactically treat or prevent an opportunistic *Pneumocystis carinii* pneumonia infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, and/or ETHAMBUTOL™ to prophylactically treat or prevent an opportunistic *Mycobacterium avium* complex infection. In another specific embodiment, Therapeutics of the invention are used in any combination with RIFABUTIN™, CLARITHROMYCIN™, and/or AZITHROMYCIN™ to prophylactically treat or prevent an opportunistic *Mycobacterium tuberculosis* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with GANCICLOVIR™,

FOSCARNET™, and/or CIDOFOVIR™ to prophylactically treat or prevent an opportunistic cytomegalovirus infection. In another specific embodiment, Therapeutics of the invention are used in any combination with FLUCONAZOLE™, ITRACONAZOLE™, and/or KETOCONAZOLE™ to prophylactically treat or prevent an opportunistic fungal infection.

- 5 In another specific embodiment, Therapeutics of the invention are used in any combination with ACYCLOVIR™ and/or FAMCICOLVIR™ to prophylactically treat or prevent an opportunistic herpes simplex virus type I and/or type II infection. In another specific embodiment, Therapeutics of the invention are used in any combination with PYRIMETHAMINE™ and/or LEUCOVORIN™ to prophylactically treat or prevent an
- 10 opportunistic *Toxoplasma gondii* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with LEUCOVORIN™ and/or NEUPOGEN™ to prophylactically treat or prevent an opportunistic bacterial infection.

- In a further embodiment, the Therapeutics of the invention are administered in combination with an antiviral agent. Antiviral agents that may be administered with the
- 15 Therapeutics of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.

- In a further embodiment, the Therapeutics of the invention are administered in combination with an antibiotic agent. Antibiotic agents that may be administered with the Therapeutics of the invention include, but are not limited to, amoxicillin, beta-lactamases,
- 20 aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin, erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin, sulfonamide, tetracyclines, trimethoprim, trimethoprim-sulfamthoxazole, and vancomycin.

- Conventional nonspecific immunosuppressive agents, that may be administered in
- 25 combination with the Therapeutics of the invention include, but are not limited to, steroids, cyclosporine, cyclosporine analogs, cyclophosphamide methylprednisone, prednisone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive agents that act by suppressing the function of responding T cells.

- In specific embodiments, Therapeutics of the invention are administered in
- 30 combination with immunosuppressants. Immunosuppressants preparations that may be administered with the Therapeutics of the invention include, but are not limited to, ORTHOCLONE™ (OKT3), SANDIMMUNE™/NEORAL™/SANGDYA™ (cyclosporin),

PROGRAF™ (tacrolimus), CELLCEPT™ (mycophenolate), Azathioprine, glucocorticosteroids, and RAPAMUNE™ (sirolimus). In a specific embodiment, immunosuppressants may be used to prevent rejection of organ or bone marrow transplantation.

In an additional embodiment, Therapeutics of the invention are administered alone or
5 in combination with one or more intravenous immune globulin preparations. Intravenous immune globulin preparations that may be administered with the Therapeutics of the invention include, but not limited to, GAMMAR™, IVEEGAM™, SANDOGLOBULIN™, GAMMAGARD S/D™, and GAMIMUNE™. In a specific embodiment, Therapeutics of the invention are administered in combination with intravenous immune globulin preparations in
10 transplantation therapy (e.g., bone marrow transplant).

In an additional embodiment, the Therapeutics of the invention are administered alone or in combination with an anti-inflammatory agent. Anti-inflammatory agents that may be administered with the Therapeutics of the invention include, but are not limited to, glucocorticoids and the nonsteroidal anti-inflammatories, aminoarylcarboxylic acid
15 derivatives, arylacetic acid derivatives, arylbutyric acid derivatives, arylcarboxylic acids, arylpropionic acid derivatives, pyrazoles, pyrazolones, salicylic acid derivatives, thiazinecarboxamides, e-acetamidocaproic acid, S-adenosylmethionine, 3-amino-4-hydroxybutyric acid, amixetrine, bendazac, benzydamine, bucolome, difenpiramide, ditazol, emorfazone, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol, paranyline,
20 perisoxal, pifoxime, proquazone, proxazole, and tenidap.

In another embodiment, compositions of the invention are administered in combination with a chemotherapeutic agent. Chemotherapeutic agents that may be administered with the Therapeutics of the invention include, but are not limited to, antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin); antiestrogens
25 (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-FU, methotrexate, floxuridine, interferon alpha-2b, glutamic acid, plicamycin, mercaptopurine, and 6-thioguanine); cytotoxic agents (e.g., carmustine, BCNU, lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate
30 sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., mephallen, chorambucil, mechlorethamine (nitrogen mustard) and thiotepa); steroids and

combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dicarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

In a specific embodiment, Therapeutics of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or
5 any combination of the components of CHOP. In another embodiment, Therapeutics of the invention are administered in combination with Rituximab. In a further embodiment, Therapeutics of the invention are administered with Rituxmab and CHOP, or Rituxmab and any combination of the components of CHOP.

In an additional embodiment, the Therapeutics of the invention are administered in
10 combination with cytokines. Cytokines that may be administered with the Therapeutics of the invention include, but are not limited to, IL2, IL3, IL4, IL5, IL6, IL7, IL10, IL12, IL13, IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha. In another embodiment, Therapeutics of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11,
15 IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21.

In an additional embodiment, the Therapeutics of the invention are administered in combination with angiogenic proteins. Angiogenic proteins that may be administered with the Therapeutics of the invention include, but are not limited to, Glioma Derived Growth Factor (GDGF), as disclosed in European Patent Number EP-399816; Platelet Derived
20 Growth Factor-A (PDGF-A), as disclosed in European Patent Number EP-682110; Platelet Derived Growth Factor-B (PDGF-B), as disclosed in European Patent Number EP-282317; Placental Growth Factor (PIGF), as disclosed in International Publication Number WO 92/06194; Placental Growth Factor-2 (PIGF-2), as disclosed in Hauser et al., Growth Factors, 4:259-268 (1993); Vascular Endothelial Growth Factor (VEGF), as disclosed in International
25 Publication Number WO 90/13649; Vascular Endothelial Growth Factor-A (VEGF-A), as disclosed in European Patent Number EP-506477; Vascular Endothelial Growth Factor-2 (VEGF-2), as disclosed in International Publication Number WO 96/39515; Vascular Endothelial Growth Factor B (VEGF-3); Vascular Endothelial Growth Factor B-186 (VEGF-B186), as disclosed in International Publication Number WO 96/26736; Vascular Endothelial
30 Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/02543; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/07832; and Vascular Endothelial Growth Factor-E (VEGF-E), as

disclosed in German Patent Number DE19639601. The above mentioned references are incorporated herein by reference herein.

In an additional embodiment, the Therapeutics of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the Therapeutics of the invention include, but are not limited to, LEUKINE™ (SARGRAMOSTIM™) and NEUPOGEN™ (FILGRASTIM™).

In an additional embodiment, the Therapeutics of the invention are administered in combination with Fibroblast Growth Factors. Fibroblast Growth Factors that may be administered with the Therapeutics of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

In additional embodiments, the Therapeutics of the invention are administered in combination with other therapeutic or prophylactic regimens, such as, for example, radiation therapy.

15

Example 14: Method of Treating Decreased Levels of the Polypeptide

The present invention relates to a method for treating an individual in need of an increased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an agonist of the invention (including polypeptides of the invention). Moreover, it will be appreciated that conditions caused by a decrease in the standard or normal expression level of a polypeptide of the present invention in an individual can be treated by administering the agonist or antagonist of the present invention. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a Therapeutic comprising an amount of the agonist or antagonist to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the agonist or antagonist for six consecutive days. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 13.

30

Example 15: Method of Treating Increased Levels of the Polypeptide

The present invention also relates to a method of treating an individual in need of a decreased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an antagonist of the invention (including polypeptides and antibodies of the invention).

In one example, antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 13.

Example 16: Method of Treatment Using Gene Therapy-Ex Vivo

15

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37 degree C for approximately one week.

25 At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

30

The cDNA encoding a polypeptide of the present invention can be amplified using

PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1 using primers and having appropriate restriction sites and initiation/stop codons, if necessary. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the
5 amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

10 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as
15 producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-
20 confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine
25 whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

Example 17: Gene Therapy Using Endogenous Genes Corresponding To Polynucleotides of
30 *the Invention*

Another method of gene therapy according to the present invention involves operably

associating the endogenous polynucleotide sequence of the invention with a promoter via homologous recombination as described, for example, in U.S. Patent NO: 5,641,670, issued June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA*, 86:8932-8935 (1989); and Zijlstra et al., *Nature*, 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made which contain a promoter and targeting sequences, which are homologous to the 5' non-coding sequence of endogenous polynucleotide sequence, flanking the promoter. The targeting sequence will be sufficiently near the 5' end of the polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol precipitation.

In this Example, the polynucleotide constructs are administered as naked polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, precipitating agents, etc. Such methods of delivery are known in the art.

Once the cells are transfected, homologous recombination will take place which results in the promoter being operably linked to the endogenous polynucleotide sequence. This results in the expression of polynucleotide corresponding to the polynucleotide in the cell. Expression may be detected by immunological staining, or any other method known in the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in DMEM + 10% fetal calf serum. Exponentially growing or early stationary phase fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining cells are subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 5 mM KCl, 0.7 mM Na₂HPO₄, 6 mM dextrose). The cells are recentrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1 mg/ml acetylated bovine serum albumin. The final cell suspension contains approximately 3X10⁶ cells/ml. Electroporation should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the locus corresponding to the polynucleotide of the invention, plasmid pUC18 (MBI Fermentas, Amherst, NY) is digested with HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on the 3' end. Two non-coding sequences are amplified via PCR: one non-coding sequence (fragment 1) is amplified with a HindIII site at the 5' end and an Xba site at the 3' end; the other non-coding sequence (fragment 2) is amplified with a BamHI site at the 5' end and a HindIII site at the 3' end. The CMV promoter and the fragments (1 and 2) are digested with the appropriate enzymes (CMV promoter - XbaI and BamHI; fragment 1 - XbaI; fragment 2 - BamHI) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap (Bio-Rad). The final DNA concentration is generally at least 120 µg/ml. 0.5 ml of the cell suspension (containing approximately 1.5X10⁶ cells) is then added to the cuvette, and the cell suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 960 µF and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a

10 cm dish and incubated at 37 degree C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.

The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce the protein product. The fibroblasts can then be introduced into a patient as described above.

Example 18: Method of Treatment Using Gene Therapy - In Vivo

Another aspect of the present invention is using *in vivo* gene therapy methods to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to increase or decrease the expression of the polypeptide. The polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata et al., Cardiovasc. Res. 35(3):470-479 (1997); Chao et al., Pharmacol. Res. 35(6):517-522 (1997); Wolff, Neuromuscul. Disord. 7(5):314-318 (1997); Schwartz et al., Gene Ther. 3(5):405-411 (1996); Tsurumi et al., Circulation 94(12):3281-3290 (1996) (incorporated herein by reference).

The polynucleotide constructs may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). The polynucleotide constructs can be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the present invention may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) Ann. NY Acad. Sci. 772:126-139 and Abdallah B. et al. (1995) Biol. Cell 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that

allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA
5 sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis,
10 ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and
15 the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such
20 as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably
25 from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial
30 space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to

arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle *in vivo* is determined as follows. Suitable template DNA for production of mRNA coding for polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology.

- 5 The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

- 10 Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

- 15 After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15 um cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be
20 determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be use to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA.

25 *Example 19: Transgenic Animals*

- The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, e.g., baboons, monkeys,
30 and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are used to express polypeptides of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (i.e., polynucleotides of the invention) into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to, pronuclear microinjection (Paterson et al., Appl. Microbiol. Biotechnol. 40:691-698 (1994); Carver et al., Biotechnology (NY) 11:1263-1270 (1993); Wright et al., Biotechnology (NY) 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., Proc. Natl. Acad. Sci., USA 82:6148-6152 (1985)), blastocysts or embryos; gene targeting in embryonic stem cells (Thompson et al., Cell 56:313-321 (1989)); electroporation of cells or embryos (Lo, 1983, Mol Cell. Biol. 3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, e.g., Ulmer et al., Science 259:1745 (1993); introducing nucleic acid constructs into embryonic pluripotent stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Lavitrano et al., Cell 57:717-723 (1989); etc. For a review of such techniques, see Gordon, "Transgenic Animals," Intl. Rev. Cytol. 115:171-229 (1989), which is incorporated by reference herein in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence (Campell et al., Nature 380:64-66 (1996); Wilmut et al., Nature 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, i.e., mosaic animals or chimeric. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., Proc. Natl. Acad. Sci. USA 89:6232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the polynucleotide transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of

the endogenous gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example, the teaching of Gu et al. (Gu et al., Science 265:103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of
5 interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA expression of the transgene in the
10 tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, *in situ* hybridization analysis, and reverse transcriptase-PCR (rt-PCR). Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies specific for the transgene product.

15 Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound transgenics that express the transgene at higher levels because of the
20 effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment expression and eliminate the need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; and breeding to place the transgene on a distinct background that is appropriate for an
25 experimental model of interest.

Transgenic animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

30

Example 20: Knock-Out Animals

Endogenous gene expression can also be reduced by inactivating or "knocking out" the gene and/or its promoter using targeted homologous recombination. (*E.g.*, see Smithies et al., *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson et al., *Cell* 5:313-321 (1989); each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional polynucleotide of the invention (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous polynucleotide sequence (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express polypeptides of the invention *in vivo*. In another embodiment, techniques known in the art are used to generate knockouts in cells that contain, but do not express the gene of interest. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the targeted gene. Such approaches are particularly suited in research and agricultural fields where modifications to embryonic stem cells can be used to generate animal offspring with an inactive targeted gene (*e.g.*, see Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be routinely adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors that will be apparent to those of skill in the art.

In further embodiments of the invention, cells that are genetically engineered to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (*e.g.*, knockouts) are administered to a patient *in vivo*. Such cells may be obtained from the patient (*i.e.*, animal, including human) or an MHC compatible donor and can include, but are not limited to fibroblasts, bone marrow cells, blood cells (*e.g.*, lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered *in vitro* using recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, *e.g.*, by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YACs, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve expression, and

preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the patient systemically, e.g., in the circulation, or intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, 5 e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, for example, Anderson et al. U.S. Patent No. 5,399,349; and Mulligan & Wilson, U.S. Patent No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, 10 they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

15 Transgenic and "knock-out" animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

20

Example 22: Assays Detecting Stimulation or Inhibition of B cell Proliferation and Differentiation

Generation of functional humoral immune responses requires both soluble and 25 cognate signaling between B-lineage cells and their microenvironment. Signals may impart a positive stimulus that allows a B-lineage cell to continue its programmed development, or a negative stimulus that instructs the cell to arrest its current developmental pathway. To date, numerous stimulatory and inhibitory signals have been found to influence B cell responsiveness including IL-2, IL-4, IL-5, IL-6, IL-7, IL10, IL-13, IL-14 and IL-15. 30 Interestingly, these signals are by themselves weak effectors but can, in combination with various co-stimulatory proteins, induce activation, proliferation, differentiation, homing, tolerance and death among B cell populations.

One of the best studied classes of B-cell co-stimulatory proteins is the TNF-superfamily. Within this family CD40, CD27, and CD30 along with their respective ligands CD154, CD70, and CD153 have been found to regulate a variety of immune responses. Assays which allow for the detection and/or observation of the proliferation and differentiation of these B-cell populations and their precursors are valuable tools in determining the effects various proteins may have on these B-cell populations in terms of proliferation and differentiation. Listed below are two assays designed to allow for the detection of the differentiation, proliferation, or inhibition of B-cell populations and their precursors.

10 **In Vitro Assay-** Agonists or antagonists of the invention can be assessed for its ability to induce activation, proliferation, differentiation or inhibition and/or death in B-cell populations and their precursors. The activity of the agonists or antagonists of the invention on purified human tonsillar B cells, measured qualitatively over the dose range from 0.1 to 10,000 ng/mL, is assessed in a standard B-lymphocyte co-stimulation assay in which purified
15 tonsillar B cells are cultured in the presence of either formalin-fixed *Staphylococcus aureus* Cowan I (SAC) or immobilized anti-human IgM antibody as the priming agent. Second signals such as IL-2 and IL-15 synergize with SAC and IgM crosslinking to elicit B cell proliferation as measured by tritiated-thymidine incorporation. Novel synergizing agents can be readily identified using this assay. The assay involves isolating human tonsillar B cells by
20 magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population is greater than 95% B cells as assessed by expression of CD45R(B220).

Various dilutions of each sample are placed into individual wells of a 96-well plate to which are added 10^5 B-cells suspended in culture medium (RPMI 1640 containing 10% FBS, 5×10^{-5} M 2ME, 100U/ml penicillin, 10ug/ml streptomycin, and 10^{-5} dilution of SAC) in a
25 total volume of 150ul. Proliferation or inhibition is quantitated by a 20h pulse (1uCi/well) with 3 H-thymidine (6.7 Ci/mM) beginning 72h post factor addition. The positive and negative controls are IL2 and medium respectively.

30 **In Vivo Assay-** BALB/c mice are injected (i.p.) twice per day with buffer only, or 2 mg/Kg of agonists or antagonists of the invention, or truncated forms thereof. Mice receive this treatment for 4 consecutive days, at which time they are sacrificed and various tissues and serum collected for analyses. Comparison of H&E sections from normal spleens and spleens treated with agonists or antagonists of the invention identify the results of the activity

of the agonists or antagonists on spleen cells, such as the diffusion of peri-arterial lymphatic sheaths, and/or significant increases in the nucleated cellularity of the red pulp regions, which may indicate the activation of the differentiation and proliferation of B-cell populations. Immunohistochemical studies using a B cell marker, anti-CD45R(B220), are used to
5 determine whether any physiological changes to splenic cells, such as splenic disorganization, are due to increased B-cell representation within loosely defined B-cell zones that infiltrate established T-cell regions.

Flow cytometric analyses of the spleens from mice treated with agonist or antagonist is used to indicate whether the agonists or antagonists specifically increases the proportion of
10 ThB+, CD45R(B220)dull B cells over that which is observed in control mice. Likewise, a predicted consequence of increased mature B-cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgM and IgA levels are compared between buffer and agonists or antagonists-treated mice.

The studies described in this example tested activity of agonists or antagonists of the
15 invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 23: T Cell Proliferation Assay

20 A CD3-induced proliferation assay is performed on PBMCs and is measured by the uptake of ³H-thymidine. The assay is performed as follows. Ninety-six well plates are coated with 100 µl/well of mAb to CD3 (HIT3a, Pharmingen) or isotype-matched control mAb (B33.1) overnight at 4 degrees C (1 µg/ml in .05M bicarbonate buffer, pH 9.5), then washed three times with PBS. PBMC are isolated by F/H gradient centrifugation from
25 human peripheral blood and added to quadruplicate wells (5 x 10⁴/well) of mAb coated plates in RPMI containing 10% FCS and P/S in the presence of varying concentrations of agonists or antagonists of the invention (total volume 200 µl). Relevant protein buffer and medium alone are controls. After 48 hr. culture at 37 degrees C, plates are spun for 2 min. at 1000 rpm and 100 µl of supernatant is removed and stored -20 degrees C for measurement of IL-2
30 (or other cytokines) if effect on proliferation is observed. Wells are supplemented with 100 µl of medium containing 0.5 uCi of ³H-thymidine and cultured at 37 degrees C for 18-24 hr. Wells are harvested and incorporation of ³H-thymidine used as a measure of proliferation.

Anti-CD3 alone is the positive control for proliferation. IL-2 (100 U/ml) is also used as a control which enhances proliferation. Control antibody which does not induce proliferation of T cells is used as the negative controls for the effects of agonists or antagonists of the invention.

- 5 The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

10 *Example 24: Effect of Agonists or Antagonists of the Invention on the Expression of MHC Class II, Costimulatory and Adhesion Molecules and Cell Differentiation of Monocytes and Monocyte-Derived Human Dendritic Cells*

- Dendritic cells are generated by the expansion of proliferating precursors found in the peripheral blood: adherent PBMC or elutriated monocytic fractions are cultured for 7-10 days with GM-CSF (50 ng/ml) and IL-4 (20 ng/ml). These dendritic cells have the characteristic phenotype of immature cells (expression of CD1, CD80, CD86, CD40 and MHC class II antigens). Treatment with activating factors, such as TNF- α , causes a rapid change in surface phenotype (increased expression of MHC class I and II, costimulatory and adhesion molecules, downregulation of FC γ RII, upregulation of CD83). These changes correlate with increased antigen-presenting capacity and with functional maturation of the dendritic cells.

- 20 FACS analysis of surface antigens is performed as follows. Cells are treated 1-3 days with increasing concentrations of agonist or antagonist of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degrees C. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

- Effect on the production of cytokines. Cytokines generated by dendritic cells, in particular IL-12, are important in the initiation of T-cell dependent immune responses. IL-12 strongly influences the development of Th1 helper T-cell immune response, and induces cytotoxic T and NK cell function. An ELISA is used to measure the IL-12 release as follows. Dendritic cells (10^6 /ml) are treated with increasing concentrations of agonists or antagonists of the

invention for 24 hours. LPS (100 ng/ml) is added to the cell culture as positive control. Supernatants from the cell cultures are then collected and analyzed for IL-12 content using commercial ELISA kit (e.g., R & D Systems (Minneapolis, MN)). The standard protocols provided with the kits are used.

5

Effect on the expression of MHC Class II, costimulatory and adhesion molecules. Three major families of cell surface antigens can be identified on monocytes: adhesion molecules, molecules involved in antigen presentation, and Fc receptor. Modulation of the expression of MHC class II antigens and other costimulatory molecules, such as B7 and ICAM-1, may result in changes in the antigen presenting capacity of monocytes and ability to induce T cell activation. Increase expression of Fc receptors may correlate with improved monocyte cytotoxic activity, cytokine release and phagocytosis.

FACS analysis is used to examine the surface antigens as follows. Monocytes are treated 1-5 days with increasing concentrations of agonists or antagonists of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degreesC. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Monocyte activation and/or increased survival. Assays for molecules that activate (or alternatively, inactivate) monocytes and/or increase monocyte survival (or alternatively, decrease monocyte survival) are known in the art and may routinely be applied to determine whether a molecule of the invention functions as an inhibitor or activator of monocytes. Agonists or antagonists of the invention can be screened using the three assays described below. For each of these assays, Peripheral blood mononuclear cells (PBMC) are purified from single donor leukopacks (American Red Cross, Baltimore, MD) by centrifugation through a Histopaque gradient (Sigma). Monocytes are isolated from PBMC by counterflow centrifugal elutriation.

Monocyte Survival Assay. Human peripheral blood monocytes progressively lose viability when cultured in absence of serum or other stimuli. Their death results from internally regulated process (apoptosis). Addition to the culture of activating factors, such as TNF-alpha

dramatically improves cell survival and prevents DNA fragmentation. Propidium iodide (PI) staining is used to measure apoptosis as follows. Monocytes are cultured for 48 hours in polypropylene tubes in serum-free medium (positive control), in the presence of 100 ng/ml TNF-alpha (negative control), and in the presence of varying concentrations of the compound to be tested. Cells are suspended at a concentration of 2×10^6 /ml in PBS containing PI at a final concentration of 5 µg/ml, and then incubated at room temperature for 5 minutes before FACScan analysis. PI uptake has been demonstrated to correlate with DNA fragmentation in this experimental paradigm.

- 10 Effect on cytokine release. An important function of monocytes/macrophages is their regulatory activity on other cellular populations of the immune system through the release of cytokines after stimulation. An ELISA to measure cytokine release is performed as follows. Human monocytes are incubated at a density of 5×10^5 cells/ml with increasing concentrations of agonists or antagonists of the invention and under the same conditions, but in the absence of agonists or antagonists. For IL-12 production, the cells are primed overnight with IFN (100 U/ml) in presence of agonist or antagonist of the invention. LPS (10 ng/ml) is then added. Conditioned media are collected after 24h and kept frozen until use. Measurement of TNF-alpha, IL-10, MCP-1 and IL-8 is then performed using a commercially available ELISA kit (e. g, R & D Systems (Minneapolis, MN)) and applying the standard protocols provided with the kit.

- Oxidative burst. Purified monocytes are plated in 96-w plate at 2×10^5 cell/well. Increasing concentrations of agonists or antagonists of the invention are added to the wells in a total volume of 0.2 ml culture medium (RPMI 1640 + 10% FCS, glutamine and antibiotics). After 3 days incubation, the plates are centrifuged and the medium is removed from the wells. To the macrophage monolayers, 0.2 ml per well of phenol red solution (140 mM NaCl, 10 mM potassium phosphate buffer pH 7.0, 5.5 mM dextrose, 0.56 mM phenol red and 19 U/ml of HRPO) is added, together with the stimulant (200 nM PMA). The plates are incubated at 37°C for 2 hours and the reaction is stopped by adding 20 µl 1N NaOH per well. The absorbance is read at 610 nm. To calculate the amount of H_2O_2 produced by the macrophages, a standard curve of a H_2O_2 solution of known molarity is performed for each experiment.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

5

Example 25: Biological Effects of Agonists or Antagonists of the Invention

Astrocyte and Neuronal Assays.

Agonists or antagonists of the invention, expressed in *Escherichia coli* and purified
10 as described above, can be tested for activity in promoting the survival, neurite outgrowth, or phenotypic differentiation of cortical neuronal cells and for inducing the proliferation of glial fibrillary acidic protein immunopositive cells, astrocytes. The selection of cortical cells for the bioassay is based on the prevalent expression of FGF-1 and FGF-2 in cortical structures and on the previously reported enhancement of cortical neuronal survival resulting from
15 FGF-2 treatment. A thymidine incorporation assay, for example, can be used to elucidate an agonist or antagonist of the invention's activity on these cells.

Moreover, previous reports describing the biological effects of FGF-2 (basic FGF) on cortical or hippocampal neurons *in vitro* have demonstrated increases in both neuron survival and neurite outgrowth (Walicke et al., "Fibroblast growth factor promotes survival of
20 dissociated hippocampal neurons and enhances neurite extension." *Proc. Natl. Acad. Sci. USA* 83:3012-3016. (1986), assay herein incorporated by reference in its entirety). However, reports from experiments done on PC-12 cells suggest that these two responses are not necessarily synonymous and may depend on not only which FGF is being tested but also on which receptor(s) are expressed on the target cells. Using the primary cortical neuronal
25 culture paradigm, the ability of an agonist or antagonist of the invention to induce neurite outgrowth can be compared to the response achieved with FGF-2 using, for example, a thymidine incorporation assay.

Fibroblast and endothelial cell assays.

30 Human lung fibroblasts are obtained from Clonetics (San Diego, CA) and maintained in growth media from Clonetics. Dermal microvascular endothelial cells are obtained from

Cell Applications (San Diego, CA). For proliferation assays, the human lung fibroblasts and dermal microvascular endothelial cells can be cultured at 5,000 cells/well in a 96-well plate for one day in growth medium. The cells are then incubated for one day in 0.1% BSA basal medium. After replacing the medium with fresh 0.1% BSA medium, the cells are incubated with the test proteins for 3 days. Alamar Blue (Alamar Biosciences, Sacramento, CA) is added to each well to a final concentration of 10%. The cells are incubated for 4 hr. Cell viability is measured by reading in a CytoFluor fluorescence reader. For the PGE₂ assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or agonists or antagonists of the invention with or without IL-1 α for 24 hours. The supernatants are collected and assayed for PGE₂ by EIA kit (Cayman, Ann Arbor, MI). For the IL-6 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or with or without agonists or antagonists of the invention IL-1 α for 24 hours. The supernatants are collected and assayed for IL-6 by ELISA kit (Endogen, Cambridge, MA).

Human lung fibroblasts are cultured with FGF-2 or agonists or antagonists of the invention for 3 days in basal medium before the addition of Alamar Blue to assess effects on growth of the fibroblasts. FGF-2 should show a stimulation at 10 - 2500 ng/ml which can be used to compare stimulation with agonists or antagonists of the invention.

Parkinson Models.

The loss of motor function in Parkinson's disease is attributed to a deficiency of striatal dopamine resulting from the degeneration of the nigrostriatal dopaminergic projection neurons. An animal model for Parkinson's that has been extensively characterized involves the systemic administration of 1-methyl-4 phenyl 1,2,3,6-tetrahydropyridine (MPTP). In the CNS, MPTP is taken-up by astrocytes and catabolized by monoamine oxidase B to 1-methyl-4-phenyl pyridine (MPP⁺) and released. Subsequently, MPP⁺ is actively accumulated in dopaminergic neurons by the high-affinity reuptake transporter for dopamine. MPP⁺ is then concentrated in mitochondria by the electrochemical gradient and selectively inhibits nicotinamide adenine disphosphate: ubiquinone oxidoreductionase (complex I), thereby interfering with electron transport and eventually generating oxygen radicals.

It has been demonstrated in tissue culture paradigms that FGF-2 (basic FGF) has trophic activity towards nigral dopaminergic neurons (Ferrari et al., Dev. Biol. 1989). Recently, Dr. Unsicker's group has demonstrated that administering FGF-2 in gel foam implants in the striatum results in the near complete protection of nigral dopaminergic
5 neurons from the toxicity associated with MPTP exposure (Otto and Unsicker, J. Neuroscience, 1990).

Based on the data with FGF-2, agonists or antagonists of the invention can be evaluated to determine whether it has an action similar to that of FGF-2 in enhancing dopaminergic neuronal survival *in vitro* and it can also be tested *in vivo* for protection of
10 dopaminergic neurons in the striatum from the damage associated with MPTP treatment. The potential effect of an agonist or antagonist of the invention is first examined *in vitro* in a dopaminergic neuronal cell culture paradigm. The cultures are prepared by dissecting the midbrain floor plate from gestation day 14 Wistar rat embryos. The tissue is dissociated with trypsin and seeded at a density of 200,000 cells/cm² on polyorthinine-laminin coated glass
15 coverslips. The cells are maintained in Dulbecco's Modified Eagle's medium and F12 medium containing hormonal supplements (N1). The cultures are fixed with paraformaldehyde after 8 days *in vitro* and are processed for tyrosine hydroxylase, a specific marker for dopaminergic neurons, immunohistochemical staining. Dissociated cell cultures are prepared from embryonic rats. The culture medium is changed every third day and the
20 factors are also added at that time.

Since the dopaminergic neurons are isolated from animals at gestation day 14, a developmental time which is past the stage when the dopaminergic precursor cells are proliferating, an increase in the number of tyrosine hydroxylase immunopositive neurons would represent an increase in the number of dopaminergic neurons surviving *in vitro*.
25 Therefore, if an agonist or antagonist of the invention acts to prolong the survival of dopaminergic neurons, it would suggest that the agonist or antagonist may be involved in Parkinson's Disease.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test
30 the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 26: The Effect of Agonists or Antagonists of the Invention on the Growth of Vascular Endothelial Cells

On day 1, human umbilical vein endothelial cells (HUVEC) are seeded at $2-5 \times 10^4$ cells/35 mm dish density in M199 medium containing 4% fetal bovine serum (FBS), 16 units/ml heparin, and 50 units/ml endothelial cell growth supplements (ECGS, Biotechnology, Inc.). On day 2, the medium is replaced with M199 containing 10% FBS, 8 units/ml heparin. An agonist or antagonist of the invention, and positive controls, such as VEGF and basic FGF (bFGF) are added, at varying concentrations. On days 4 and 6, the medium is replaced.

On day 8, cell number is determined with a Coulter Counter.

An increase in the number of HUVEC cells indicates that the compound of the invention may proliferate vascular endothelial cells, while a decrease in the number of HUVEC cell indicates that the compound of the invention inhibits vascular endothelial cells.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 27: Rat Corneal Wound Healing Model

This animal model shows the effect of an agonist or antagonist of the invention on neovascularization. The experimental protocol includes:

- a) Making a 1-1.5 mm long incision from the center of cornea into the stromal layer.
- b) Inserting a spatula below the lip of the incision facing the outer corner of the eye.
- c) Making a pocket (its base is 1-1.5 mm from the edge of the eye).
- d) Positioning a pellet, containing 50ng- 5ug of an agonist or antagonist of the invention, within the pocket.
- e) Treatment with an agonist or antagonist of the invention can also be applied topically to the corneal wounds in a dosage range of 20mg - 500mg (daily treatment for five days).

The studies described in this example tested activity of agonists or antagonists of the

invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 28: Diabetic Mouse and Glucocorticoid-Impaired Wound Healing Models

5

A. Diabetic db+/db+ Mouse Model.

To demonstrate that an agonist or antagonist of the invention accelerates the healing process, the genetically diabetic mouse model of wound healing is used. The full thickness wound healing model in the db+/db+ mouse is a well characterized, clinically relevant and
10 reproducible model of impaired wound healing. Healing of the diabetic wound is dependent on formation of granulation tissue and re-epithelialization rather than contraction (Gartner, M.H. *et al.*, *J. Surg. Res.* 52:389 (1992); Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)).

The diabetic animals have many of the characteristic features observed in Type II
15 diabetes mellitus. Homozygous (db+/db+) mice are obese in comparison to their normal heterozygous (db+/+m) littermates. Mutant diabetic (db+/db+) mice have a single autosomal recessive mutation on chromosome 4 (db+) (Coleman *et al.* *Proc. Natl. Acad. Sci. USA* 77:283-293 (1982)). Animals show polyphagia, polydipsia and polyuria. Mutant diabetic mice (db+/db+) have elevated blood glucose, increased or normal insulin levels, and
20 suppressed cell-mediated immunity (Mandel *et al.*, *J. Immunol.* 120:1375 (1978); Debray-Sachs, M. *et al.*, *Clin. Exp. Immunol.* 51(1):1-7 (1983); Leiter *et al.*, *Am. J. of Pathol.* 114:46-55 (1985)). Peripheral neuropathy, myocardial complications, and microvascular lesions, basement membrane thickening and glomerular filtration abnormalities have been described in these animals (Norido, F. *et al.*, *Exp. Neurol.* 83(2):221-232 (1984); Robertson *et al.*,
25 *Diabetes* 29(1):60-67 (1980); Giacomelli *et al.*, *Lab Invest.* 40(4):460-473 (1979); Coleman, D.L., *Diabetes* 31 (Suppl):1-6 (1982)). These homozygous diabetic mice develop hyperglycemia that is resistant to insulin analogous to human type II diabetes (Mandel *et al.*, *J. Immunol.* 120:1375-1377 (1978)).

The characteristics observed in these animals suggests that healing in this model may
30 be similar to the healing observed in human diabetes (Greenhalgh, *et al.*, *Am. J. of Pathol.* 136:1235-1246 (1990)).

Genetically diabetic female C57BL/KsJ (db+/db+) mice and their non-diabetic

(db+/+m) heterozygous littermates are used in this study (Jackson Laboratories). The animals are purchased at 6 weeks of age and are 8 weeks old at the beginning of the study. Animals are individually housed and received food and water ad libitum. All manipulations are performed using aseptic techniques. The experiments are conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

Wounding protocol is performed according to previously reported methods (Tsuboi, R. and Rifkin, D.B., *J. Exp. Med.* 172:245-251 (1990)). Briefly, on the day of wounding, animals are anesthetized with an intraperitoneal injection of Avertin (0.01 mg/mL), 2,2,2-tribromoethanol and 2-methyl-2-butanol dissolved in deionized water. The dorsal region of the animal is shaved and the skin washed with 70% ethanol solution and iodine. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is then created using a Keyes tissue punch. Immediately following wounding, the surrounding skin is gently stretched to eliminate wound expansion. The wounds are left open for the duration of the experiment. Application of the treatment is given topically for 5 consecutive days commencing on the day of wounding. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of surgery and at two day intervals thereafter. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

An agonist or antagonist of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology and immunohistochemistry. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Three groups of 10 animals each (5 diabetic and 5 non-diabetic controls) are evaluated: 1) Vehicle placebo control, 2) untreated group, and 3) treated group.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and

obtaining the total square area of the wound. Contraction is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm², the corresponding size of the dermal punch. Calculations are made using the following formula:

5

$$[\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using a Reichert-Jung microtome.

- 10 Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds are used to assess whether the healing process and the morphologic appearance of the repaired skin is altered by treatment with an agonist or antagonist of the invention. This assessment included verification of the presence of cell accumulation, inflammatory cells, capillaries, fibroblasts, re-epithelialization and
- 15 epidermal maturity (Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)). A calibrated lens micrometer is used by a blinded observer.

- Tissue sections are also stained immunohistochemically with a polyclonal rabbit anti-human keratin antibody using ABC Elite detection system. Human skin is used as a positive tissue control while non-immune IgG is used as a negative control. Keratinocyte growth is
- 20 determined by evaluating the extent of reepithelialization of the wound using a calibrated lens micrometer.

- Proliferating cell nuclear antigen/cyclin (PCNA) in skin specimens is demonstrated by using anti-PCNA antibody (1:50) with an ABC Elite detection system. Human colon cancer served as a positive tissue control and human brain tissue is used as a negative tissue
- 25 control. Each specimen included a section with omission of the primary antibody and substitution with non-immune mouse IgG. Ranking of these sections is based on the extent of proliferation on a scale of 0-8, the lower side of the scale reflecting slight proliferation to the higher side reflecting intense proliferation.

- Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is
- 30 considered significant.

B. Steroid Impaired Rat Model

The inhibition of wound healing by steroids has been well documented in various *in vitro* and *in vivo* systems (Wahl, Glucocorticoids and Wound healing. In: Anti-Inflammatory Steroid Action: Basic and Clinical Aspects. 280-302 (1989); Wahlet *et al.*, *J. Immunol.* 115: 476-481 (1975); Werb *et al.*, *J. Exp. Med.* 147:1684-1694 (1978)). Glucocorticoids retard wound healing by inhibiting angiogenesis, decreasing vascular permeability (Ebert *et al.*, *An. Intern. Med.* 37:701-705 (1952)), fibroblast proliferation, and collagen synthesis (Beck *et al.*, *Growth Factors.* 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978)) and producing a transient reduction of circulating monocytes (Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", In: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989)). The systemic administration of steroids to impaired wound healing is a well establish phenomenon in rats (Beck *et al.*, *Growth Factors.* 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", In: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989); Pierce *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 2229-2233 (1989)).

To demonstrate that an agonist or antagonist of the invention can accelerate the healing process, the effects of multiple topical applications of the agonist or antagonist on full thickness excisional skin wounds in rats in which healing has been impaired by the systemic administration of methylprednisolone is assessed.

Young adult male Sprague Dawley rats weighing 250-300 g (Charles River Laboratories) are used in this example. The animals are purchased at 8 weeks of age and are 9 weeks old at the beginning of the study. The healing response of rats is impaired by the systemic administration of methylprednisolone (17mg/kg/rat intramuscularly) at the time of wounding. Animals are individually housed and received food and water *ad libitum*. All manipulations are performed using aseptic techniques. This study is conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

The wounding protocol is followed according to section A, above. On the day of wounding, animals are anesthetized with an intramuscular injection of ketamine (50 mg/kg) and xylazine (5 mg/kg). The dorsal region of the animal is shaved and the skin washed with 70% ethanol and iodine solutions. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is created using a Keyes tissue punch. The

wounds are left open for the duration of the experiment. Applications of the testing materials are given topically once a day for 7 consecutive days commencing on the day of wounding and subsequent to methylprednisolone administration. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

5 Wounds are visually examined and photographed at a fixed distance at the day of wounding and at the end of treatment. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

10 The agonist or antagonist of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

 Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for
15 histology. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

 Four groups of 10 animals each (5 with methylprednisolone and 5 without glucocorticoid) are evaluated: 1) Untreated group 2) Vehicle placebo control 3) treated groups.

20 Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total area of the wound. Closure is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm², the corresponding size of the dermal punch. Calculations are made using the following formula:

25

$$[\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using an Olympus microtome. Routine
30 hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds allows assessment of whether the healing process and the morphologic appearance of the repaired skin is improved by treatment with an agonist or

antagonist of the invention. A calibrated lens micrometer is used by a blinded observer to determine the distance of the wound gap.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

- 5 The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 29: Lymphadema Animal Model

10

- The purpose of this experimental approach is to create an appropriate and consistent lymphedema model for testing the therapeutic effects of an agonist or antagonist of the invention in lymphangiogenesis and re-establishment of the lymphatic circulatory system in the rat hind limb. Effectiveness is measured by swelling volume of the affected limb, quantification of the amount of lymphatic vasculature, total blood plasma protein, and histopathology. Acute lymphedema is observed for 7-10 days. Perhaps more importantly, the chronic progress of the edema is followed for up to 3-4 weeks.

- Prior to beginning surgery, blood sample is drawn for protein concentration analysis. Male rats weighing approximately ~350g are dosed with Pentobarbital. Subsequently, the right legs are shaved from knee to hip. The shaved area is swabbed with gauze soaked in 70% EtOH. Blood is drawn for serum total protein testing. Circumference and volumetric measurements are made prior to injecting dye into paws after marking 2 measurement levels (0.5 cm above heel, at mid-pt of dorsal paw). The intradermal dorsum of both right and left paws are injected with 0.05 ml of 1% Evan's Blue. Circumference and volumetric measurements are then made following injection of dye into paws.

- Using the knee joint as a landmark, a mid-leg inguinal incision is made circumferentially allowing the femoral vessels to be located. Forceps and hemostats are used to dissect and separate the skin flaps. After locating the femoral vessels, the lymphatic vessel that runs along side and underneath the vessel(s) is located. The main lymphatic vessels in this area are then electrically coagulated or suture ligated.

 Using a microscope, muscles in back of the leg (near the semitendinosus and adductors) are bluntly dissected. The popliteal lymph node is then located. The 2 proximal

and 2 distal lymphatic vessels and distal blood supply of the popliteal node are then and ligated by suturing. The popliteal lymph node, and any accompanying adipose tissue, is then removed by cutting connective tissues.

Care is taken to control any mild bleeding resulting from this procedure. After
5 lymphatics are occluded, the skin flaps are sealed by using liquid skin (Vetbond) (AJ Buck). The separated skin edges are sealed to the underlying muscle tissue while leaving a gap of ~0.5 cm around the leg. Skin also may be anchored by suturing to underlying muscle when necessary.

To avoid infection, animals are housed individually with mesh (no bedding).
10 Recovering animals are checked daily through the optimal edematous peak, which typically occurred by day 5-7. The plateau edematous peak are then observed. To evaluate the intensity of the lymphedema, the circumference and volumes of 2 designated places on each paw before operation and daily for 7 days are measured. The effect plasma proteins on lymphedema is determined and whether protein analysis is a useful testing perimeter is also
15 investigated. The weights of both control and edematous limbs are evaluated at 2 places. Analysis is performed in a blind manner.

Circumference Measurements: Under brief gas anesthetic to prevent limb movement, a cloth tape is used to measure limb circumference. Measurements are done at the ankle bone and dorsal paw by 2 different people then those 2 readings are averaged. Readings are
20 taken from both control and edematous limbs.

Volumetric Measurements: On the day of surgery, animals are anesthetized with Pentobarbital and are tested prior to surgery. For daily volumetrics animals are under brief halothane anesthetic (rapid immobilization and quick recovery), both legs are shaved and equally marked using waterproof marker on legs. Legs are first dipped in water, then dipped
25 into instrument to each marked level then measured by Buxco edema software(Chen/Victor). Data is recorded by one person, while the other is dipping the limb to marked area.

Blood-plasma protein measurements: Blood is drawn, spun, and serum separated prior to surgery and then at conclusion for total protein and Ca²⁺ comparison.

Limb Weight Comparison: After drawing blood, the animal is prepared for tissue
30 collection. The limbs are amputated using a quillitine, then both experimental and control legs are cut at the ligature and weighed. A second weighing is done as the tibio-cacaneal joint is disarticulated and the foot is weighed.

Histological Preparations: The transverse muscle located behind the knee (popliteal) area is dissected and arranged in a metal mold, filled with freezeGel, dipped into cold methylbutane, placed into labeled sample bags at - 80EC until sectioning. Upon sectioning, the muscle is observed under fluorescent microscopy for lymphatics..

- 5 The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

10 *Example 30: Suppression of TNF alpha-induced adhesion molecule expression by a Agonist or Antagonist of the Invention*

- 15 The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules (CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

Tumor necrosis factor alpha (TNF-a), a potent proinflammatory cytokine, is a stimulator of all three CAMs on endothelial cells and may be involved in a wide variety of inflammatory responses, often resulting in a pathological outcome.

- 25 The potential of an agonist or antagonist of the invention to mediate a suppression of TNF-a induced CAM expression can be examined. A modified ELISA assay which uses ECs as a solid phase absorbent is employed to measure the amount of CAM expression on TNF-a treated ECs when co-stimulated with a member of the FGF family of proteins.

- 30 To perform the experiment, human umbilical vein endothelial cell (HUVEC) cultures are obtained from pooled cord harvests and maintained in growth medium (EGM-2; Clonetics, San Diego, CA) supplemented with 10% FCS and 1% penicillin/streptomycin in a 37 degree C humidified incubator containing 5% CO₂. HUVECs are seeded in 96-well

plates at concentrations of 1×10^4 cells/well in EGM medium at 37 degree C for 18-24 hrs or until confluent. The monolayers are subsequently washed 3 times with a serum-free solution of RPMI-1640 supplemented with 100 U/ml penicillin and 100 mg/ml streptomycin, and treated with a given cytokine and/or growth factor(s) for 24 h at 37 degree C. Following incubation, the cells are then evaluated for CAM expression.

Human Umbilical Vein Endothelial cells (HUVECs) are grown in a standard 96 well plate to confluence. Growth medium is removed from the cells and replaced with 90 ul of 199 Medium (10% FBS). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 ul volumes). Plates are incubated at 37 degree C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to remove medium and 100 μ l of 0.1% paraformaldehyde-PBS(with Ca^{++} and Mg^{++}) is added to each well. Plates are held at 4°C for 30 min.

Fixative is then removed from the wells and wells are washed 1X with PBS(+Ca,Mg)+0.5% BSA and drained. Do not allow the wells to dry. Add 10 μ l of diluted primary antibody to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10 μ g/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA.

Then add 20 μ l of diluted ExtrAvidin-Alkaline Phosphatase (1:5,000 dilution) to each well and incubated at 37°C for 30 min. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA. 1 tablet of p-Nitrophenol Phosphate pNPP is dissolved in 5 ml of glycine buffer (pH 10.4). 100 μ l of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphatase in glycine buffer: $1:5,000 (10^0) > 10^{-0.5} > 10^{-1} > 10^{-1.5}$. 5 μ l of each dilution is added to triplicate wells and the resulting AP content in each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 μ l of pNPP reagent must then be added to each of the standard wells. The plate must be incubated at 37°C for 4h. A volume of 50 μ l of 3M NaOH is added to all wells. The results are quantified on a plate reader at 405 nm. The background subtraction option is used on blank wells filled with glycine buffer only. The template is set up to indicate the concentration of AP-conjugate in each standard well [5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

The studies described in this example tested activity of agonists or antagonists of the

invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 31: Production Of Polypeptide of the Invention For High-Throughput Screening Assays

The following protocol produces a supernatant containing polypeptide of the present invention to be tested. This supernatant can then be used in the Screening Assays described in Examples 33-42.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in Examples 8-10, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on

PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem 1 complex to the odd wells first, then to the even wells, to
5 each row on the 24-well plates. Incubate at 37 degree C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or HGS CHO-5 media (116.6 mg/L of CaCl₂ (anhyd); 0.00130 mg/L CuSO₄·5H₂O; 0.050 mg/L of Fe(NO₃)₃·9H₂O; 0.417 mg/L of FeSO₄·7H₂O; 311.80 mg/L of KCl; 28.64 mg/L of MgCl₂; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of
10 NaHCO₃; 62.50 mg/L of NaH₂PO₄·H₂O; 71.02 mg/L of Na₂HPO₄; 4320 mg/L of ZnSO₄·7H₂O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of
15 Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L- Arginine-HCL; 7.50 mg/ml of L-Asparagine-H₂O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H₂O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L- Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L- Histidine-HCL-H₂O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75
20 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H₂O; and 99.65 mg/ml of L- Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00
25 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin
30 complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal Acetate. Adjust

osmolarity to 327 mOsm) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

5 The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37 degree C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

10 On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 33-40.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide of the present invention directly (e.g., as a secreted protein) or by polypeptide of the present invention inducing expression of other proteins, which are then secreted into the supernatant.

15 Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 32: Construction of GAS Reporter Construct

20 One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

25 GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class 1, cells after treatment with IL-12. Stat5 was originally called

30 mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon

tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

5 The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN- α , IFN- γ ,
10 and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:1686)).

 Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is
15 encompassed in the Jaks-STATs signal transduction pathway.

 Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter
20 molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>JAKs</u>				<u>STATS GAS(elements) or ISRE</u>	
		<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>		
	<u>IFN family</u>						
5	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS
	(IRF1>Lys6>IFP)						
	IL-10	+	?	?	-	1,3	
10	<u>gp130 family</u>						
	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS
	(IRF1>Lys6>IFP)						
	IL-11(Pleiotrohic)	?	+	?	?	1,3	
	OnM(Pleiotrohic)	?	+	+	?	1,3	
15	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
20	<u>g-C family</u>						
	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP
	>>Ly6)(IgH)						
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
25	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
	<u>gp140 family</u>						
30	IL-3 (myeloid)	-	-	+	-	5	GAS
	(IRF1>IFP>>Ly6)						
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS

510

Growth hormone family

	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
5	EPO	?	-	+	-	5	GAS(B-
	CAS>IRF1=IFP>>Ly6)						

Receptor Tyrosine Kinases

	EGF	?	+	+	-	1,3	GAS (IRF1)
10	PDGF	?	+	+	-	1,3	
	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 33-34, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

10 5':GCGCCTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCGAAATGATTTCCTCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:1687)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:1688)

15 PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

20 5':CTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCGAAATGATTTCCTCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTA
25 GGCTTTTTGCAAAAAGCTT:3' (SEQ ID NO:1689)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter
30 molecules that can be used instead of SEAP include chloramphenicol

acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and
5 XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-
10 SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding
15 as described in Examples 33-34.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 35 and 36. However, many other promoters can be substituted using the protocols described
20 in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

25

Example 33: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, and determining whether supernate containing a polypeptide of the invention
30 proliferates and/or differentiates T-cells. T-cell activity is assessed using the

GAS/SEAP/Neo construct produced in Example 32. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC
5 Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately
10 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells
15 containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

20 During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37 degree C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

25 The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing polypeptide of the present invention or polypeptide of the present invention induced polypeptides as produced by the protocol described in Example 31.

30 On the day of treatment with the supernatant, the cells should be washed and

resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

- 5 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

 After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12
10 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

 The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul
15 samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20 degree C until SEAP assays are performed according to Example 37. The plates containing the remaining treated cells are placed at 4 degree C and serve as a source of material for repeating the assay on a specific well if desired.

20 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

 The above protocol may be used in the generation of both transient, as well as, stable transfected cells, which would be apparent to those of skill in the art.

25

Example 34: High-Throughput Screening Assay Identifying Myeloid Activity

 The following protocol is used to assess myeloid activity of polypeptide of the present invention by determining whether polypeptide of the present invention
30 proliferates and/or differentiates myeloid cells. Myeloid cell activity is assessed using

the GAS/SEAP/Neo construct produced in Example 32. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 5 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 32, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml
10 penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37 degrees C for 45 min.

- 15 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37 degree C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 20 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- Add 50 ul of the supernatant prepared by the protocol described in Example
25 31. Incubate at 37 degree C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 37.

- 30 *Example 35: High-Throughput Screening Assay Identifying Neuronal Activity.*

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed by polypeptide of the present invention.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells by polypeptide of the present invention can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO: 1690)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO: 1691)

Using the GAS:SEAP/Neo vector produced in Example 32, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter

sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 31. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 31, 37 degree C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 37.

Example 36: High-Throughput Screening Assay for T-cell Activity

NF-KB (Nuclear Factor KB) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF-KB
5 regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- KB appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- KB is retained in the cytoplasm with I-KB (Inhibitor KB). However, upon stimulation, I- KB is phosphorylated and degraded,
10 causing NF- KB to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- KB include IL-2, IL-6, GM-CSF, ICAM-1 and class I MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF-KB promoter element are used to screen the supernatants
15 produced in Example 31. Activators or inhibitors of NF-KB would be useful in treating, preventing, and/or diagnosing diseases. For example, inhibitors of NF-KB could be used to treat those diseases related to the acute or chronic activation of NF-KB, such as rheumatoid arthritis.

To construct a vector containing the NF-KB promoter element, a PCR based
20 strategy is employed. The upstream primer contains four tandem copies of the NF-KB binding site (GGGGACTTTCCC) (SEQ ID NO:1692), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:

5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
25 TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:1693)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:1688)

PCR amplification is performed using the SV40 promoter template present in
30 the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is

digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)
Sequencing with the T7 and T3 primers confirms the insert contains the following
sequence:

5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC
5 ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCC
ATCCCGCCCCTAACTCCGCCCAGTTCGCCCATTCTCGCCCCATGGCTGA
CTAATTTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTA
TTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAA
GCTT:3' (SEQ ID NO:1694)

10 Next, replace the SV40 minimal promoter element present in the pSEAP2-
promoter plasmid (Clontech) with this NF-KB/SV40 fragment using XhoI and
HindIII. However, this vector does not contain a neomycin resistance gene, and
therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF-KB/SV40/SEAP
15 cassette is removed from the above NF-KB/SEAP vector using restriction enzymes
Sall and NotI, and inserted into a vector containing neomycin resistance. Particularly,
the NF-KB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the
GFP gene, after restricting pGFP-1 with Sall and NotI.

Once NF-KB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are
20 created and maintained according to the protocol described in Example 33. Similarly,
the method for assaying supernatants with these stable Jurkat T-cells is also described
in Example 33. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to
wells H9, H10, and H11, with a 5-10 fold activation typically observed.

25 *Example 37: Assay for SEAP Activity*

As a reporter molecule for the assays described in Examples 33-36, SEAP
activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the
following general procedure. The Tropix Phospho-light Kit supplies the Dilution,
30 Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 ul of 2.5x dilution buffer into Optiplates containing 35 ul of a supernatant. Seal the plates with a plastic sealer and incubate at 65 degree C for 30 min. Separate the Optiplates to avoid uneven heating.

- 5 Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 ml Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below).. Add 50 ul Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it
10 takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

15 Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6

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23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 38: High-Throughput Screening Assay Identifying Changes in Small

Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-4 (Molecular Probes, Inc.; catalog no. F-14202), used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-4 is made in 10% pluronic acid DMSO. To load the cells with fluo-4, 50 ul of 12 ug/ml fluo-4 is added to each well. The plate is incubated at 37 degrees C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to $2-5 \times 10^6$ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-4 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37 degrees C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1×10^6 cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley Cell Wash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-4. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event caused by the a molecule, either polypeptide of the present invention or a molecule induced by polypeptide of the present invention, which has resulted in an increase in the intracellular Ca^{++} concentration.

Example 40: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, identifying whether polypeptide of the present invention or a molecule induced by polypeptide of the present invention is capable of activating tyrosine

kinase signal transduction pathways is of interest. Therefore, the following protocol is designed to identify such molecules capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately
5 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from
Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with
100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr
with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or
polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St.
10 Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or
calf serum, rinsed with PBS and stored at 4 degree C. Cell growth on these plates is
assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of
cell number through use of alamarBlue as described by the manufacturer Alamar
Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from
15 Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen
Plates. Falcon Microtest III cell culture plates can also be used in some proliferation
experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of
Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium.
20 Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20
minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in
Example 31, the medium was removed and 100 ml of extraction buffer ((20 mM
HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM
Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from
25 Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is
shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a
vacuum transfer manifold and the extract filtered through the 0.45 mm membrane
bottoms of each well using house vacuum. Extracts are collected in a 96-well
catch/assay plate in the bottom of the vacuum manifold and immediately placed on
30 ice. To obtain extracts clarified by centrifugation, the content of each well, after

detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4 degree C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described
5 here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and
10 PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂⁺ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride,
15 pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30 degree C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of
20 120mM EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37 degree C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul
25 of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37 degree C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the
30 absorbance of the sample at 405 nm by using ELISA reader. The level of bound

peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

Example 41: High-Throughput Screening Assay Identifying Phosphorylation Activity

5

As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 40, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

15 Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4 degree C until use.

20 A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 31 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

25 After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit)
30

antibody (1 µg/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation by polypeptide of the present invention or a molecule induced by polypeptide of the present invention.

Example 42: Assay for the Stimulation of Bone Marrow CD34+ Cell Proliferation

10

This assay is based on the ability of human CD34+ to proliferate in the presence of hematopoietic growth factors and evaluates the ability of isolated polypeptides expressed in mammalian cells to stimulate proliferation of CD34+ cells.

It has been previously shown that most mature precursors will respond to only a single signal. More immature precursors require at least two signals to respond. Therefore, to test the effect of polypeptides on hematopoietic activity of a wide range of progenitor cells, the assay contains a given polypeptide in the presence or absence of other hematopoietic growth factors. Isolated cells are cultured for 5 days in the presence of Stem Cell Factor (SCF) in combination with tested sample. SCF alone has a very limited effect on the proliferation of bone marrow (BM) cells, acting in such conditions only as a "survival" factor. However, combined with any factor exhibiting stimulatory effect on these cells (e.g., IL-3), SCF will cause a synergistic effect. Therefore, if the tested polypeptide has a stimulatory effect on a hematopoietic progenitors, such activity can be easily detected. Since normal BM cells have a low level of cycling cells, it is likely that any inhibitory effect of a given polypeptide, or agonists or antagonists thereof, might not be detected. Accordingly, assays for an inhibitory effect on progenitors is preferably tested in cells that are first subjected to *in vitro* stimulation with SCF+IL-3, and then contacted with the compound that is being evaluated for inhibition of such induced proliferation.

30 Briefly, CD34+ cells are isolated using methods known in the art. The cells

are thawed and resuspended in medium (QBSF 60 serum-free medium with 1% L-glutamine (500ml) Quality Biological, Inc., Gaithersburg, MD Cat# 160-204-101). After several gentle centrifugation steps at 200 x g, cells are allowed to rest for one hour. The cell count is adjusted to 2.5×10^5 cells/ml. During this time, 100 μ l of
5 sterile water is added to the peripheral wells of a 96-well plate. The cytokines that can be tested with a given polypeptide in this assay is rhSCF (R&D Systems, Minneapolis, MN, Cat# 255-SC) at 50 ng/ml alone and in combination with rhSCF and rhIL-3 (R&D Systems, Minneapolis, MN, Cat# 203-ML) at 30 ng/ml. After one hour, 10 μ l of prepared cytokines, 50 μ l of the supernatants prepared in Example 31
10 (supernatants at 1:2 dilution = 50 μ l) and 20 μ l of diluted cells are added to the media which is already present in the wells to allow for a final total volume of 100 μ l. The plates are then placed in a 37°C/5% CO₂ incubator for five days.

Eighteen hours before the assay is harvested, 0.5 μ Ci/well of [3H] Thymidine is added in a 10 μ l volume to each well to determine the proliferation rate. The
15 experiment is terminated by harvesting the cells from each 96-well plate to a filtermat using the Tomtec Harvester 96. After harvesting, the filtermats are dried, trimmed and placed into OmniFilter assemblies consisting of one OmniFilter plate and one OmniFilter Tray. 60 μ l Microscint is added to each well and the plate sealed with TopSeal-A press-on sealing film. A bar code 15 sticker is affixed to the first plate for
20 counting. The sealed plates is then loaded and the level of radioactivity determined via the Packard Top Count and the printed data collected for analysis. The level of radioactivity reflects the amount of cell proliferation.

The studies described in this example test the activity of a given polypeptide to stimulate bone marrow CD34+ cell proliferation. One skilled in the art could
25 easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof. As a nonlimiting example, potential antagonists tested in this assay would be expected to inhibit cell proliferation in the presence of cytokines and/or to increase the inhibition of cell proliferation in the presence of cytokines and a given polypeptide.
30 In contrast, potential agonists tested in this assay would be expected to enhance cell

proliferation and/or to decrease the inhibition of cell proliferation in the presence of cytokines and a given polypeptide.

The ability of a gene to stimulate the proliferation of bone marrow CD34+ cells indicates that polynucleotides and polypeptides corresponding to the gene are useful for the diagnosis and treatment of disorders affecting the immune system and hematopoiesis. Representative uses are described in the "Immune Activity" and "Infectious Disease" sections above, and elsewhere herein.

Example 43: Assay for Extracellular Matrix Enhanced Cell Response (EMECR)

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The objective of the Extracellular Matrix Enhanced Cell Response (EMECR) assay is to identify gene products (e.g., isolated polypeptides) that act on the hematopoietic stem cells in the context of the extracellular matrix (ECM) induced signal.

15 Cells respond to the regulatory factors in the context of signal(s) received from the surrounding microenvironment. For example, fibroblasts, and endothelial and epithelial stem cells fail to replicate in the absence of signals from the ECM. Hematopoietic stem cells can undergo self-renewal in the bone marrow, but not in *in vitro* suspension culture. The ability of stem cells to undergo self-renewal *in vitro* is dependent upon their interaction with the stromal cells and the ECM protein fibronectin (fn). Adhesion of cells to fn is mediated by the $\alpha_5\beta_1$ and $\alpha_4\beta_1$ integrin receptors, which are expressed by human and mouse hematopoietic stem cells. The factor(s) which integrate with the ECM environment and responsible for stimulating stem cell self-renewal has not yet been identified. Discovery of such factors should be of great interest in gene therapy and bone marrow transplant applications

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Briefly, polystyrene, non tissue culture treated, 96-well plates are coated with fn fragment at a coating concentration of $0.2 \mu\text{g}/\text{cm}^2$. Mouse bone marrow cells are plated (1,000 cells/well) in 0.2 ml of serum-free medium. Cells cultured in the presence of IL-3 (5 ng/ml) + SCF (50 ng/ml) would serve as the positive control,

conditions under which little self-renewal but pronounced differentiation of the stem cells is to be expected. Gene products of the invention (e.g., including, but not limited to, polynucleotides and polypeptides of the present invention, and supernatants produced in Example 31), are tested with appropriate negative controls in the presence and absence of SCF(5.0 ng/ml), where test factor supernates represent 10% of the total assay volume. The plated cells are then allowed to grow by incubating in a low oxygen environment (5% CO₂, 7% O₂, and 88% N₂) tissue culture incubator for 7 days. The number of proliferating cells within the wells is then quantitated by measuring thymidine incorporation into cellular DNA. Verification of the positive hits in the assay will require phenotypic characterization of the cells, which can be accomplished by scaling up of the culture system and using appropriate antibody reagents against cell surface antigens and FACScan.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof.

If a particular polypeptide of the present invention is found to be a stimulator of hematopoietic progenitors, polynucleotides and polypeptides corresponding to the gene encoding said polypeptide may be useful for the diagnosis and treatment of disorders affecting the immune system and hematopoiesis. Representative uses are described in the "Immune Activity" and "Infectious Disease" sections above, and elsewhere herein. The gene product may also be useful in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types.

Additionally, the polynucleotides and/or polypeptides of the gene of interest and/or agonists and/or antagonists thereof, may also be employed to inhibit the proliferation and differentiation of hematopoietic cells and therefore may be employed to protect bone marrow stem cells from chemotherapeutic agents during chemotherapy. This antiproliferative effect may allow administration of higher doses of chemotherapeutic agents and, therefore, more effective chemotherapeutic treatment.

Moreover, polynucleotides and polypeptides corresponding to the gene of interest may also be useful for the treatment and diagnosis of hematopoietic related disorders such as, for example, anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia.

Example 44: Human Dermal Fibroblast and Aortic Smooth Muscle Cell Proliferation

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The polypeptide of interest is added to cultures of normal human dermal fibroblasts (NHDF) and human aortic smooth muscle cells (AoSMC) and two co-assays are performed with each sample. The first assay examines the effect of the polypeptide of interest on the proliferation of normal human dermal fibroblasts (NHDF) or aortic smooth muscle cells (AoSMC). Aberrant growth of fibroblasts or smooth muscle cells is a part of several pathological processes, including fibrosis, and restenosis. The second assay examines IL6 production by both NHDF and SMC. IL6 production is an indication of functional activation. Activated cells will have increased production of a number of cytokines and other factors, which can result in a proinflammatory or immunomodulatory outcome. Assays are run with and without co-TNF α stimulation, in order to check for costimulatory or inhibitory activity.

Briefly, on day 1, 96-well black plates are set up with 1000 cells/well (NHDF) or 2000 cells/well (AoSMC) in 100 μ l culture media. NHDF culture media contains: Clonetics FB basal media, 1mg/ml hFGF, 5mg/ml insulin, 50mg/ml gentamycin, 2%FBS, while AoSMC culture media contains Clonetics SM basal media, 0.5 μ g/ml hEGF, 5mg/ml insulin, 1 μ g/ml hFGF, 50mg/ml gentamycin, 50 μ g/ml Amphotericin B, 5%FBS. After incubation at 37°C for at least 4-5 hours, culture media is aspirated and replaced with growth arrest media. Growth arrest media for NHDF contains fibroblast basal media, 50mg/ml gentamycin, 2% FBS, while growth arrest media for AoSMC contains SM basal media, 50mg/ml gentamycin, 50 μ g/ml Amphotericin B,

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0.4% FBS. Incubate at 37°C until day 2.

On day 2, serial dilutions and templates of the polypeptide of interest are designed such that they always include media controls and known-protein controls. For both stimulation and inhibition experiments, proteins are diluted in growth arrest
5 media. For inhibition experiments, TNF α is added to a final concentration of 2ng/ml (NHDF) or 5ng/ml (AoSMC). Add 1/3 vol media containing controls or polypeptides of the present invention and incubate at 37°C/5% CO₂ until day 5.

Transfer 60 μ l from each well to another labeled 96-well plate, cover with a plate-sealer, and store at 4°C until Day 6 (for IL6 ELISA). To the remaining 100 μ l in
10 the cell culture plate, aseptically add Alamar Blue in an amount equal to 10% of the culture volume (10 μ l). Return plates to incubator for 3 to 4 hours. Then measure fluorescence with excitation at 530nm and emission at 590nm using the CytoFluor. This yields the growth stimulation/inhibition data.

On day 5, the IL6 ELISA is performed by coating a 96 well plate with 50-100
15 μ l/well of Anti-Human IL6 Monoclonal antibody diluted in PBS, pH 7.4, incubate ON at room temperature.

On day 6, empty the plates into the sink and blot on paper towels. Prepare Assay Buffer containing PBS with 4% BSA. Block the plates with 200 μ l/well of Pierce Super Block blocking buffer in PBS for 1-2 hr and then wash plates with wash
20 buffer (PBS, 0.05% Tween-20). Blot plates on paper towels. Then add 50 μ l/well of diluted Anti-Human IL-6 Monoclonal, Biotin-labeled antibody at 0.50 mg/ml. Make dilutions of IL-6 stock in media (30, 10, 3, 1, 0.3, 0 ng/ml). Add duplicate samples to top row of plate. Cover the plates and incubate for 2 hours at RT on shaker. Plates are washed with wash buffer and blotted on paper towels. Dilute EU-labeled Streptavidin
25 1:1000 in Assay buffer, and add 100 μ l/well. Cover the plate and incubate 1 h at RT. Plates are again washed with wash buffer and blotted on paper towels. Add 100 μ l/well of Enhancement Solution and shake for 5 minutes. Read the plate on the Wallac DELFIA Fluorometer. Readings from triplicate samples in each assay are tabulated and averaged.

30 A positive result in this assay suggests AoSMC cell proliferation and that the

polypeptide of the present invention may be involved in dermal fibroblast proliferation and/or smooth muscle cell proliferation. A positive result also suggests many potential uses of polypeptides, polynucleotides, agonists and/or antagonists of the polynucleotide/polypeptide of the present invention which gives a positive result.

5 For example, inflammation and immune responses, wound healing, and angiogenesis, as detailed throughout this specification. Particularly, polypeptides of the present invention and polynucleotides of the present invention may be used in wound healing and dermal regeneration, as well as the promotion of vasculargenesis, both of the blood vessels and lymphatics. The growth of vessels can be used in the treatment of,

10 for example, cardiovascular diseases. Additionally, antagonists of polypeptides and polynucleotides of the invention may be useful in treating diseases, disorders, and/or conditions which involve angiogenesis by acting as an anti-vascular (e.g., anti-angiogenesis). These diseases, disorders, and/or conditions are known in the art and/or are described herein, such as, for example, malignancies, solid tumors, benign

15 tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; arteriosclerotic plaques; ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, uveitis and Pterygia (abnormal blood vessel growth) of the eye;

20 rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization; telangiectasia;

25 hemophiliac joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis. Moreover, antagonists of polypeptides and polynucleotides of the invention may be useful in treating anti-hyperproliferative diseases and/or anti-inflammatory known in the art and/or described herein.

One skilled in the art could easily modify the exemplified studies to test the

30 activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or

antagonists and fragments and variants thereof.

Example 45: Cellular Adhesion Molecule (CAM) Expression on Endothelial Cells

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The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules (CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves
10 intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an
15 inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

Briefly, endothelial cells (e.g., Human Umbilical Vein Endothelial cells (HUVECs)) are grown in a standard 96 well plate to confluence, growth medium is removed from the cells and replaced with 100 μ l of 199 Medium (10% fetal bovine
20 serum (FBS)). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 μ l volumes). Plates are then incubated at 37°C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to remove medium and 100 μ l of 0.1% paraformaldehyde-PBS(with Ca++ and Mg++) is added to each well. Plates are held at 4°C for 30 min. Fixative is
25 removed from the wells and wells are washed 1X with PBS(+Ca,Mg) + 0.5% BSA and drained. 10 μ l of diluted primary antibody is added to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10 μ g/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed three
30 times with PBS(+Ca,Mg) + 0.5% BSA. 20 μ l of diluted ExtrAvidin-Alkaline

Phosphatase (1:5,000 dilution, referred to herein as the working dilution) are added to each well and incubated at 37°C for 30 min. Wells are washed three times with PBS(+Ca,Mg)+0.5% BSA. Dissolve 1 tablet of p-Nitrophenol Phosphate pNPP per 5 ml of glycine buffer (pH 10.4). 100 µl of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphatase in glycine buffer: $1:5,000 (10^0) > 10^{-0.5} > 10^{-1} > 10^{-1.5}$. 5 µl of each dilution is added to triplicate wells and the resulting AP content in each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 µl of pNPP reagent is then added to each of the standard wells. The plate is incubated at 37°C for 4h. A volume of 50 µl of 3M NaOH is added to all wells. The plate is read on a plate reader at 405 nm using the background subtraction option on blank wells filled with glycine buffer only. Additionally, the template is set up to indicate the concentration of AP-conjugate in each standard well [5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

Example 46: Alamar Blue Endothelial Cells Proliferation Assay

This assay may be used to quantitatively determine protein mediated inhibition of bFGF-induced proliferation of Bovine Lymphatic Endothelial Cells (LECs), Bovine Aortic Endothelial Cells (BAECs) or Human Microvascular Uterine Myometrial Cells (UTMECs). This assay incorporates a fluorometric growth indicator based on detection of metabolic activity. A standard Alamar Blue Proliferation Assay is prepared in EGM-2MV with 10 ng /ml of bFGF added as a source of endothelial cell stimulation. This assay may be used with a variety of endothelial cells with slight changes in growth medium and cell concentration. Dilutions of the protein batches to be tested are diluted as appropriate. Serum-free medium (GIBCO SFM) without bFGF is used as a non-stimulated control and Angiostatin or TSP-1 are included as a known inhibitory controls.

Briefly, LEC, BAECs or UTMECs are seeded in growth media at a density of 5000 to 2000 cells/well in a 96 well plate and placed at 37-C overnight. After the

overnight incubation of the cells, the growth media is removed and replaced with GIBCO EC-SFM. The cells are treated with the appropriate dilutions of the protein of interest or control protein sample(s) (prepared in SFM) in triplicate wells with additional bFGF to a concentration of 10 ng/ ml. Once the cells have been treated
5 with the samples, the plate(s) is/are placed back in the 37° C incubator for three days. After three days 10 ml of stock alamar blue (Biosource Cat# DAL1100) is added to each well and the plate(s) is/are placed back in the 37°C incubator for four hours. The plate(s) are then read at 530nm excitation and 590nm emission using the CytoFluor fluorescence reader. Direct output is recorded in relative fluorescence units.

10 Alamar blue is an oxidation-reduction indicator that both fluoresces and changes color in response to chemical reduction of growth medium resulting from cell growth. As cells grow in culture, innate metabolic activity results in a chemical reduction of the immediate surrounding environment. Reduction related to growth causes the indicator to change from oxidized (non-fluorescent blue) form to reduced
15 (fluorescent red) form. i.e. stimulated proliferation will produce a stronger signal and inhibited proliferation will produce a weaker signal and the total signal is proportional to the total number of cells as well as their metabolic activity. The background level of activity is observed with the starvation medium alone. This is compared to the output observed from the positive control samples (bFGF in growth medium) and
20 protein dilutions.

Example 47: Detection of Inhibition of a Mixed Lymphocyte Reaction

This assay can be used to detect and evaluate inhibition of a Mixed
25 Lymphocyte Reaction (MLR) by gene products (e.g., isolated polypeptides). Inhibition of a MLR may be due to a direct effect on cell proliferation and viability, modulation of costimulatory molecules on interacting cells, modulation of adhesiveness between lymphocytes and accessory cells, or modulation of cytokine production by accessory cells. Multiple cells may be targeted by these polypeptides

since the peripheral blood mononuclear fraction used in this assay includes T, B and natural killer lymphocytes, as well as monocytes and dendritic cells.

Polypeptides of interest found to inhibit the MLR may find application in diseases associated with lymphocyte and monocyte activation or proliferation. These include, but are not limited to, diseases such as asthma, arthritis, diabetes, inflammatory skin conditions, psoriasis, eczema, systemic lupus erythematosus, multiple sclerosis, glomerulonephritis, inflammatory bowel disease, crohn's disease, ulcerative colitis, arteriosclerosis, cirrhosis, graft vs. host disease, host vs. graft disease, hepatitis, leukemia and lymphoma.

Briefly, PBMCs from human donors are purified by density gradient centrifugation using Lymphocyte Separation Medium (LSM[®], density 1.0770 g/ml, Organon Teknika Corporation, West Chester, PA). PBMCs from two donors are adjusted to 2×10^6 cells/ml in RPMI-1640 (Life Technologies, Grand Island, NY) supplemented with 10% FCS and 2 mM glutamine. PBMCs from a third donor is adjusted to 2×10^5 cells/ml. Fifty microliters of PBMCs from each donor is added to wells of a 96-well round bottom microtiter plate. Dilutions of test materials (50 μ l) is added in triplicate to microtiter wells. Test samples (of the protein of interest) are added for final dilution of 1:4; rhIL-2 (R&D Systems, Minneapolis, MN, catalog number 202-IL) is added to a final concentration of 1 μ g/ml; anti-CD4 mAb (R&D Systems, clone 34930.11, catalog number MAB379) is added to a final concentration of 10 μ g/ml. Cells are cultured for 7-8 days at 37°C in 5% CO₂, and 1 μ C of [³H] thymidine is added to wells for the last 16 hrs of culture. Cells are harvested and thymidine incorporation determined using a Packard TopCount. Data is expressed as the mean and standard deviation of triplicate determinations.

Samples of the protein of interest are screened in separate experiments and compared to the negative control treatment, anti-CD4 mAb, which inhibits proliferation of lymphocytes and the positive control treatment, IL-2 (either as recombinant material or supernatant), which enhances proliferation of lymphocytes.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or

antagonists and fragments and variants thereof.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties. Moreover, the hard copy of and the corresponding computer readable form of the Sequence Listing of Serial No. 60/124,270 are also incorporated herein by reference in their entireties.

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Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209059
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Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209060
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Date of deposit 20 May 1997	Accession Number 209061
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D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209061

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 209061

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

548

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209062
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209062

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 209062

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application number	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209063
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209063

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 209063

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209064
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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ATCC Deposit No. 209064

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 209064

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA106PCT	557 International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>20 May 1997</u>	Accession Number <u>209065</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
<u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit") 	

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ATCC Deposit No. 209065

CANADA

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NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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Page 2

ATCC Deposit No. 209065

DENMARK

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560

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209066
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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ATCC Deposit No. 209066

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No. 209066

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

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Applicant's or agent's file reference number	PA106PCT	International application I	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>20 May 1997</u>	Accession Number <u>209067</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
<u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Authorized officer <u>Processing Div.</u> <u>(703) 305-3039</u>

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Authorized officer

ATCC Deposit No. 209067

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 209067

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

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Applicant's or agent's file reference number	PA106PCT	International application?	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209068
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209068

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 209068

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

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Applicant's or agent's file reference number	PA106PCT	International application?	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209069
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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ATCC Deposit No. 209069

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 209069

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

572

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 12 January 1998	Accession Number 209579
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209579

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 209579

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by an applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>12 January 1998</u>	Accession Number <u>209578</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
<u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit") 	

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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209578

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 209578

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

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578

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 16 July 1998	Accession Number 203067
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Authorized officer Judy McDowell PCT/Intemat'l Appl Processing Div. (703) 305-6639	Authorized officer

Form PCT/RO/134 (July 1992)

ATCC Deposit No. 203067**CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 203067

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

581

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 16 July 1998	Accession Number 203068
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application Authorized officer Jared McDowell PCT/Intemat'l Appl Processing Div. (703) 305-3339	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 203068

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 203068

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 1 February 1999	Accession Number 203609
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 203609

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 203609

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

587

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 1 February 1999	Accession Number 203610
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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ATCC Deposit No. 203610

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 203610

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

590

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 17 November 1998	Accession Number 203485
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application Authorized officer: PCT/Internat'l Appl Processing Div. (703) 305-3639	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer:
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ATCC Deposit No. 203485

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. 203485

DENMARK

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NETHERLANDS

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593

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 18 June 1999	Accession Number PTA-252
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Authorized officer J. M. Powell PCT/Internat'l Appl Processing Div. (703) 305-3839	Authorized officer

ATCC Deposit No. PTA-252

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. PTA-252

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

596

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 18 June 1999	Accession Number PTA-253
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input checked="" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Jerry McDowell Authorized officer PCT/US00/05882 Appl Processing Div. (703) 305-3639	Authorized officer

Form PCT/RO/134 (July 1992)

ATCC Deposit No. PTA-253**CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

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UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

ATCC Deposit No. PTA-253

DENMARK

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SWEDEN

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NETHERLANDS

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599

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>121</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>22 December 1999</u>	Accession Number <u>PTA-1081</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
<u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit") 	

For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application Authorized officer <u>Janet Chen</u> <u>PCT/Internat'l Appl Processing Div.</u> <u>(703) 305-3639</u>	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
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Form PCT/RO/134 (July 1992)

600

ATCC Deposit No. PTA-1081

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

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Page 2

ATCC Deposit No. PTA-1081

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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
- 5 (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- 10 (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- (c) a polynucleotide encoding a polypeptide fragment of a polypeptide encoded by SEQ ID NO:X or a polypeptide fragment encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- 15 (d) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- (e) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- 20 (f) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X, having biological activity;
- (g) a polynucleotide which is a variant of SEQ ID NO:X;
- 25 (h) a polynucleotide which is an allelic variant of SEQ ID NO:X;
- (i) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
- (j) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide
- 30

sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a protein.

5

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X.

10

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X.

15

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

20

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

25

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

30

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.
11. An isolated polypeptide comprising an amino acid sequence at least
5 95% identical to a sequence selected from the group consisting of:
- (a) a polypeptide fragment of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
 - (b) a polypeptide fragment of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone, having biological activity;
 - 10 (c) a polypeptide domain of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
 - (d) a polypeptide epitope of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
 - (e) a full length protein of SEQ ID NO:Y or of the sequence encoded by the
15 cDNA included in the related cDNA clone;
 - (f) a variant of SEQ ID NO:Y;
 - (g) an allelic variant of SEQ ID NO:Y; or
 - (h) a species homologue of the SEQ ID NO:Y.
- 20 12. The isolated polypeptide of claim 11, wherein the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.
- 25 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.
14. A recombinant host cell that expresses the isolated polypeptide of claim 11.
- 30 15. A method of making an isolated polypeptide comprising:

(a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and

(b) recovering said polypeptide.

5 16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

10

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

15 (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

20 (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

25 20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

(a) contacting the polypeptide of claim 11 with a binding partner; and

(b) determining whether the binding partner effects an activity of the polypeptide.

30

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.
22. A method of identifying an activity in a biological assay, wherein the method comprises:
- 5 (a) expressing SEQ ID NO:X in a cell;
- (b) isolating the supernatant;
- (c) detecting an activity in a biological assay; and
- (d) identifying the protein in the supernatant having the activity.
- 10 23. The product produced by the method of claim 20.

SEQUENCE LISTING

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<211> 901
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<211> 731
<212> DNA
<213> Homo sapiens

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<222> (106)
<223> n equals a,t,g, or c

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<210> 7

<211> 2774

<212> DNA

<213> Homo sapiens

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<222> (2652)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2698)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2714)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2756)

<223> n equals a,t,g, or c

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<210> 8

<211> 2613

<212> DNA

<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1246)

<223> n equals a,t,g, or c

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<211> 1101

<212> DNA

<213> Homo sapiens

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<221> misc feature

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<220>
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<223> n equals a,t,g, or c

<220>
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<222> (1055)
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<211> 1373
<212> DNA
<213> Homo sapiens

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<222> (1364)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1373)
<223> n equals a,t,g, or c

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<211> 3804

<212> DNA

<213> Homo sapiens

<400> 11

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<210> 12

<211> 2157

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (806)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (846)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1517)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2110)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2116)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2137)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2150)

<223> n equals a,t,g, or c

<400> 12

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<210> 13

<211> 1117

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1102)

<223> n equals a,t,g, or c

<400> 13

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<210> 14

<211> 885
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (869)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (884)
<223> n equals a,t,g, or c

<400> 14
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<210> 15
<211> 1024
<212> DNA
<213> Homo sapiens

<220>
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<222> (938)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1005)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1012)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1019)
<223> n equals a,t,g, or c

<400> 15
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gccagatgct caaggaggga gcgaaacact tttcaggatt agaaggagct gtgtatagaa 180
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<210> 16
<211> 545
<212> DNA
<213> Homo sapiens

<220>
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<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (403)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (476)
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (507)

<223> n equals a,t,g, or c

<400> 16

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ctcaagagat gattcaaaaa acacgytgta tytgcaaatg aacagcctga aaaccngagg 480
acacagccgt gtattactgt accacangac ccctaattac tatgatagta rtgcaaaaag 540
ctttt 545
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<210> 17

<211> 623

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (15)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (613)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (616)

<223> n equals a,t,g, or c

<400> 17

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tggcagagct cacgtgcctc aacgaagcct cggtgttgca caacctcaag gagcgttact 540
actcagggtc catctacgta agtggctgcc gtggcaccgc gcaggctggg tctgagggtc 600
ccgaggtggg gngngnggcg ggt 623
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<210> 18

<211> 559

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (371)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (531)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (544)
<223> n equals a,t,g, or c

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<222> (547)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (556)
<223> n equals a,t,g, or c

<400> 18
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<210> 19
<211> 1355
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (1045)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1355)
<223> n equals a,t,g, or c

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<210> 20
<211> 1280
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1043)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1162)
<223> n equals a,t,g, or c

<400> 20
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<210> 21

<211> 1191

<212> DNA

<213> Homo sapiens

<400> 21

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caagtgttct caccacacaa acccaaagg aactatgttc tcaccacaca aaccacaaag 900
gaactatgta ttaattagct tgattgtggg aaccatttca caatgtatac atttgccaaa 960
acattatgtt gtatacctgg aatatataat tttatttatc aattatacct caataaagct 1020
gaaagagggg attactaatt cccacaaaat acagatttaa caaaaacttt tattcaacaa 1080
acagtgttat gaagttgtaa attggaaaca aaagaaataa aatttcatcc acagtcttct 1140
catcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaactcgtag g 1191
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<210> 22

<211> 853

<212> DNA

<213> Homo sapiens

<400> 22

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gtttgccata ctgaacawct tttttcttgt ggaatttaaa gtccagctgt gttttctttt 600
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accattaacc taaaacttac tatttaacct agtggtttttg ttgatgaggt ttacattatg 720
tgaatacatg cacatttggt tcttatacag gtgggtgtgaa ctctagggcc tatactagaa 780
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atgtaaatat ata 853
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<210> 23

<211> 474

<212> DNA

<213> Homo sapiens

<400> 23

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tcctctcgct tccctgccgg gcaggcgcca tggcggaagc tcggcgacgg gcgcctgcgg 180
agaggcgatg gcagcgccgg aaggtctctc gggcccggcg ggcttgactc tgggcccggg 240
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gacgggcttc tccggcatga agggctgagg ctgcaaggtc ccgcagaggc gctgtcaaaa 360
ctcctggcgg gactgamgcy gccggacktk cggccccgct gggccggggc ctkgtkgtk 420
gccargaara agcgtcccag gaagccggcc tgccggcaag agcggggccc agcc 474
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<210> 24

<211> 2280

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (13)

<223> n equals a,t,g, or c

<400> 24

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gcatcaagag cttcaagaac aaggggccgc atgtggaaac aatgcgaaga catagaaatg 180
aagtgcagtg ggaactgcgg aagaacaaaa gagatgaaca cttattgaaa aagagaaatg 240
ttccccaaga agaaagtcta gaagattcag atgttgatgc tgattttaaa gcacaaaatg 300
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taaccctaga agctatattg cagaatgcc aagtgtataa cccagtgggc caattgagtg 360
ctgtccaggc agcaagaaaa ctgttatcca gtgacagaaa tccaccgatt gatgacttaa 420
taaaaatctgg gattttacca attctagtca aatgtctaga aagggatgat aatccttcat 480
tacagtttga agctgcttgg gcattaacta acatagcatc aggracttct gcacagactc 540
aagctgttgt gcagtctaata gcagtacctc tttttctgag acttcttctg tcaccacatc 600
agaatgtttg tgaacaagca gtatgggctt tgggaaacat tataaggatg ggtcctcaat 660
gtagagatta tgtcatatca ctgggagttg tcaaacctct tctgtccttc atcagtcctt 720
ccatccccat cacccttctt cggaacgtca catgggtcat tgtcaatctc tgcaggaata 780
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tcccaaatct cttatcacac ccaaaagaga agataaataa ggaagcagtg tggttccttt 1140
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cctccacaaa catattttca tattctttat gtggaagaat agattttaaa gtacaagcca 2160
aatgattttc attggtggaa ctgacacaaa aaaaagtaact taaaaacaag aaacttggtt 2220
attgaataaa cagataagtt taaaaaaaaa aaaaactact tcatctacca gtaattgatg 2280

<210> 25

<211> 1061

<212> DNA

<213> Homo sapiens

<400> 25

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atggcaggct ctgaagagct ggggtctcgg gaagacacgc tgagggtcct agctgccttc 180
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gaagagccaa cagacttctt gagccgcctt cgaagatgtc ttccttgctc cctggggcgga 300
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ctggtccaag agcagctgaa atctccgccc agcccagaat tacagggtcc cccatcgaca 480
gagaaggaag ccatactgag gaggtggtg gccctgctgg aggaggaggc agaagtcatt 540
aaccagaagc tggcctcgga ccccgccctg cgcacaagct ggtccgcctg tcctccgact 600
ctttcgcccc cctggtggag ctgttctgta gccgggatga cagctctcgc ccaagccgag 660

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catgccccgg gccccgcct ccttccccgg agcccctggc ccgcctggcc cttagccatgg 720
agctgagccg gcgcgtggcc gggctggggg gcaccctggc cggactcagc gtggagcacg 780
tgcacagctt cacgccctgg atccaggcca cgggggctgg gagggcatcc tggctgtttc 840
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cacctcatgt ccctgccctc ttcgtgtgct ttccaagtc ttcctattcc actcagggt 960
gtgggggtgt ggttgcccta cctgtttttg ccaaaaataa attgtttaaa acttttctta 1020
ttaaaaacgt tacaaaaaaa aaaaaaaaam aggggggccc c 1061

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<210> 26

<211> 1572

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (19)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (28)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1491)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1527)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1555)

<223> n equals a,t,g, or c

<400> 26

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gggcagctgc ggacatgtcg accccggccc ggaggaggct catgcgggat ttcaagcgg 180
tacaagagga cccacctgtg ggtgtcagt gcgcaccatc tgaaaacaac atcatgcagt 240
ggaatgcagt tatatttga ccagaaggga caccttttga agatggtact tttaaactag 300
taatagaatt ttctgaagaa tatccaaata aaccaccaac tgtaggttt ttatccaaaa 360
tgtttcatcc aaatgtgtat gctgatggt gcatatgttt agatatcctt cagaatcgat 420
ggagtccaac atatgatgta tcttctatct taacatcaat tcagtctctg ctggatgaac 480
cgaatcctaa cagtcagcc aatagccagg cagcacagct ttatcaggaa aacaaacgag 540
aatatgagaa aagagtttcg gccattgttg acaaagctg gaatgattca taatagacaa 600
ctggtctgtt aatctttttc atcattgttg tgtataattt acctctcatt agaaaggcta 660
acaaatttta agtgcacag gttttaagg ttctgcagaa aaaaaagaaa aaagtccttc 720

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agtttagaac ctacaaaagc ttgtgtatct tgattaatgt actttttatt gcatgggtg 780
aactaagtta ttgctgcata aatttgtaat atatcctgtt tgtatttttt tccaagtgt 840
taatgttgggt gtggagtttt catgacagaa tatacacatt ttgtaaatct gtactttttt 900
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agactttgtc acttatttcc ttatgtgtgt aggaggggtt aataagtctc tagctctcca 1080
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gccatttggt acagtttctt catgcattac ttactgttaa aactgtacct ttgcgattt 1320
cacagttggc acttctgcca tgagcagaga actgatgcga cttgttttgc tgcttggtag 1380
cactttaaaa aattttttga ttaatgaagg aaagtaaaac cataaacatt tgccaaaaat 1440
tcatgccccca gtattaggca atggaattag gttgcattgg gtttgaggaa ngggcacatt 1500
ggggggggga atcttgggggt gttaacnttt aaattatttt gggaaaattt acccntttta 1560
tgccatggc ct 1572

<210> 27

<211> 2005

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1976)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1977)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1978)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1979)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1986)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1988)

<223> n equals a,t,g, or c

<400> 27

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gcggacgcgt gggtcgccma cgcgygcgca agcagcgggt tagtggtcgc gcgcccagacc 60
tccgcagtc cagccgagcc gcgacccttc cggccgtccc caccacacct cgccgccatg 120
cgccctccgc gcctagcgct gttcccgggt gtggcgctgc ttcttgccgc ggcccgctc 180
gccgctgcct ccgacgtgct agaactcacg gacgacaact tcgagagtcg catctccgac 240
acgggctctg cgggcctcat gctcgtcgag ttcttcgcyc cctgggtgtg acactgcaag 300
agacttgac ctgagtatga agctgcagct accagattaa aaggaatagt ccattagca 360
aagggttgatt gactgccaa cactaacacc tgtaataaat atggagtcag tggatatcca 420
accctgaaga tatttagaga tggggaagaa gcagggtgctt atgatggacc taggactgct 480
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gaggaagaat ttaagaaatt cattagtgt aaagatgcct ctatagtagg ttttttcgat 600
gattcattca gtgaggctca ctccgagttc ctaaaagcag ccagcaactt gagggataac 660
taccgatttg cacatacgaa tgttgagtct ctggtgaacg agtatgatga taatggagag 720
ggtatcatct tatttcgtcc ttcacatctc actaacaagt ttgaggacaa gactgtggca 780
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cactgtttat ggaaatacca ggaccagttt atgtttgtg ttttgggaaa aattatttgt 1860
gttgggggaa atgttggtgg ggtggggtg agttgggggt attttcta attttttgt 1920
catttggaac agtgacaata aatgagacc ctttaaaaa aaaaaaaa aaaaannnn 2005
gggggncnc cagtcctt cgcc
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<210> 28

<211> 1408

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (11)

<223> n equals a,t,g, or c

<400> 28

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acacgtacga cgagtacaaa aagggttcc tggaccaggc atctgggagt gcagtgtgc 180
tgctcaggcc cggagaccgg tgttcctcca gatgccctca gaacaggctg caggactgta 240
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tgccgggcag tatgtccact cctccttttc aggatattta ttgtatccca tgtaaaaaaca 300
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tccaaatgaa aaacataatt gcttcaaaac acttacacag ttggaaagtt atatgtaagt 420
gaaaatttgg accattgtgt acaaataaaa actaagatgc atgtttaata ctccacacag 480
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cccactggaa tcatatttagc tgttttatgt tatatgcttc cacagtaacc tgcttattca 600
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tctgttttagc atgtatgcaa actggata                                     1408
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<210> 29

<211> 917

<212> DNA

<213> Homo sapiens

<400> 29

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ggaccatgtg cgcgtcccgg gacgactggc gctgtgcgct ccatgcacga kttttccgcc 180
aaggacatcg acgggcacat ggtaacctg gacaagtacc ggggcttcgt gtgcatcgtc 240
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cacgcccgat acgctgagtg tggtttgagg atcctggcct tcccgtgtaa ccagttccggg 360
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aagttcctca tcgacaagaa cggctgctgt gtgaagcgt acggacccat ggaggagccc 600
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ctgctgggct tggctcggcg cccccacccc tggctacctt gtgggaataa acagacaaat 840
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aaaaaaaaaa aaaaaaaa                                     917
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<210> 30

<211> 577

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (501)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (534)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (568)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (575)
<223> n equals a,t,g, or c

<400> 30
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ggtgactcac atctgtaatc ccagcacttt gggaggccaa ggcaggcaga acacttgaag 120
gagttcaaga ccagcgtggc caacgtggtg aaccctgtct ctactaaaaa tacaaaaatt 180
gtttagctct gtttttcata atagaaatag aaaaggtaaa attgcttttc ttctgaaaag 240
aacaagtatt gttcatccaa gaagggtttt tgtgactgaa tcagcagtgc ctgccctagt 300
catagctgtg cttcagaaac ctcagcatga ttagtgttkg agcmmaacaa ggragcaaag 360
caaawcwtg ttttgaaatt ctatctgttg cttgaactat tttgtaataa ttaaactttg 420
gatgttgaga aatcacaaact ttattggtac acttcattgc aacttgaaat tccatgggtc 480
ttaaagtgag attggaattc naatgggagg cctttaaaaa gtaattccca accnttaagg 540
ttaaacccca ggaaattggg gccaatcnaa aaccngg 577

<210> 31
<211> 2059
<212> DNA
<213> Homo sapiens

<400> 31
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aacaagagac tggaggagac ataaatttaa atggagaaag gaccctcaag acaaatgacc 240
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cccgagaaac ccctgcctca tcaatgagtgt tgtccgagtgt aaggaggagg tctttataca 1080
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<210> 32

<211> 549

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (337)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (378)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (497)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (537)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (546)

<223> n equals a,t,g, or c

<400> 32

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tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc tatagtgtca 180
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acttgccagc gccctagcgc ccgctccttt cgctttcttc ccttcctttc tcgccacgtt 480
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ctttanggt 549
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<210> 33

<211> 841

<212> DNA

<213> Homo sapiens

<400> 33

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gcagcccccac agaccatggt catgccaggt ggttgacta caatcccaga gtcagaccta 180
gaagaaaagat cagtagaaca agactctaca gaactgttta ccaaccacag acatctcact 240
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ttgtttggtt gagaggaaca tccccatctc aaggccgaac ctgtgtgaac ctcatgcaa 360
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gattcagatc caaaataatt tcatacccca ttttttcaca gaattcttat atagtaaag 660
tatcaagttt aataaagcat ctcatgtgca aataatatct tggattttat ttataattag 720
agggatttat gagtgattgc tctacattat ttcttcaaag gaaaggaaag gaattgaaga 780
ctttgctact ctctggtgag acttgaatgt gattatttta taaataaaaag aaccactatg 840
a 841
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<210> 34

<211> 863

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (19)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (29)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (44)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (58)

<223> n equals a,t,g, or c

<400> 34

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tggaatcccc ccggggcctt caaggaattc ggcacgagtt tgcttaggcg cagacgggga 120
agcggagcca acatgccagt ggcccgagc tgggtttgtc gcaaaactta tgtgacccc 180
cggagaccct tcgagaaatc tcgtctcgac caagagctga agctgatcgg cgagtatggg 240
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atcctggggc tgaagataga ggatttctta gagagacgcc tgcagacca ggtcttcaag 480
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gtccgcaagc aggtggtgaa catcccgtcc ttcattgtcc gcctggattc ccagaagcac 600
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gctttacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840
aaaaaaaaaa aaaaaaaaaa ttt 863
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<210> 35

<211> 1230

<212> DNA

<213> Homo sapiens

<400> 35

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ggtgggtggt ccagctggaa gtaacccctt ccgggagcct agatcctgtg ctttactctg 240
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tgggtgaagg aatagaattt taaatagtaa taactgcttg ttttttttgt gcaagtactt 480
ttatacataa gataaacaaa aaccttacca ccaaacatac caaaatgcac ctctttcata 540
agtgaattac taagatttct atacctggaa tatcatgtat gtttcattta ctggatgttt 600
acattttagg aaggaaaata gtttgtttta tttaaacaac tgaatactta taaactgttg 660
ttcctggaag ttattttatt cataaaaaat ttgttctttt ctcatgaatt tataattcct 720
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1230

<210> 36

<211> 640

<212> DNA

<213> Homo sapiens

<400> 36

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ctatccgcac tagaaagttc atgaccaacc gactacttca gaggaacaa atggtcattg 180
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aaatgtacaa gaccacaccg gatgtcatct ttgtatttg attcagaact cattttggtg 300
gtggcaagac aactggcttt ggcattgatt atgattccct ggattatgca aagaaaaatg 360
aaccctaaaca tagacttgca agacatggcc tgtatgagaa gaaaaagacc tcaagaaagc 420
aacgaaagga acgcaagaac agaataaga aagtcagggg gactgcaaag gccaatgttg 480
gtgctggcaa aaagccgaag gagtaaaggt gctgcaatga tgtagctgt ggccactgtg 540
gatttttcgc aagaacatta ataaactaaa aacttcaaaa aaaaaaaaaa aaaaaaaaaa 600
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagg 640

<210> 37

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (10)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (15)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (32)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (556)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (558)

<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (567)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (590)
<223> n equals a,t,g, or c

<400> 37
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gtccggcagc gccagcccta cactcgcccg cgccatggcc tctgtctccg agctcgctg 180
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tgccctcatt aaagcagccg gtgtaaatgt tgagcctttt tggcctggct tgtttgcaaa 300
ggccttgcc aacgtcaaca ttgggagcct catctgcaat gtaggggccg gtggacctgc 360
tccagcagct ggtgctgcac cagcaggagg tcctgcccc tccactgctg ctgctccagc 420
tgaggagaag aaagtgaag caaagaaaga agaatccgag gagtctgatg atgacatggg 480
ctttggtctt ttgtactaaa cctcttttat aacatgttca ataaaaagct gaactttaaa 540
aaaaaaaaa aaaaancncg ggggggnccg ctttaaaggg tccaagttan gtacggg 597

<210> 38
<211> 624
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<400> 38
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gaggagacca tcgagggcat gctcctcagg ctggaagagt ttgacagcct ggctgacctg 180
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camctgsacc kgtgcccggt acgtacgagc tgcccacact gtataggacg gaggactatt 480
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ctttgtggtc ttcccatcag gaacactgga aagtgcatt gtgtacacgc tgcagcttgg 600
gggttttttc ttgtattgc tggt 624

<210> 39
<211> 1029
<212> DNA
<213> Homo sapiens

<400> 39
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cctaattgaa tcgargarcc cagggacaca cgcttcagg tttgctcarg ggttcataatt 300
tggtgcttag acaaattcaa aatgaggaaa catcggcact tgccttagt ggccgtcttt 360
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<210> 40

<211> 1107

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1098)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1106)

<223> n equals a,t,g, or c

<400> 40

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ttattagcca tttcctgctg ttgatwatgt tacacatgty catttactca aaaacgtgtt 420
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acaaattggt gttctaaatg tcttaagaac ctaattaaat agctgactac aaaaaaaaa 1020

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<210> 41

<211> 1051

<212> DNA

<213> Homo sapiens

<400> 41

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tgtggctgct ggtgaaaagc ttctccgaga gtggaatcaa ctatgaaatt ataatacatg 180
atgatggaag ccagatgga acaagggatg ttgctgaaca gttggagaag atctatgggt 240
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atggaatgaa acatgccaca ggaaactaca tcattattat ggatgctgat ctctcacacc 360
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<210> 42

<211> 2192

<212> DNA

<213> Homo sapiens

<400> 42

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ttggaaaata tttttttcct ttgcattcat ctctcaaact tagtttttat ctttgaccaa 2100
ccgaacatga ccaaaaacca aaagtgcatt caaccttacc aaaaaaaaaa aaaaaaaaaa 2160
actcgggggg ggcccgtac caattggcct aa 2192
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<210> 43

<211> 353

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (37)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (348)

<223> n equals a,t,g, or c

<400> 43

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ccgggtcgac ccacgcgtcc ggtggggcctt caccaagttc aatgctgatg aatttgaaga 120
catggtggct gaaaagcggc tcatcccaga tggctgtggg gtcaagtaca tcccagtcg 180
tggccctctg gacaagtggc gggccctgca ctcatgagg cttccaatgt gctgcccccc 240
tcttaatact caccaataaa ttctacttcc tgtccaaaaa aaaaaaaaaa aaaaaaaaaa 300
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaanaa aag 353
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<210> 44

<211> 3490

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (782)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1311)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2298)

<223> n equals a,t,g, or c

<400> 44

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acgcgtccgg tgaaaactgt tgcattatcc ctccatcctg tctggaatac accaggtcaa 120
caccagagat ctccagatcag aatcagagat ctccagagggg aataagttca tcctcatggg 180
atggtgaggg gcakgaaagc ggctgggctc ttggacacct gggtctcaga gaaccctgtg 240
atgatcacc cagccccagg ctgtcttagc ccctggagtt cagaagtcct ctctgtaaag 300
cctgcctccc amtargtcaa gaggaactag agtacctttg gatttatcag gaccctcatg 360
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tgccctcgat ctatttccct ctccctctctg acctccctccc aggcactctt acttctagcc 480
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```



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cagcatcagg tcagatcayt gaaattaaaa aatgtgaatt aagttcatat ccaccttttg 3240
gggaagcagg acaaacacc accccaccaa gtgtgtgact tctccatata ccactgcagt 3300
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gtttgagacc ctgttactgt ttgaaaatgc atgcagtgtt cgatgaatct ccaacctgag 3420
gaaaaaaata aaactcaaaa agctttgtgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3480
aaaaaaaaacct                                     3490
```

<210> 45

<211> 781

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (750)

<223> n equals a,t,g, or c

<400> 45

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atcagatgga gggtaggggc tgcccagcaa atgtcagtgt gtgtcaacat ttactgcagg 180
ttcagagctc cctccagggt ccctgagtac atcatgtgct cctgagagtt ttaagggaaa 240
gccaagtaaa gacgtgatga tgttctaaac ccaagcaatt aataaaygcc acggaaatca 300
gtcattcact taccaagtat ttctctgctt tctgccatgt cacgggscca tgatcccctg 360
gagattgagg gaaataagat cacaggagct cccagtctga gtgagaaaag gcagctgctc 420
tgtggtactg tgcaactggc ctgggaatgg cctaaggaga caagcattga gggctgagct 480
cagaagccag ggagaagagc tcagaacccc aggagaggag ctcagaaccc tgggagagga 540
gctcagaacc ctgggagggc ttggtaacct tcgaggatgt ggccgtggag ttcacccagg 600
aggagtgggc gttgctggac cctgccccaa ggacactgta cagggatgtg atgctggaga 660
actgcaggac ctggcctcac targgtgtcg tgtaataaaa cccagtctga tatcccagtt 720
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t                                                                                   781
```

<210> 46

<211> 1431

<212> DNA

<213> Homo sapiens

<400> 46

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gagataaaga cactttttca aaaatggcaa tggatcaga attcctcaag caggcctggt 120
ttattgaaaa tgaagagcag gaatatgttc aaactgtgaa gtcattccaa ggtgggtccc 180
gatcagcggg gagcccttat cctaccttca atccatcctc ggatgtcgct gccttgcata 240
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acagggtcta cagagaggaa ctgaagagag atctggccaa agacataacc tcagacacat 600
ctggagattt tcggaacgct ttgctttctc ttgctaaggg tgaccgatct gaggactttg 660
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ataaggcatt gatcaggatt atgggtttccc gttctgaaat tgacatgaat gatatcaaa 1020
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agtttcttca acaggattac agtgtagcta cctacatgct gaaaaatata gcctttaaat 1260
catttttata ttataactct gtataataga gataagtcca ttttttaaaa atgttttccc 1320
caaaccataa aacctatac aagttgttct agtaacaata catgagaaag atgtctatgt 1380
agctgaaaaa aaaatgacgt cacaagacaa aaaaaaaaaa aaaaaaaaaa a 1431
```

<210> 47

<211> 1913

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (43)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1878)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1896)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1905)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1907)

<223> n equals a,t,g, or c

<400> 47

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agccaggcta gtgacagaaa tggattcgaa ataycagtgt gtgaagctga atgatgggtca 120
cttcatgcct gtcctgggat ttggcaccta tgcgcctgca gaggttccta aaagtaaagc 180
tytagaggcc rycaaatgg caatwgaagc yggsttcrc catattgatt ctgcwcatkt 240
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gaagagagaa gacatattct acacttcaaa gctttggwgc aattcccatc gaccagagtt 360
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taaagatgca ggattggcca agtccatcgg ggtgtccaac ttcaaccrca ggcagctgga 600
gatgatcctc aacaagccag ggctcaagta caagcctgtc tgcaaccagg tggaatgtca 660
tccttacttc aaccagagaa aactgctgga tttctgcaag tcaaaagaca ttgttctggt 720
tgccatatagt gctctgggat ccacaycgaga agaaccatgg gtggaccga actccccggt 780
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ccatttaaga ttcatttctg cagtgggagt ggggtggagt tcacctctg ggaaaggggc 1440
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tgttcataaa agaaaacttt ccacattgtt ttaacaaacc ccacagctgg agagttcagg 1800
cctggaatct ttggatgtgt gccagttca cagattggac cctattggtt tgtggtgggg 1860
ccagggcac caaagacntc attgactaa ttcacnttcc cccgnanagc ccc 1913
```

<210> 48

<211> 1761

<212> DNA

<213> Homo sapiens

<400> 48

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acagcatcta tggcccagat ggggccccct tctacaacta cctgggcccc gaggacaccc 180
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tccctgagcc tgccttcccc aacacagccg gtcactcagc ggaccgcaca cccatccttg 240
agtctccttt gcagccctca gaactccagc cccactacgt ggccagccat ccagagcccc 300
cagccggctt cgaagggtt caggcggagg agtgccgcat cctgaacggc tgtgagaatg 360
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cgggatattgt ggctgaggca gggccccccc actgcactgc caaggagtag cagtcagggg 600
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tcctagctgg gaagacaccg tgacatcagg ccagagggtt ccaatcagcc ttgcctgctt 720
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ggcaggcatt cctctgagtt tacaagcaga gactcactcc aacccaaact agctgggagt 1680
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aaaaaaaaa aaaaaaaaaa g 1761

<210> 49

<211> 956

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (37)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (352)

<223> n equals a,t,g, or c

<400> 49

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cgccgcccgc ccgcaaacct tcgtgcccgg cccgtcctcg ccccgccctc cgccaccgcc 120
tcggcccgcga gagcttgccc cctccccacc cgcagacatg tccgagtcca agagcggccc 180
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gccggagcag atcatgaagt ccatcatccc agtggatcat gctggcatca tngycatcta 360
cggcctgggt gtggcagtc tcatcgccaa ctccctgaat gacgacatca gcctctacaa 420

```

gagcttcctc cagctgggag ccggcctgag cgtgggcctg agcggcctgg cagccggctt 480
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cgtgggcatg atcctgattc tcattctcgc cgaggtgctc ggctctacg gtctcatcgt 600
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traagaccac ccctcctcat cgccctcca ggccccggc gccccacccc ctagagtgt 720
ctgtgtatgc ggatgattta gaattgtcat ttctctttac tggatgttta ttataaaaga 780
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wmcgkcccggt ggccctgcgc ggagctgtgt ccaataaagt tcttggatgt gaaaaa 956

```

<210> 50

<211> 563

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (510)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (519)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (530)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (558)

<223> n equals a,t,g, or c

<400> 50

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gccacaccgc cgtgcctca gtcagccga agcagagtt ctctgtggac atgacctgtg 120
gaggctgtgc tgaagctgtc tctcgggtcc tcaataagct tggaggagtt aagtatgaca 180
ttgacctgcc caacaagaag gtctgcattg aatctgagca cagcatggac actctgcttg 240
caacctgaa gaaaacagga aagactgttt cctaccttg ccttgagtag caggggcctg 300
gtccccacag cccacaggat ggaccaaagg ggcaggatg ctgacctcc cgctggcttc 360
cagacagacc tgggacttgg cagtcatgcc gggatgatgg gttcctgcgg agaccctcag 420
ttgtcctatt ccttcctagc ttccctgcaa taaaatcaag ctgcttttgt tggaaaaaaa 480
aaaaaaaaa gggggcgtct aaaaaccaan ttatttcnt gatgaaatcn acctctttgt 540
tccattcat ccggcctnaa aaa 563

```

<210> 51

<211> 3215

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3196)

<223> n equals a,t,g, or c

<400> 51

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cgctcccttc cctccatagc cacgctccaa accccagggt agccatggcc gggtaaagca 180
agggccattt agattaggaa ggtttttaag atccgcaatg tggagcagca gccactgcac 240
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ttgggcgga agtgagagcc agcagcaaaa actacatttt gcaacttggt ggtgtggatc 360
tattggctga tctatgcctt tcaactagaa aattctaagt attggcaagt cacgttggtt 420
tcaggtccag agtagtttct ttctgtctgc tttaaatggr aacagactca taccacactt 480
acaattaagg tcaagcccag aaagtgataa gtgcaggag gaaaagtga agtccattat 540
gtaatagtga cagcaaagg accaggggag aggcattgcc ttctctgccc acagtcttcc 600
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<210> 52

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (571)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (572)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (573)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (618)

<223> n equals a,t,g, or c

<400> 52

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ctggcccggg catcaggga ctatgccacc gttatctccc acaaccctga gaccaagaag 180
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gttgggtgtg tggctggagg tggccgaatt gacaaacca tcttgaaggc tggccgggag 300
taccacaaat ataaggcaaa gaggaactgc tggccacgag tacgggggtg ggccatgaat 360
cctgtggagc atccttttgg aggtggcaac caccagcaca tcggcaagcc ctccaccatc 420
cgcagagatg ccctgtctgg ccgcaaagtg ggtctcattg ctgcccgcgc gactggacgt 480
ctccggggaa ccaagactgt gcaggagaaa gagaactagt gctgagggcc tcaataaagt 540
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ggggccaact tacccttnca tgcaaa 626

<210> 53

<211> 920

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (617)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (621)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (725)

<223> n equals a,t,g, or c

<400> 53

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tggaactcag cagagtcctg gtgggtgagc agcagcagtg ccasgatgcc aagagccagc 180
agaaggagca gatgttgctg ctggagaaka agagtgtctg ttactcccag gtgcttctcc 240
gctgcctcac ttgctgcag aggtctcttc aagaacaccg gctgaagact caatccgagc 300
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ggatggagga gctaaagatt ttgtccgaca cttactctgt tgagaaagtg gaagttcatc 420
gtctgattag ggaccgtttg gagggagcca ttcacctaca ggagcaggac atggagaact 480
caagacaggt cctgaactcc tatgaggtcc ttggggagga gtttgacagg ctggtgaaag 540
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ggaanatstt acgcttgaac cactgcagtc atttaggcac tctcctggtt tctctttatt 780
ttttatgact gggcctcttc tggaaaatct agcaaggaga tttatataat ttttatgcat 840
agctgtgtgt cagtgtcagc cctgtattgt atttgattat ctctgaata aagttatgat 900
attawaaaaa aaaaaaaaaa 920
```

<210> 54

<211> 1090

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1024)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1034)

<223> n equals a,t,g, or c

<400> 54

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tctctggagt, gactttttct cctcgaattg aaacaagtct atggcaaaag aagctgcatt 120
tttttcacaa aagggaagat ggtaacaatg gtcacttcaa acttttgggc taaattatat 180
gtacacagaa atgttcaaaa tcatagtttt aatgtgtttt gaaaaggcca cacaattata 240
ctttatcttt tcttaataat cctgcaaata tctgccctgg aatccgaaat ctgaaaatgt 300
actggcttga acaaaatttg ttttgtgtgt tagagttata aatcattaat ctttatttcg 360
gggtgtttac gtttatgcca gttcctttat atttaaattt cttgttttat atattttgaa 420
tgtctttata gatttcttta aatttcctta tagaaccatt aatagaaaat cattacattt 480
aaaatatacc ttacagcaaa agcatccaaa taagtatagg gtttatgtcc ttatttttct 540
ttcagctgaa tacgaatgaa cacagtgggt gaatttctga aggggaagtga tgaaattata 600
tttatttcag tgggcacttt tccattttac cactgtacca ttatttgggt cctggagtta 660
tacactaatt ttcagtatat tactgttaaa ttaccaacac aaggcaattt atttgaaaga 720
ttccgtttat cctgccattg ctttgaaaag cagcaggaaa cgaaatcctt tgacttgtat 780
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atatctttga acttgctgtt ttcaatatgg gcagcacaaa ggtgagagat acatattaat 1020
agtngtatgt attnctctta tacattagat acctatattt aaatgaaagg gccaatattg 1080
aaacatatac                                     1090
```

<210> 55

<211> 1464

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (766)

<223> n equals a,t,g, or c

<400> 55

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gacgctctca gctctcggcg cacggcccag cttcctcaa aatgtctact gttcacgaaa 120
tcctgtgcaa gctcagcttg gagggatgac actctacacc cccaagtga tatgggtctg 180
tcaaagccta tactaacttt gatgctgagc gggatgcttt gaacattgaa acagccatca 240
agaccaaagg tgtggatgag gtcaccattg tcaacatttt gaccaaccgc agcaatgcac 300
agagacagga tattgccttc gcctaccaga gaaggaccaa aaaggaactt gcatcagcac 360
tgaagtcagc cttatctggc cacctggaga cggatgattt gggcctattg aagacacctg 420
ctcagtatga cgcttctgag ctaaaagctt ccatgaaggg gctgggaacc gacgaggact 480
ctctcattga gatcatctgc tccagaacca accaggagct gcaggaaatt aacagagtct 540
acaaggaaat gtacaagact gatctggaga aggacattat ttcggacaca tctggtgact 600
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caagagaaaag tacggcaagt ccctgtacta ttatatccag caagacacta agggcgacta 1080
ccagaaagcg ctgctgtacc tgtgtggtgg agatgactga agcccagacac ggcctgagcg 1140
```

```

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ttgcctaagc attgcctggc cttcctgtct agtctctcct gtaagccaaa gaaatgaaca 1320
ttccaaggag ttggaagtga agtctatgat gtgaaacact ttgcctcctg tgtactgtgt 1380
cataaacaga tgaataaact gaatttgtac ttaraaaaa aaaaaaaaaa aactyrgggg 1440
ggggcccgka cccattggcc ttag                                     1464

```

<210> 56

<211> 985

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (647)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (875)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (962)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (973)

<223> n equals a,t,g, or c

<400> 56

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gactggagga tcttgtaccc agagattccc cgtaagctcc gagagctgga agccgagggc 180
tacaagctgg tgatcttcac caaccagatg agcatcgggc gcgggaagct gccagccgag 240
gagttcaagg ccaaggtgga ggctgtggtg gagaagctgg gggccccctt ccaggtgctg 300
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gccggacgcc cggccaactg ggccccgggg cggaagaaga aagacttctc ctgcgccgat 480
cgctgtttg ccctcaacct tggcctgccc ttcgccacgc ctgaggagtt ctttctcaag 540
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gcgccaggtg cgtccartgt gcccgagccg cggngtacc cctgccgctg cttcctcttc 900
accgccactc tggagcaggc gcgccacaac aaccgggtga gcccgcttca gcccgggaca 960
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<210> 57
<211> 1246
<212> DNA
<213> Homo sapiens

<400> 57
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gcagaggggt tctacaacag cttcctggag cagctgcgta aaacatacag gccggagctt 420
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cgacgtgtcc tctgaacggg agccgtagct caggaggcag aattcagtgt gttatcattg 720
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tctccaayac actcacactg tccatgttct ttttattgcc agggcccgtg ttgaagtgtc 1140
aagagagcaa tcatcaatga taatgtattg tgtgagacct ttgcatcttg taaattttct 1200
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<210> 58
<211> 1966
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1926)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1942)
<223> n equals a,t,g, or c

<400> 58
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tgaaccttca caatttggtt aaatccaaga accttggttt aaacaaatcg ccaagtgtgt 180
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catgagtttg atagargaaa actctaactg catccttccc atcatgtttt ccagccttta 300
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caaaggtgca tcgtgaccaa attgtttaaa aaaaaaaaac aaaaaaaca aaatctaggg 1860
ctgtatttta tatatatata tatatatata tatatatata tatatatata tatatatgtc 1920
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<210> 59

<211> 1611

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<400> 59

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aatatttaat tttcaaaaac ataatagatta atgttccaat tatgcatcac tccccccagk 1560
ataaaaycagg aatgkttgtg agaaaccatt gggaactata ctctttttta a 1611

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<210> 60

<211> 1849

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (100)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (977)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1846)

<223> n equals a,t,g, or c

<400> 60

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tccactttgg ggcgaaaact agagacttgc ttgggggctg cagaagtgcc ctctcctcga 600
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaggngga 1849
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<210> 61
<211> 233
<212> DNA
<213> Homo sapiens
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<400> 61
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tattattccc ttgactcac taattacact gctggaatat aaagaaatga tcctaaatat 180
atatgtagtt ttatggtcct aaatatgtat aaagctttat gatcactcgt gcc 233
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<210> 62
<211> 2333
<212> DNA
<213> Homo sapiens
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<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c
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<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c
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<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c
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<220>
<221> misc feature
<222> (14)
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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2327)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2331)

<223> n equals a,t,g, or c

<400> 62

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ggtgcaatcc agtttgtgac tcagtatcag cattcaagtg ggcagagacg catccgagtg 180
accaccattg ctaggaaactg ggcagatgct caaactcaaa tccaaaacat tgetgcatct 240
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cctgatgaga gttcatatta tcgtcaccat tttatgctgc aagatctgac ccagtctcta 540
attatgattc agcctatcct gtatgcgtat tcttttagtg gaccaccaga gccggttctt 600
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<210> 63

<211> 1470

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1410)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1414)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1419)

<223> n equals a,t,g, or c

<400> 63

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gaggacgcaa cgctcgagaac atgamgatct tgcgtctaata gctgctccac atcaaatacc 180
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gccgctgtgt gccattgcc aagcgcgagc tactgtgggc tggctctgcc gggctggcct 360
gctggctggc aggagtcatc ttcctcgacc ggaagcgcac gggggatgcc atcagtgtca 420
tgtctgaggt cgcctcagacc ctgctcaccg aggacgtgag ggtctgggtg tttcctgagg 480
gaacgagaaa ccacaatggc tccatgctgc ccttcaaacg tggcgccctc catcttgagc 540
tgacggccca ggttcccat gtcccatag tcatgtctc ctaccaagac ttctactgca 600
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cggaagggct gacaccagat gacgtcccag ctctggctga cagagtccg cactccatgc 720
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<210> 64

<211> 939

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<400> 64
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cagggaaccc agccagcaca gcagcagcag ccttgccctct atgagatcaa acagtttctg 480
gagtgtgccc agaaccaggg tgacatcaag ctctgtgagg gtttcaatga ggtgctgaaa 540
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gaagtggggg tgtccctact ctgtagaatc tgggactggg caaatgtttg tgtggcctcc 780
ttaaactagc tgttatgtta tgattttatt ctttgtgagt taattagaat aaagtcattt 840
tcttccaagg tatggttcat ttagtctata gtctctggtt atgaaattag catcctccca 900
gatctgacag ctccctgagg ggttatataa ggagtagct 939

<210> 65
<211> 2068
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (308)
<223> n equals a,t,g, or c

<400> 65
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cgggcagcag gctcctgact acaggtccat tctgagcatt agtgacgarg cagccagggc 120
acaagccctg aacgagcacc tcagcacgcg tagtatgtcc aggggtactc actgtcccag 180
gcagacgtgg acgcgttcag gcagctctcg gccccgcccg ctgaccccca gctcttcac 240

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atcaagaggg cccggcagaa ccacctgttc gagcagtatc gggagaagag gcctgaagcg 660
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gaggacagct ccctgggatt cccggtcgga gggcctggaa ccagcctcag tctcgaggcc 2040
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2068

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<210> 66

<211> 1391

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (16)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (20)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (27)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1343)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1358)
<223> n equals a,t,g, or c

<400> 66
nccacgcgtc cgcggnacgn tggngnttt taaaatgggt ttttttgttg ttgttgatgg 60
ggggggagag ggtccagcat tttttaaatg ttttcacatc gtgtgttcca aaaataactg 120
gttagcctaa gtcacttcca ccctccaatg ttgtgaatgc agtctctagc attcgctatt 180
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aaaaaaaaaa aaaaaaaagg cngggccgca ggcttttnc ctttggtggg ggttattttt 1380
ggcttgccc t 1391

<210> 67
<211> 659
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (139)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (475)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (585)
<223> n equals a,t,g, or c

<400> 67
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gcgcagggcg gtttcctcgg tggcggggtc cgcggttgga gccgagcccg ggcttcgggt 120
gctggccgtg cagcgyttnc ccgtagagca gcgttctgcc gggcttgcca gaccccaaac 180
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cgagggacgc ccagaatcgg acgcggcaga tcatactggg cccaagtgtg acatcgatat 300
gatggtttca cttctgaggc aagaaaatgc aagagacatt tgtgtgatcc argttcctcc 360
agaaatgaga tatacagatt actttgtgat tgtagtgga acttctaccc gacacttaca 420
tgccatggcy ttctacgttg tgaaaatgta caaacacctg aaatgtaaac gtganccctc 480
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tggattcatt tgaatgcttc cagaaaacca gagaaatcta tgganttaga gaaattatgg 600
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<210> 68
<211> 2981
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2858)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2948)
<223> n equals a,t,g, or c

<400> 68
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tcattgttgc tgtgtagtgt ctgtcctaac agtaagaatt ccacggtgac tcgcctcatt 240
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gaaacttact tgaagaagat tcctggattt tgtgaagggg gatttaaaat ccatgagggt 360

gatataaatg cagataaaga ttgtgatgtg ctggttggtt ataaagctgt gtatcggatc 420
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gttgttgcca tgataggggc cgccctcttc atcctcattc agctgggtgct gctggtagat 660
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<210> 69

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature
<222> (584)
<223> n equals a,t,g, or c

<220>
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<222> (590)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (595)
<223> n equals a,t,g, or c

<400> 69
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<210> 70
<211> 1101
<212> DNA
<213> Homo sapiens

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<222> (195)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1080)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1081)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1090)
<223> n equals a,t,g, or c

<400> 70

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<210> 71

<211> 714

<212> DNA

<213> Homo sapiens

<400> 71

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gacagtgttc caggcactta cagaaaagtg gtggctgctc gagccccag aaagggtgctt 180
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cattgcattg tgttctaatt acaagtatgt tgtatttgag atttgcttag attgttgtag 600
tgctgccatt tttattggtg tttgattatt ggaatgggtc catattgtca ctccttctac 660
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<210> 72

<211> 2890

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (555)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2853)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2882)
<223> n equals a,t,g, or c

<400> 72
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<210> 73

<211> 2488

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (277)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (446)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2382)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2412)

<223> n equals a,t,g, or c

<400> 73

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<210> 74

<211> 711

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (696)

<223> n equals a,t,g, or c

<400> 74

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<210> 75
<211> 906
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (362)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (889)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (894)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (897)
<223> n equals a,t,g, or c

<400> 75
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cttaca 906

<210> 76
<211> 271
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<400> 76
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caagtgtggg tctactctt ctagtctctg a 271

<210> 77
<211> 673
<212> DNA
<213> Homo sapiens

<400> 77
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<211> 367
<212> DNA
<213> Homo sapiens

<400> 78
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<211> 1344

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<213> Homo sapiens

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<222> (1319)

<223> n equals a,t,g, or c

<400> 79

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<211> 3748

<212> DNA

<213> Homo sapiens

<400> 80

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<210> 81

<211> 1891

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1869)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1879)

<223> n equals a,t,g, or c

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<210> 82

<211> 1954

<212> DNA

<213> Homo sapiens

<400> 82

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<210> 83

<211> 936

<212> DNA

<213> Homo sapiens

<220>

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<222> (895)

<223> n equals a,t,g, or c

<220>

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<222> (930)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (936)

<223> n equals a,t,g, or c

<400> 83

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<210> 84

<211> 1513

<212> DNA

<213> Homo sapiens

<400> 84

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<211> 1298

<212> DNA

<213> Homo sapiens

<220>

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<222> (3)

<223> n equals a,t,g, or c

<400> 85

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<210> 86

<211> 2009

<212> DNA

<213> Homo sapiens

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<222> (1955)
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<220>
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<400> 87
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<210> 88
<211> 4302
<212> DNA
<213> Homo sapiens

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<222> (1015)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4270)
<223> n equals a,t,g, or c

<220>
<221> misc feature
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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4296)

<223> n equals a,t,g, or c

<400> 88

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<210> 89

<211> 2782

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (82)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (743)

<223> n equals a,t,g, or c

<400> 89

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<210> 90

<211> 1037

<212> DNA

<213> Homo sapiens

<400> 90

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<210> 91

<211> 1052

<212> DNA

<213> Homo sapiens

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<220>

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<222> (962)

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<220>

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<220>

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<222> (1044)

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<220>

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<222> (1048)

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<400> 91

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<210> 92

<211> 1234

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1115)

<223> n equals a,t,g, or c

<400> 92

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<210> 93

<211> 1571

<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (1497)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1516)
<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1546)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1571)
<223> n equals a,t,g, or c

<400> 93
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aaaggggggg n 1571

<210> 94

<211> 1872

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (6)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (51)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1271)

<223> n equals a,t,g, or c

<400> 94

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aatgttgtaa taaatattcc tttgatcttg gtgtttgcaa aaaaaaaaaa aaaaaaaact 1860
cgagactagc gg 1872

<210> 95

<211> 1516

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1505)

<223> n equals a,t,g, or c

<400> 95

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aaggcgcccc caccccaact ccacgggaat ataaacaatt tgtattttcc gatcagggtg 300
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<210> 96

<211> 1770

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (485)

<223> n equals a,t,g, or c

<400> 96

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cgaaatgtag ttttgccaca gactcggggc tcgagtttca gagccacata cctcagcacc 480
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<210> 97

<211> 938

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (183)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (293)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (360)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (938)
<223> n equals a,t,g, or c

<400> 97
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<210> 98
<211> 311
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (297)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (309)
<223> n equals a,t,g, or c

<400> 98
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accaactctc accgctgtct ctttcgtccc cagctccagg ccatgcccgc agccggaggt 180
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taccacagna t 311

<210> 99
<211> 620
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (368)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (570)
<223> n equals a,t,g, or c

<400> 99
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<210> 100
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<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (28)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2456)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2488)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2511)

<223> n equals a,t,g, or c

<400> 100

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<211> 2981

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (293)

<223> n equals a,t,g, or c

<400> 101

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<210> 102

<211> 2804

<212> DNA

<213> Homo sapiens

<400> 102

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<211> 722

<212> DNA

<213> Homo sapiens

<400> 103

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<210> 104

<211> 1636

<212> DNA

<213> Homo sapiens

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<210> 105

<211> 1561

<212> DNA

<213> Homo sapiens

<400> 105

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<211> 486

<212> DNA

<213> Homo sapiens

<400> 106

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<210> 107

<211> 800

<212> DNA

<213> Homo sapiens

<400> 107

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<210> 108

<211> 1058

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (895)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1019)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1054)

<223> n equals a,t,g, or c

<400> 108

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<210> 109

<211> 1076

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (780)

<223> n equals a,t,g, or c

<400> 109

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gctccggggc aatgcagagg cctcccgaa caagcagcag gattgaagct tcggcctccc 960
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa waaaaaaaaa ttgggggggg cccctt 1076

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<210> 110

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 110

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gttgggtggag ttctgcccgg atggaagctc cggccgcgga gtgatggtgg cctcagcgaa 60
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cagcagcgcg agcgtgaaat caacttggtg gcctatcatg gggcatgcca tggggctggt 480
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<210> 111

<211> 3630

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3606)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3608)

<223> n equals a,t,g, or c

<400> 111

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cggccgctcc tcgctgcgct tcgcctccgc ctccctcggac tcggactcgg gtttatatcg 180
cgccctcact catcccagtc ccgggcgagc agcgttggtt ttatgtcttt atttgacgaa 240
aacgacagaa gataccaaaa agttgcaatc aaagatctct tcattctatt gataaagcca 300
ctaataagcc aaaatgtctg tcaatgtcaa ccgcagcgtg tcagaccagt tctatcgcta 360
caagatgcc cgtctgattg ccaaggttga gggcaaaggc aatggaatca agacagttat 420
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aacaataggt aattcttgta aagcctgtgg ctatcgaggc atgcttgaca cacatcataa 720
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gtttgttctg taatgccttt tacatttgga cacatagttt atsetttttt ttggtgtaag 2640
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```

<210> 112

<211> 1526

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1496)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1511)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1512)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1515)

<223> n equals a,t,g, or c

<400> 112

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tcgaccacg cgtccgcagc aggccctgcg cgcggcaaca tggcggggtc caggtggagg 60
tcttgaggct atcagatcgg tatggcattg gcgtccgggc ccgcaaggcg ggcgctagct 120
ggctccgggc agctcggcct tgggggcttc ggggccccga gacgcggggc gtatgagtg 180
ggcgtgcgct ccacgcggaa gtcggagcct cctcccctgg atagggtgta cgagatccct 240
ggactggagc ccatcacctt tgcggggaag atgcacttcg tgccctggct ggcgcgggcc 300
atctttccgc cctgggaccg cggctacaag gacccaaggt tctaccgctc gccccctctt 360

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cacgagcatc cgctgtacaa agaccaggcc tgctatatct ttcaccaccg ttgccgcctt 420
ctcgaggggtg taaagcaggc cctctggctc accaagacca agttaataga aggccttccc 480
gagaaagtgc ttagccttgt tgatgatcca aggaaccaca tagagaacca agacgagtgc 540
gttctgaatg tgatctctca cgcccgtctc tggcagacca ctgaggaaat cccaagaga 600
gagacctact gcccggtcat cgtggacaac ctaatacagc tgtgtaaate tcagattctc 660
aagcatcctt ctctggccag gaggatctgt gtccaaaact ccacgttttc tgctacctgg 720
aaccgagagt ctcttctcct tcaagtccgt ggttctgggt gagcccgact gagcactaag 780
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ccctcttgcc tctcttccac ggaagaggcc tgggccccgt ggagcctcag tgcccgtttg 1440
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ggccgctcaa nnggncccaa gttagt 1526

<210> 113

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (422)

<223> n equals a,t,g, or c

<400> 113

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tggtgttggg attaggagat ctgcacatcc cacaccgggt caacagtttg ccagctaaat 120
tcaaaaaact cctggtgcca ggaataatc agcacattct ctgcacagga aacctttgca 180
ccaaagagag ttatgactat ctcaagactc tggctggtga tgttcatatt gtgagaggag 240
acttcgatga gaatctgaat tatccagaac agaaagtgt gactgttggg cagttcaaaa 300
ttggtctgat ccatggacat caagttattc catggggaga tatggccagc ttagccctgt 360
tgagaggcca atttgatgtg gacattctta tctygggaca cacacacaaa tttgaagcat 420
tngagcatga aaataaatc tacattaatc caggttctgc cactggggca tataatgcct 480
tggaacaaa cattattyca tcattgtgtt gatggatatc caggcttcta cagtggkac 540
ctatgtgtaa tcagctaatt ggagatgaag tgaaagtaga acgga 585

<210> 114

<211> 501

<212> DNA

<213> Homo sapiens

<400> 114

gatgaaaaga aggtttttgc tcttcaaatg cttaagtaaa ctaaaaggca gagctggaaa 60
taaagcccgt attgtggact ccaagtaatg ctctttctgc tacaccatac tttgtggtgt 120

```

ctgctcccat gtgcttcttc gctaaggctg atcaaaaaag ttagtaggtt gcttcagcta 180
taagaatttg atggtcttcc ttagtcatca tagtctgcag caatcatttt tgttcatcat 240
tgggatgtct gcttactcct gttgagtaaa tgtgatctat tcacccttgg ragctccttg 300
cacaccaaca gtattcttgg atagggacaa gtgttgctta agtcagtgc gatttcttta 360
gcataataaa aggtccatg taggatgcta atacttgagt gaaatatgct tcataagcag 420
ccttgttttg acagagttgg tgtaaagtga gggtatgtct tggcctgagc gtcttcaaag 480
catgtgccac tttgtgcac t 501

```

<210> 115

<211> 1965

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (338)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (343)

<223> n equals a,t,g, or c

<400> 115

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agaggcggca ctggcggcaa gagcagacgc ccgaaccgag cgagaagagc ggcagagcct 60
tatcccctga agccggggccc cgcgtcccag mcctggccca aaggcaggag cagcagacaa 120
gagtgcagtg gtggctgccg ccgcaccagc ctacgtggca gatgacacac cccccccga 180
gcgtcggaac aagagcggta tcatcagtga gcccctcaac aagagcctgc gccgctccc 240
cccgtctctc cactactctt cttttggcag cagtgggtgt agtggcgggt gcagcatgat 300
gggaggagag tctgctgaca aggccactgc ggctgcanc tgnctccct gttggccaat 360
gggcatgacc tggcggcgcc catggcgggt gacaaaagca accctacct aaagcacaaa 420
agtgggtgct tggccagcct gctgagcaag gcagagcggg ccacggagct ggcagccgag 480
ggacagctga cgctgcagca gtttgcgcag tccacagaga tgctgaagcg cgtggtgcag 540
gagcatctcc cgctgatgag cgaggcgggt gctggcctgc ctgacatgga ggctgtggca 600
ggtgccgaag ccctcaatgg ccagtccgac ttccctacc tgggcgcttt ccccatcaac 660
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gcgggcctgg ctgagtacc catgcaggga gagctggcct ctgccatcag ctccggcaag 780
aagaagcggg aacgctgcgg catgtgcgcg ccctgccggc ggcgcacaa ctgcgagcag 840
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gaactcaaaa agaagccttc cgctgctctg gagaaggtga tgcttccgac gggagccgcc 960
ttccggtggt ttcagtgcg cggcggaac ccaaagctgc cctctccgtg caatgtcact 1020
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acaaaaaata ttctctcaca gatttcattc ctgtttttat atatatattt tttgtgtc 1140
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tccgaccatg aaatagtga tagtttgctt ggagaatcca ctcacgttca taaagagaat 1500
gttgatggcg ccgtgtagaa gccgctctgt atccatccac gcgtgcagag ctgccagcag 1560
ggagctcaca gaaggggagg gagcaccagg ccagctgagc tgcaccacaa gtcccagac 1620

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tgggatcccc caccccaaca gtgatttttg aaaaaaaaaat gaaagttctg ttcgtttatc 1680
cattgcgatac tggggagccc catctcgata tttccaatcc tggctacttt tcttagagaa 1740
aataagtccct ttttttcttg ccttgctaata ggcaacagaa gaaagggctt ctttgcgtgg 1800
tcccctgctg gtgggggttg tcccagggg cccctgctg ctgggcccc ctsccacggc 1860
cagcttcctg ctgatgaaca tgctgtttgt attgttttag gaaaccaggc tgttttgtga 1920
ataaaacgaa tgcattgttg tgacacgaar maaaaaaaaa aaaaa 1965

<210> 116

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (299)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1060)

<223> n equals a,t,g, or c

<400> 116

gaaacacata cattggatat gggaagatgg cggctgtgtc ggtgtatgct ccaccagttg 60
gaggcttctc ttttgataac tgccgcagaa tgccgtcttg gaagccgatt ttgcaaagag 120
gggatacaag cttccaaagg yccggaaaac tggcacgacc atcgctgggg tggctataaa 180
ggatggcata gttcttgagg cagatacaag agcaactgaa gggatggttg ttgctgacaa 240
gaactgttca aaaatacact tcatactctc taatatattat tggtgtggtg ctgggacanc 300
tgcagacaca gacatgacaa cccagctcat ttcttccaac ctggagctcc actccctctc 360
cactggccgt cttcccagag ttgtgacagc caatcggatg ctgaagcaga tgcttttcag 420
gtatcaagggt tacattggtg cagccctagt tttaggggga gtagatgtta ctggacctca 480
cctctacagc atctatcctc atggatcaac tgataagttg ccttatgtca ccatgggttc 540
tggctccttg gcagcaatgg ctgtatttga agataagttt aggccagaca tggaggagga 600
ggaagccaag aatctggtga gcgaagccat cgcagctggc atcttcaacg acctgggctc 660
cggaagcaac attgacctct gcgtcatcag caagaacaag ctggattttc tccgcccata 720
cacagtggcc aacaagaagg ggaccaggct tggccgggtac aggtgtgaga aagggactac 780
tgcatgcctc actgagaaaa tcaactcctc ggagattgag gtgctggaag aaacagtcca 840
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gagcattgag gccagtaag acactcatgt ggctagtgtt tgccgaatga aactcaactc 960
aataaaaaac aaaaccacaa ttgggcagct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1060

<210> 117

<211> 709

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (174)

<223> n equals a,t,g, or c

<400> 117

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gacttgtctg atcacccaat ggaagtggat acttgtaaag tctacaccac tgtacttggc 120
gttaaatctt gctgaattcg tggtaagctg ttaccatgtc tacattttgt agantgattt 180
tggctctgcag caaaattcga ttctacttct cataccctt tccttccact tgaaatgcaa 240
tttagacaga ggccctgtgg tgaaagtgc aatattaagt ttmcccttag aagatcccyt 300
cctcaaacct cagaaccct agcagtgtta ccctwaaaca aaaatgagct cgagaaaaaa 360
gtagctcagt tacagagaag caaatcgagt tatttcccca cataaaaagt ttccccagat 420
tctaagaatt gcagtatcct gtaccctaaa atttttcaag gtgactcctg ttgtcgtctg 480
ttgataactt taataaaggc catttaagga cataagtttt taaagactcc caaagtgaaa 540
cttaaacatt ttcgggatta tcgattgcat atatcagttt atgctgtgtg ctgaattact 600
atgccatgtg ctatttttagt gtttggggaa aatgaaaaat aaaatttggt ctttagctta 660
ataaatatgt cttattttta aaaaaaaaaa aaaaaactcg agactagct 709
```

<210> 118

<211> 2053

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (813)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2049)

<223> n equals a,t,g, or c

<400> 118

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ctccttggcg cctgtcccca cgcccccg agcgtgacca cgatgctccc cataccccac 60
ccattcccga tacaccttac ttactgtgtg ttggcccgagc cagagtgagg aaggagtgtg 120
gccacattgg agatggcggg actgagcaga catgccccca cgagtagcct gactccctgg 180
tgtgtcctcg gaaggaagat cttggggacc cccccaccgg agcacacca rggatcatct 240
ttgcccgtct cctggggacc cccaagaaa tgtggagtcc tcgggggccc tgcaactgatg 300
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gggggagtgc tgggtagga agtggtcccg ggagattttg gatggaaaag tcaggaggat 420
tgacagcaga cttgcagaat tacatagaga aattaggaac ccccaaattt catgtcaatt 480
gatctattcc cctcttttgt ttcttggggc atttttcctt tttttttttt ttttgtttt 540
tttttaccct tccttagctt tatgcgtca gaaaccaa ataaaccccc ccccatgtaa 600
caggggggca gtgacaaaag caagaacgca cgaagccagc ctggagacca ccacgtcctg 660
cccccgcca ttatcgccc tgattggatt ttgttttca tctgtccctg ttgcttgggt 720
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ggggggggnc cgg 2053

<210> 119

<211> 1824

<212> DNA

<213> Homo sapiens

<400> 119

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gctgagtgggt tacactttgc aagctgtgggt gaagatcaca ctgtgaagat acacagagtc 1800
aataaatgtg cactgtaatg gaaa 1824

<210> 120

<211> 606

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (144)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (155)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (598)

<223> n equals a,t,g, or c

<400> 120

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aggccttgac ttaaaaacttt ctttgtactg tgatttcctt ttgggtgtat ttgctaagt 480
gaaacttggt aaattttttg ttaactaaat ttttttctta aaataaagac tttttcacia 540
wraaaaaaaa aaaaaaaaaa actcgagggg gggcccgtac ccaatgcct gtgatgtntc 600
gtatac 606

<210> 121

<211> 838

<212> DNA

<213> Homo sapiens

<400> 121

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<210> 122

<211> 656

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (41)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (218)

<223> n equals a,t,g, or c

<400> 122

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaggggggg gggcggacgc gtgggc 656

<210> 123

<211> 1386

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1283)

<223> n equals a,t,g, or c

<400> 123

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cattgg 1386

<210> 124

<211> 845

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (823)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (825)

<223> n equals a,t,g, or c

<400> 124

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catcgtgggt gagtactgtg aaccttgcgg cttcgaggcg acctacctgg agctggccag 180
tgctgtgaag gagcagatc cgggcatcga gatcgagtcg cgctcgggg gcacaggtgc 240
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cttcgcctcg gtaatacctg tctgatgcc aagatattat ttattctccc ctaaccacag 720
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa atntnggggg ggggcccccc 840
cccccc 845

<210> 125

<211> 1656

<212> DNA

<213> Homo sapiens

<400> 125

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gcagtgcagg gccccacact cccartgcgg aggctgctga gccagaggcc agactggcgg 240
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<210> 126

<211> 837

<212> DNA

<213> Homo sapiens

<400> 126

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aaaattccag ttattttatt ccaaaatggt ttgaaacagt ataatttgac aaagaaaaat 180
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<210> 127

<211> 1217

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1168)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1169)

<223> n equals a,t,g, or c

<400> 127

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<210> 128

<211> 1349

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (57)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1133)

<223> n equals a,t,g, or c

<400> 128

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<210> 129

<211> 2318

<212> DNA

<213> Homo sapiens

<400> 129

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<210> 130

<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (787)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (819)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1518)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2116)
<223> n equals a,t,g, or c

<220>
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<222> (2147)
<223> n equals a,t,g, or c

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<210> 131
<211> 1020

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (11)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1019)

<223> n equals a,t,g, or c

<400> 131

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<210> 132

<211> 2319

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (10)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2246)

<223> n equals a,t,g, or c

<400> 132

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ttgggaccgg cggtgatgc aggatgacaa ccggggccta ggccaagggc tcaaggacaa 180
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caagagaacc tgcaaccgtt tccgcctcct gctagagcgg cgaaccrtgg gcagtgaggt 240
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gaacgccccg gcgctcgctc tgctgtagc caggatgcag ctcccaggcc ctggctctgcg 360
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actaagacca ctctgaacga tgataatgag tttgggggt 2319

<210> 133

<211> 1373

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (403)

<223> n equals a,t,g, or c

<400> 133

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ttttattttt caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1373

<210> 134

<211> 1657

<212> DNA

<213> Homo sapiens

<400> 134

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gtaaaacaga ccatacagta catttcagga tttaatgaaa cctgcttgag atggagaagc 180
atcaagacag ctgatatgga ggagatgtat ttattccaca tttggggcca gagatggtat 240
cagaaggaat ttgccagga aatgacctt aatatcagta gcagcagccg agatcccgag 300
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<210> 135

<211> 2360

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1517)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2330)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2353)

<223> n equals a,t,g, or c

<400> 135

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aactgttagt ttttttgaag tagtttttcc cakgtttaat ttgtatttgg ttaaaaaaac 2280
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tccaatttaa cntgggatt 2360

<210> 136

<211> 1042

<212> DNA

<213> Homo sapiens

<400> 136

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cccggccggc ctgctgagtt tctcatctca caaccgcgc ttcggggccgc gcgaaggaca 180
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aatgacttat ttgaaaatcc agtcctttat taatagaatg gaggaagcc tgaatatagt 720
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<210> 137

<211> 1037

<212> DNA

<213> Homo sapiens

<400> 137

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ccggccggcg gaccgaagaa cgcaggaaag gggccggggg gacccgcccc cgccggcgcc 180
cagccatgaa ctccaacgtg gagaacctac cccgcacat catccgctg gtgtacaagg 240

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<210> 138

<211> 1490

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1225)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1239)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1348)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1452)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1487)

<223> n equals a,t,g, or c

<400> 138

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caagacagta aggattcaaa ccatttgcca aaaatgagtc taagtgcatt tactctcttc 120
ctggcattga ttggtggtac cagtggccag tactatgatt atgattttcc cctatcaatt 180
tatgggcaat catcaccaaa ctgtgcacca gaatgtaact gccctgaaag ctaccaagt 240
gccatgtact gtgatgagct gaaattgaaa agtgtaccaa tggtgccctc tggaatcaag 300

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tatctttacc ttaggaataa ccagattgac catattgatg aaaaggcctt tgagaatgta 360
actgatctgc agtggctcat tctagatcac aaccttctag aaaactccaa gataaaagg 420
agagttttct ctaaattgaa acaactgaag aagctgcata taaaccacaa caacctgaca 480
gagtctgtgg gccacttcc caaatctctg gaggatctgc agcttactca taacaagatc 540
acaaagctgg gctcttttga aggattggta aacctgacct tcatccatct ccagcacaat 600
cggctgaaag aggatgctgt ttcagctgct tttaaaggtc ttaaatcact cgaatacctt 660
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gttgaggaa acagccagtt ttaaaatcct taaacttaag ttctcaagc tggataaaac 1440
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<210> 139

<211> 1684

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (93)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (201)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1657)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1659)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1682)

<223> n equals a,t,g, or c

<400> 139

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gctcccctgc ccctccggga gcgcgcgggg cngggcgggg cggggcgggg ccaggcgggc 120
gagctggggc ctcgccctc cctcgggcgg tcacctgggc acgggcgctg cagggtgcgg 180
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ggaargaamc gctctcgstt cgtcctacac ttgcgcaaat gtctccgagc ttactcacat 360
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aaaagtgaat ttaaataagg agatcatcag tcaaggaaga cccactggag aggacagaaa 480
atgaagcagt gttttatcat gtgtatttca gcaggctctt ttgaaattta actaaaaata 540
tgactgctct ctcttcagag aactgctctt ttcagtacca gttacgtcaa acaaacaccg 600
ccctagatgt taactatctg ctattcttga tcatacttgg gaaaatatta ttaaatatcc 660
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cactagcatt cgttgatctt ttacttttgg taaacatttc cattatattg tatttcagg 780
attttgact ttaagcatt aggttcaact aataccacat ctgcctattt actcaaatta 840
tttcctttac ttatggcttt ttgcattatc cagttttcct gacagcttgt atagattatt 900
gcctgaattt ctctaaaaca accaagcttt catttaagtg tcaaaaatta ttttatttct 960
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tcttatattt tcctttttca tcccactcca gttatactgt gagatctaaa aaaatattct 1260
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cnac 1684
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<210> 140

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (395)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (417)

<223> n equals a,t,g, or c

<400> 140

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cctccaagcc tgctgccagc tccttgcaag cccctcaggt tgggccttgc cacggtgcc 120
gcaggcagcc ctgggctggg ggtaggggac tccctacagg cagcagccc tgagacctca 180
gagggccacc ccttgagggt ggccaggccc ccagtggcca acctgagtc tgccctctgc 240
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accagccctg ctggcccctg gttccgctgg cccccagat gcctggctga gacacgcat 300
ggcccttcag ctggcccaca cytyttcccg gscctggaa kttggcaytg cagcagacag 360
ytccytgggc accagrcagy taacaggaca cagcngccag cccaaacagc agcgggnatg 420
ggggcag 427

<210> 141
<211> 889
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (60)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (698)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (889)
<223> n equals a,t,g, or c

<400> 141
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ccgttgggga aggattgaat acagagacgc tgtctgcttg ctgccttaag acagctagct 180
gaattgctga ttaactttta aaatacccag cttgggttat ttttcttaga atctgttgct 240
aagactgggg acgctgtttt cttttacaaa gggaaatcta agttaatttc aaggcattcg 300
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ttaaaaaggc ttaccgaaaa caagccctca aatttcatcc ggacaagaac aaatctcctc 420
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catttttcgg aggtccaac ccctttgaaa ttttcttttg aagacgaatg ggtgggtggt 660
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<210> 142
<211> 1505
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1493)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1499)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1500)
<223> n equals a,t,g, or c

<400> 142
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acttcacgca gcaaaagcgc cccccgtcta tatcatatcg cctctcggtc ctcctaaaag 180
tcgtatgaga tggagctgga ggaggggaag gcaggcagcg gactccgcca atattatctg 240
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caggcacaga ggaacgaact aaatgctaaa gtgcgcctat tgcgggagga gctacagctg 360
ctgcaggagc agggctccta tgtgggggaa gtagtccggg ccatggataa gaagaaagtg 420
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tcaacttatg agatgattgg tggactggac aaacagatca aggagatcaa agaagtgatc 660
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aagttagtgg acagcctttg tgtgtatctc tccaataaag ctctgtgggc caagtcaaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aanggggggnn 1500
cccccc 1505

<210> 143
<211> 1235
<212> DNA
<213> Homo sapiens

<400> 143
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ctccgcggag gaccacaggag agccggacta ggaccagggc cctgggcctc cccacactcc 180
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<210> 144

<211> 1420

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1385)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1396)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1400)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1410)

<223> n equals a,t,g, or c

<400> 144

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actcacagcc catctgatct gttcaaagct gtcttttcca cctgctgaaa ttcattaaat 180
cactggaggc atgcataatg aatggagaat gagtgaactt ccaatgcaac ttggattcac 240
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<210> 145

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1882)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1898)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1919)

<223> n equals a,t,g, or c

<400> 145

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<210> 146

<211> 1379

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (925)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1371)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1377)

<223> n equals a,t,g, or c

<400> 146

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cgattctggc agaataaaca ggtgttttta gttttcccac tgtctgagcc aagcaggacc 180
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<210> 147

<211> 514

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (406)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (412)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (418)

<223> n equals a,t,g, or c

<400> 147

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cagtacaatt taaagaccac tatgtgtccc cggagaccaa cctgtttatt tccctgaaag 240
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gacgcgtggg cggacgcgtg ggcggacgcg tggg 514

<210> 148

<211> 2058

<212> DNA

<213> Homo sapiens

<400> 148

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tctgcgttca gggacctcgt cctttgctgg ctgtggagcg gactgggcag cgccccctgt 180
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2058

<210> 149

<211> 1781

<212> DNA

<213> Homo sapiens

<400> 149

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taactcccag ggggttgact ggtggggtaa ctgagcctgc tttgcagtag gtcaccctgc 180
caaacaagct aatatggaaa ccacatgtaa cttagccaga ctataccttg tgtagcttca 240
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<210> 150

<211> 1709

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1612)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1660)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1678)

<223> n equals a,t,g, or c

<400> 150

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gttgaggggc tgagttttga caccaatgag cagtcgctgg agcaggtctt ctcaaagtac 180
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<210> 151

<211> 922

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (906)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (915)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (922)

<223> n equals a,t,g, or c

<400> 151

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cacctcgggg acattattgc gcgtggaacg gctgctttt gaagactatt gccagaaga 180
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<210> 152

<211> 635

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (13)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (594)

<223> n equals a,t,g, or c

<220>

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<222> (614)

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<222> (616)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (628)

<223> n equals a,t,g, or c

<400> 152

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ggtcgggcta agcggcggtat gcagtacaac cggcgctttg tcaacgttgt gccacacctt 480
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ttscctata gggngncgtt taaattcntt ggcgg 635

<210> 153

<211> 2328

<212> DNA

<213> Homo sapiens

<400> 153

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<210> 154
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<212> DNA
<213> Homo sapiens

<220>
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<222> (80)
<223> n equals a,t,g, or c

<400> 154
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<211> 1006

<212> DNA

<213> Homo sapiens

<400> 156

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<210> 157

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 157

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<210> 158

<211> 4147

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (13)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (292)

<223> n equals a,t,g, or c

<220>

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<222> (4145)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4146)

<223> n equals a,t,g, or c

<400> 158

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<211> 1242

<212> DNA

<213> Homo sapiens

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<222> (1235)

<223> n equals a,t,g, or c

<220>

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<222> (1236)

<223> n equals a,t,g, or c

<400> 159

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<210> 160

<211> 2229

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (29)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (43)

<223> n equals a,t,g, or c

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<222> (55)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (59)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (128)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (301)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2226)

<223> n equals a,t,g, or c

<400> 160

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<210> 161

<211> 1920

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (119)

<223> n equals a,t,g, or c

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<222> (1755)
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<222> (1766)
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<222> (1832)
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<222> (1841)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (1915)
<223> n equals a,t,g, or c

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<210> 162

<211> 2619

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (2546)

<223> n equals a,t,g, or c

<400> 162

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<210> 163

<211> 1419

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (230)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (624)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (697)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1187)

<223> n equals a,t,g, or c

<400> 163

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<210> 164

<211> 3810

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (189)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2523)

<223> n equals a,t,g, or c

<400> 164

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<210> 165

<211> 817

<212> DNA

<213> Homo sapiens

<400> 165

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<210> 166

<211> 1578

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (16)

<223> n equals a,t,g,,or c

<220>

<221> misc feature

<222> (38)

<223> n equals a,t,g, or c

<400> 166

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aatcttcg gggggggg 1578

<210> 167

<211> 1694

<212> DNA

<213> Homo sapiens

<400> 167

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aaaaaaaaact cgag 1694

<210> 168

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 168

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<210> 169

<211> 667

<212> DNA

<213> Homo sapiens

<400> 169

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tacccaa 667

<210> 170

<211> 3598

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (16)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (22)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (964)

<223> n equals a,t,g, or c

<400> 170

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<210> 171

<211> 940

<212> DNA

<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (12)

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<220>

<221> misc feature

<222> (919)

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<221> misc feature
<222> (935)
<223> n equals a,t,g, or c

<220>
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<222> (938)
<223> n equals a,t,g, or c

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<210> 172
<211> 1458
<212> DNA
<213> Homo sapiens

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<210> 173

<211> 2709

<212> DNA

<213> Homo sapiens

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<222> (2595)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2622)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2659)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2670)

<223> n equals a,t,g, or c

<400> 173

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<210> 174

<211> 1013

<212> DNA

<213> Homo sapiens

<400> 174

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<210> 175

<211> 1697

<212> DNA

<213> Homo sapiens

<400> 175

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aaaaaaaaa aaaaaaa 1697

<210> 176

<211> 1409

<212> DNA

<213> Homo sapiens

<400> 176

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aaaaaaaaaa aaaaaaaaaa aaactcgag 1409

<210> 177

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 177

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<210> 178
<211> 1378
<212> DNA
<213> Homo sapiens

<220>
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<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (82)
<223> n equals a,t,g, or c

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<210> 179
<211> 2251
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2020)
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2050)

<223> n equals a,t,g, or c

<400> 179

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<210> 180

<211> 1000

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (20)

<223> n equals a,t,g, or c

<400> 180

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actgtttgga ttttaattgt gatgcagaag ttatagtaac aaacatttg tttgtacag 900
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aaaaaaaaaa aaaaaaaaaa maaaaaaggg gggggccccc 1000
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<210> 181

<211> 1429

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (761)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1407)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1420)

<223> n equals a,t,g, or c

<400> 181

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actgggactc ccagcagagc ccaccagcca gccctggccc acccccagc ctccagagaa 60
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gcatgatgcc ctcccctcag cgcaggctgc agagcccggc cccacctccc tgcgcccttg 180
agggggcccca gcgtctgcag ggtgacgcct garacagcac cactgctgag gagtgaggac 240
tgtcctccca cagacctga gtgaggggcc ctccatgcgc agatgagggg ccactgacct 300
acctgcgctt ctgctggagg aggggaagct gggcccaaag gccmgsgrag gcagcgtggg 360
ctctgccaat gtgggctgcc cctcgcacac agggctcaca gggcaggcct tgctggggtc 420
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cagggctggt ggaggacccc gagggctgag gagcagcagg acccgctgc tcccatcctc 480
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<210> 182

<211> 2725

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2713)

<223> n equals a,t,g, or c

<400> 182

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tacagccagg cctgccaccc cttaggctcc aaagtccgga ggtgcagaaa gccaggacca 180
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tatgggattc acctctactt caccatctg gacattgagc tgcagagaa ctgtgcgtat 420
gactcagtgc agataatctc aggagacact gaagaaggga ggctctgtg acagaggagc 480
agtaacaatc cccactctcc aattgtggaa gagttccaag tccatacaa caaactccag 540
gtgatcttta agtcagactt ttccaatgaa gacgtttta cggggtttgc tgcatactat 600
gttgccacag acataaatga atgcacagat tttgtagatg tccctgtag ccacttctgc 660
aacaatttca ttggtggtta ctctgtctcc tgcccccg aatatttcct ccatgatgac 720
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gactaatcca gatacatccc accagcctct ccaagggtgg tgaccaatgc attaccttct 2340
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tggtcataca tttgtgttct gactccttgg ggtcctttcc ccggagtacc tattgtatag 2520
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aaaaaaaaa aaaaaaaaaa aaaag 2725

<210> 183

<211> 1751

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (344)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (416)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1617)

<223> n equals a,t,g, or c

<400> 183

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gtggtctgtg ggtctcaga gcagaccacc tgccaggaag tggatcatgc actagcccaa 180
gcaataggcc agactggcgg ctttgtgctt gtgcagcgcc ttcgggagaa ggagcggcag 240
ttgctgccac aagagtgtcc agtgggcgcc caggccacct gcggacagtt tgccagcgat 300

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tgtccacccc cggaacgctg cctaattcgt gccagcctcc ctgtaaagcc acgggntgcg 420
ctgggctgtg agccccgcaa aacactgacc cccgagccag cccccagcct ctcacgccct 480
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cgggagaggt ccttcactgt gtgtacacag caagagcatg tgtgtgccac ttccccctacc 1680
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aaaaaaaaa a 1751
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<210> 184

<211> 2200

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2096)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2140)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2157)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2181)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2184)

<223> n equals a,t,g, or c

<400> 184

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catgtgtgtg aaaccatcat ccgcatcttt aaaagacatg gagctgttca gttgtgtact 120
ccactactgc ttccccgaaa cagacaaata tatgagcaca acgaagctgc cctattcatg 180
gaccacagcg ggatgctggt gatgcttcct ttgacctgc ggatcccttt tgcaagatat 240
gtggcaagaa ataatatatt gaatttaaaa cgatactgca tagaacgtgt gttcaggccg 300
cgcaagttag atcgatttca tcccaaagaa cttctggagt gtgcatttga tattgtcact 360
tctaccacca acagctttct gccactgct gaaattatct acactatcta tgaaatcatc 420
caagagtttc cagcacttca ggaaagaaat tacagtatct atttgaacca taccatgtta 480
tgaaagcaa tactcttaca ctgtgggac ccagaagata aactcagtca agtctacatt 540
attctgtatg atgctgtgac agagaagctg acgaggagag aagtgggaagc taaattttgt 600
aatctgtctt tgtcttctaa tagtctgtgt cgactctaca agtttattga acagaaggga 660
gatttgcaag atcttatgcc aacaataaat tcattaataa aacagaaaac aggtattgca 720
cagttggtga agtatggctt aaaagaccta gaggagggtt ttggactgtt gaagaaactc 780
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tactggaata atggaatgtt gtacattcat cataatttaa aattaaattc taagaagagg 1920
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gcttgaaacc aggagtttga gaccagcctg agcaacaaag caagacccca tctctataaa 2040
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tgagatggat catctgagcc tcaggagggt gacgctgcan tgactgtgac tgcgccnctg 2160
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<210> 185

<211> 1987

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (523)

<223> n equals a,t,g, or c

<400> 185

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ggaaatatga ctttgattct tcggagggtc ttcagggact ggactttttt ggaaacaaga 180
agtctgtccc aggtgtgtgt ggagcatcac aaacacatca gaagcccaa aatggagaga 240
aaaaagaaga gaggctaact gaaaggaaga gggagcagag caagaaaaaa aggaagacga 300
tgacttcaga aattgcttcc caagaagaag gtgctactat acagtggatg tcactctgtag 360
aagcaaagat tgaagacaaa aaagttcaga gagaaagtaa actaacttcc ggaaagtgg 420
agaatctcag aaaagaaaag ataaacttct tgcggaataa acacaaaatt cagtcctaag 480
gaaccgatct tcctgaccca attgctacat ttcagcaact tgnaccagga atataaaatc 540
aattctcgac tacttcagaa cattctagat gcaggtttcc aaatgcctac gccaatccaa 600
atgcaagcca tcccagttat gctgcatggt cgggaacttc tggttctgct tccaactgga 660
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aagaaaaaga tgattaagaa accattggaa agggagagca ttagtacaac tccaaaatgt 1740
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gtagctcttg aagacaaaag ttaaaaacag actttaaaaa tactgtccca gaaatgtaat 1860
tttatgatcc cagcatgaat gttattttca tggaataact gaagtcttac agtcacctgt 1920
accaaacatt tgaatcaac tacaagtaca tgggactggt gataaatgat cctaaactat 1980
caagtca 1987
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<210> 186

<211> 1737

<212> DNA

<213> Homo sapiens

<400> 186

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ggatgatatg tgggcaaaat cacttatgaa agtagaagca agaatacagt gggttgctac 180
cacataaagc catgctgttt ttggtcaaac tgtgtaaact ggaaaaattc acatcatttc 240
tgagtttaat cacttttaga tatattcaca ttgttttggg gaatttgctg aattgaattg 300
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aagggaata aaagtctttt gaaggtagct atactagcac ttttgatcat cttcagggcc 540
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gtatatattt cttgccataa tggtaaagga ctgattgata tatttaagag ttaataaatt 1680
tgtgatttct gctgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1737
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<210> 187

<211> 1132

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1131)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1132)

<223> n equals a,t,g, or c

<400> 187

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agatcctgga gtcccagagg cccctgcag gcacccctgt agcccatcc agtggtgag 180
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gtcacatatc accgtggtga tggcgtcacg tggccatgta gacgtcacga agagatatag 480
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<210> 188

<211> 1267

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (12)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (25)

<223> n equals a,t,g, or c

<400> 188

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<210> 189

<211> 3787

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (22)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (155)

<223> n equals a,t,g, or c

<400> 189

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<210> 190

<211> 554

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (520)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (542)

<223> n equals a,t,g, or c

<400> 190

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<210> 191

<211> 874

<212> DNA

<213> Homo sapiens

<400> 191

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<210> 192

<211> 2103

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (140)

<223> n equals a,t,g, or c

<400> 192

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<210> 193

<211> 1317

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1314)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1315)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1316)

<223> n equals a,t,g, or c

<400> 193

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<210> 194

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1231)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1240)

<223> n equals a,t,g, or c

<400> 194

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<210> 195

<211> 1688

<212> DNA

<213> Homo sapiens

<400> 195

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ccaaggcatc cgctgaagac caacccatca cctcagttgt tttttatatt tctaataaag 1620
tcatgtctcc cttcatgttt tttttttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1680
aaaaaaaaa 1688

<210> 196

<211> 756

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (756)

<223> n equals a,t,g, or c

<400> 196

ggcacgagcc gccctcggcg tcctctgtag cgggacacct aggccgggg acccgagcg 60
aggtagaggc cagggcagcg cgtccgggag cggagtccgc gcccgccgc gccatgccg 120


```

acagctggga caaggatgtg taccctgagc ccccgcgccg cacgccggtg cagcccaatc 180
ccatcgctcta catgatgaaa gcgttcgacc tcatcggtga ccgacccgtg accctcgtga 240
gagaatttat agagcggcag caccgaaaaga acaggtatta ctactaccac cggcagtacc 300
gccgcgtgcc agacatcact gaggcaagg aggaggacat catgtgcatg tatgaagccg 360
aaatgcagtg gaagagggac tacaaagtcg accaagaaat tatcaacatt atgcaggatc 420
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tggagcagtt caccaggtg gccaaaggct accaggaccg ctatcaggac ctgggggcct 540
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ctgcaaaaaga ggcgcgcgt gccacctcct gaggcagctg tgggtgcccc tgcgtgtgtg 660
ctctgtatga ctgttctga aatataaagc cctgcaacct gaaaaaaaaa aaaaaaaaaa 720
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaattn 756

```

<210> 197

<211> 1471

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (458)

<223> n equals a,t,g, or c

<400> 197

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ccaagcgttc ctctgccgga catacaagag ttccccaact atgaggtgat tgatgagcag 120
acaccctgt actcagcaga tccaaacgcc atcgatacgg actattacc cggaggctac 180
gacatcgaaa gtgattttcc tccaccccca gaagacttcc ccgcagctga tgagctacca 240
ccgttaccgc ccgaattcag caatcagttt gaatccatcc accctcctag agacatgcct 300
gccgcgggta gcttgggttc ttcacaaaga aaccggcaga ggttcaactt gaatcagtat 360
ttgcccaatt tttatccctt cgatatgtct gaacctcaaa caaaaggcac tggtgagaat 420
agtacttgta gagaacccca tgccccttac ccgccagngt atcaaagaca cttcgaggcg 480
cccgtgtcg agagcatgcc catgtctgtg tacgcctcca ccgcctcctg ctctgacgtg 540
tcagcctgct gcgaagtgga gtccgaggtc atgatgagt actatgagag cggggacgac 600
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ctctcaactc ccccaaaagt gcctgacttt agtgaaccta gaggtgatgt gagtaatccg 720
cgctgttctt tgcagcagtg cttccaagct ttttttggtg agccgaatgg gcatggctgc 780
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cctgttttaga accaaaacca ccatgacaca gtttttatag tgtctgtata tttgtgatgc 1380
aatggtcttg taaaggtttt taatgaaaac taccattagc cagcttttct tactgacaat 1440
aaattattaa taaaataaaa aaaaaaaaaa a 1471

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<210> 198

<211> 692

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (43)

<223> n equals a,t,g, or c

<400> 198

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gtgaattggt aattcgacct cccctatagg gccgaatttg ggntaccggg cccccccctt 60
agtgcggcct gctcttgga gttcaggctc ggttgtcttt tgggagccat ggagagtgc 120
ttttatctgc gttactacgt ggggcacaag ggcaagtctg gccacgagtt cctggagttt 180
gagtttcgac cggacgggaa gttaagatat gccacaaca gcaattacaa gaatgatgtc 240
atgatcagaa aagaggctta tgtacataaa agcgtgatgg aggaactgaa gagaataatt 300
gacgacagtg aaattaccaa agaggatgat gcattgtggc ctccctcctga ccgagtgggc 360
cggcaggagc ttgaaatcgt cattggagat gaacacattt cttttacaac atcaaaaatt 420
ggttccctta ttgatgtcaa tcaatccaag gatccagaag gcttacgagt attttattat 480
cttgtccagg acctgaagtg tttggtcttc agtcttattg gattacactt caagattaaa 540
ccaatctaga ctgaatattg gtgtggacat ggggggtggg tgggagtaga aaattttgtg 600
tatatcaggg cagtattttt ttatgaacta taaatgattg tctttaataa atatgtgata 660
aatccaatt tttattattt tataaagacc tg 692
```

<210> 199

<211> 1573

<212> DNA

<213> Homo sapiens

<400> 199

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ctcgtgccga attcggcacg agccggcgcc agctacgccg ctgccgctgt cactatggcc 60
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gtgctggaca cgctgaccaa ggtgttggtg gccttatatg aagaaccaga gaaacctaac 180
agtgcctttg attttttaaa gcatcactta ggagctgcta ctccagaaaaa tccagaaata 240
gagctgcttc gcctagaact ggccgaaatg aaagagaagt atgaagctat tgtagaagaa 300
aataaaaaac tgaaagcaaa gcttgctcag tatgaaccac ctccaggagga gaagcgtgct 360
gaataggatt ctctcagtt tgaaagacaa tgaaaaatgg ttttgtatga cttgaatagt 420
ttgtatagta tataatcttt tctgaacaga tgctatagaa ctcttttaat atgtttaatt 480
cacctatcac actctgttaa aaacacatag aatcatcaat aaaaactcaa tataactttc 540
tttgggtctt aaagcaggag aatccaaaat aaatcctgaa caaaacctaa acacagccat 600
ctaactcatt accttaaaag acattctgkt tattagtctg attaggaatg atggcactgg 660
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acacaggtac agtcattctt tgaaggtgac actgttctgt atattcccta taggcagctg 780
gagagatctg tgtgacacaa gatgcttttg tacgggttcc catgaatctt ctgctcttgt 840
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agccttgaat tcattttatc ttcattatcc ctgtgaagta ggtgggacaa gtataagggg 1320
aagagggggt ctgaattttt aggcacaaag ctgatattaa tacaatcac tcactaactg 1380
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aaaaaaaaaa aaa 1573

<210> 200

<211> 2742

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (26)

<223> n equals a,t,g, or c

<400> 200

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gtgtcttcgt caaattacag aagccaaatg ctgccatccg agactgtgac agagccattg 180
aaataaatcc tgattcagct cagccttaca agtggcgggg gaaagcacac agacttctag 240
gccactggga agaagcagcc catgatcttg cccttgccctg taaattggat tatgatgaag 300
atgctagtgc aatgctgaaa gaagttcaac ctagggcaca gaaaattgca gaacatcgga 360
gaaagtatga gcgaaaacgt gaagagcgag agatcaaaga aagaatagaa cgagttaaga 420
aggctcgaga agagcatgag agagcccaga gggagggaaga agccagacga cagtcaggag 480
ctcagtatgg ctcttttcca ggtggctttc ctgggggaat gcctggtaat tttcccgagg 540
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aaccgatttt ttttatccaa tgtgaattat aaatgagata atccacagtt attcattgtg 2040
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cctaattata ttctaattatt gcaaatatta ccataagtgg gtaaaagtaa aattcctctt 2700
ctgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaggggggg gg 2742
```

<210> 201

<211> 1417

<212> DNA

<213> Homo sapiens

<400> 201

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aatgtcatag gtatgcataa gatgactcca ccaattaaag atctgctgcc tagactcacc 180
cccattctaa agaacagaca tgaaaaagta caagagaatt gtattgatct tgttggtcgt 240
attgctgaca ggggagctga atattgatct gcaagagagt ggatgaggat ttgctttgag 300
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ggttatattg caaaggccat tggccctcat gatgtattgg ctacacttct gaacaacctc 420
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ctcgaggggg gcccgtaacc aattcgccgt atagtga 1417
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<210> 202

<211> 1512

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (855)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1512)

<223> n equals a,t,g, or c

<400> 202

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aacttgagaga gtactcgggt tcgtgaactt cccggaggcg caatgagctg cattaacctg 120
cccactgtgc tgccyggctc cccagcaag acccgggggc agatccagggt gattctcggg 180
ccgatgttct caggaaaaag cacagagttg atgagacgcg tccgtcgctt ccagattgct 240
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acacatgacc ggaacacccat ggaggcrctg cccgcctgcc tgctccgaga cgtggcccag 360
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gagttctgcg aggccatggc caacgccggg aagaccgtaa ttgtggctgc actggatggg 480
accttycaga ggaagccatt tggggccatc ctgaacctgg tgccgctggc cgagagcgtg 540
gtgaaagctga cggcgggtgtg catggagtgcc ttccgggaag ccgcctatac caagaggctc 600
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tgggacttgg atcccagggt cttatctctt caagtgtgga gagggcaggg tccacgcctc 1440
tgctgtagct tatgaaatta actaattgaa aattcaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa an 1512
```

<210> 203

<211> 419

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (384)

<223> n equals a,t,g, or c

<400> 203

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cctgggcaga gccggtggca agggcctccc ctgccgctgt gccaggcagg cagtgccaaa 60
tccggggagc ctggagctgg ggggaaggcc ggggacagcc cggccctgcc ccctcccccg 120
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tgggcagggt cccgctggcc tgggtgcttg cgctgtgcgg ctggggcgtg catggcccc 240
aggggcacgc argctgaaga aagtcccttc gtgggcaacc cagggaatat cacagggtgcc 300
```

cggggactca cgggcaccct tcggtgtcag ctccaggttc agggagagcc ccccgaggta 360
cattggcttc gggatggaca gatnctggag ctgcgggaca gcacccagac ccaggtgtt 419

<210> 204

<211> 2833

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2802)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2822)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2831)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2832)

<223> n equals a,t,g, or c

<400> 204

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tgaggagcag ccagcgggag gcggcggcga gtcggtgagc agctgggaag agcagaaccg 120
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caagagcccc ccagtgtga gccacgaatt cgtcctgcag aatcacgcgg acatcgtctc 240
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catttttgtt actcttcagt acaatgtcac cctcccagca acagaagaac aagctactga 360
atcagtgtcc ctttattact atggcatcaa agatttggt actgttttct tctacatgct 420
agtggcgata attattcatg ccgtaattca agagtatatg ttggataaaa ttaacaggcg 480
aatgcacttc tccaaaacaa aacacagcaa gttaaatgaa tctggtcagc ttagtgcggt 540
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aggaacagaa aatggtgtga atggaacatt aacttcaaat gtagcagact ctccccggaa 1260
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<212> DNA

<213> Homo sapiens

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<223> n equals a,t,g, or c

<400> 206

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<210> 207

<211> 1996

<212> DNA

<213> Homo sapiens

<400> 207

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<211> 1668

<212> DNA

<213> Homo sapiens

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<220>

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<222> (1565)

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<220>

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<220>

<221> misc feature

<222> (1620)

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<211> 2250

<212> DNA

<213> Homo sapiens

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<222> (23)

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<400> 209

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atttttacat tatgtatatt cttaactgga ctgtctcggt tagactgtat acatcataatc 2040
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2250
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<210> 210

<211> 838

<212> DNA

<213> Homo sapiens

<400> 210

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cccgcgagct tacaccggct tctctctgtc ctccgcccgc gcgccgccat cgccgtcatg 120
ctgggcccgc ctctccggcg ctgcgctgtg gccgcaacca cccgggcccga ccctcgaggc 180
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tatttgaaca agttttcctt tattgagtac caagccatgt aatggtaact tggactttaa 720
taaaagggaa atgagtttga actgaaaaaa aaaaaaaaaa aaactcatc agactgaagc 780
gcggtgatta aataatgaaa gagttcgacg cgccgggaa ttaggaggt aaatatcc 838
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<210> 211

<211> 1213

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1206)

<223> n equals a,t,g, or c

<400> 211

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gaaccggtt cgggcctcag agcgtctggt gagatgctgt tgccgctgct gctgctgcta 180
cccatgtgct gggccgtgga ggtcaagagg ccccgggcg tctccctcac caatcatcac 240
ttctacgat agtccaagcc ttccacctgc ctggacggtt cgccaccat cccatttgat 300
caggtaacg atgactattg cgactgaaa gatggctctg acgagccagg cacggctgcc 360
tgtcctaag gcagcttcca ctgcaccaac actggctata agccctgta tatccctcc 420
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aaccgggtca acgatgggtg ttgtgactgc tgcgatggaa cagacgagta caacagcggc 480
gtcatctgtg agaacacctg caaagagaag ggccgtaagg agagagagtc cctgcagcag 540
atggccgagg tcacccgcga agggttccgt ctgaagaaga tccttattga ggactggaag 600
aaggcacggg aggagaagca gaaaaagctc attgagctac aggctgggaa gaagtctctg 660
gaagaccagg tggagatgct gcggacagtg aaggagggaag ctgagaagcc agagagagag 720
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ccagccctgt cctgccacc cctcctagtg gggactagt aatgacttga cctgtgacct 1140
caatacaata aatgtgatcc cccaccctaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaaanaaaa aaa 1213
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<210> 212

<211> 969

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (922)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (955)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (958)

<223> n equals a,t,g, or c

<400> 212

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gttgatgta aaagctaagg aaaccttttc ttttgaaga tcagtataaa catgctgctt 180
ttgtaaaat tcttttgagc cattttcatc taaatataac ttctgtttca ttttttttc 240
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cagcgcctat attaaggcac atttgaataa attctattac cagttaaaaa aaaaaaaaaa 900
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aaaaaaaaa aaaaaaaaaa anaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaanccncg 960
gggggggggg 969

<210> 213

<211> 1694

<212> DNA

<213> Homo sapiens

<400> 213

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gcgatggcca aggtgtcggt gctgaacgtg gcggtccttg agaaccggag ccctttccac 180
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cctgagctgc gtgagaaccc gcccatgaag ccagatttct cccagctcca gcggaacatc 540
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aaaaaaaaa aaaa 1694

<210> 214

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 214

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tggttaccat tatccccaac ttcagtctgg acaagatcta cctcatcggg ggggacctgg 180
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tgagggatca tgaacgaaag gaagaaactt ttacccaat gccagccct tactacatgg 360

aacttacgaa gctcctgtta aatcatgctt cagacaacat cccgaaggca gacgaaatcc 420
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<210> 215

<211> 1776

<212> DNA

<213> Homo sapiens

<400> 215

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gtcgggcttc ctcggcggt gaggtctcc gccttggcgg gcgctggtcg cttttgcatt 180
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gactcctctc cgcagctgtg gcccgaaacc gatttcagga atccgccaaag gaaggcgtct 300
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cctggaatcc tgactcaggc attacttgaa gctggtgcca aagtgttgc gctcgaaagt 480
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atgtattgtc aagtactgta caatgaaatt gtttaaatat taatatgatt taagcttttt 1740

agaaattaaa atatttttaa taagaaaaaa aaaaaa

1776

<210> 216

<211> 1418

<212> DNA

<213> Homo sapiens

<400> 216

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gccatacaga attgtgtatt caccagcatc atgaaacagt tgtggtcttt tgagttgatc 180
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cagaagaaaa gcaggaagaa tttaaatgtt taattttttt tttaaattga ctttctagt 480
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aaagaagaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1418
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<210> 217

<211> 2200

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2188)

<223> n equals a,t,g, or c

<400> 217

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cacgagtgcc gccagcatgt ctgacaaact gccctacaaa gtgcgcgaca tcggcctggc 120
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<210> 218

<211> 1853

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (890)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1794)

<223> n equals a,t,g, or c

<400> 218

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tggtgggcgc cgtgaagagc cttcaggcgc tgggcgaggt catcgaggct gaacttcggt 180
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<210> 219

<211> 1093

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1090)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1091)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1092)

<223> n equals a,t,g, or c

<400> 219

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<211> 2155

<212> DNA

<213> Homo sapiens

<400> 220

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<210> 221

<211> 1264

<212> DNA

<213> Homo sapiens

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<221> misc feature

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (22)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (125)

<223> n equals a,t,g, or c

<400> 221

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<210> 222

<211> 2085

<212> DNA

<213> Homo sapiens

<400> 222

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<210> 223

<211> 2921

<212> DNA

<213> Homo sapiens

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<220>

<221> misc feature

<222> (2919)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2920)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2921)

<223> n equals a,t,g, or c

<400> 223

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<211> 4395

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (4382)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4391)

<223> n equals a,t,g, or c

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<211> 3035

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2911)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2959)

<223> n equals a,t,g, or c

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<211> 1511

<212> DNA

<213> Homo sapiens

<400> 226

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<210> 227

<211> 2239

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2238)

<223> n equals a,t,g, or c

<400> 227

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<210> 228

<211> 2346

<212> DNA

<213> Homo sapiens

<400> 228

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<211> 2246

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2235)

<223> n equals a,t,g, or c

<400> 229

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<210> 230

<211> 2002

<212> DNA

<213> Homo sapiens

<400> 230

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<210> 231

<211> 994

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (394)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (853)

<223> n equals a,t,g, or c

<400> 231

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<210> 232

<211> 486

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature
<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (440)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (485)
<223> n equals a,t,g, or c

<400> 232
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gcgccaccac cgatgccggc gccagaggyc caactcctgt gacagggcag tggtcagcaa 360
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gagacaagcg atctttggan gaaacaagaa ttccaagag gccagaaca gccccatctg 480
gaagnc 486

<210> 233
<211> 2081
<212> DNA
<213> Homo sapiens

<400> 233
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<210> 234

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (490)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (498)

<223> n equals a,t,g, or c

<400> 234

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ctgtaggctt cgggacttta tctggcgaac catggaactc tctcamacgg gagctggtct 420
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<210> 235

<211> 1129

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (807)

<223> n equals a,t,g, or c

<400> 235

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aatggaactg aggaagatta taactttgtc ttcaagggtg tgctgatcgg cgaatcaggt 300
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ctatcaciaa tacctctttt atctgtccac ccctcacaga ctaggaccct caaataaagg 1080
tgttttatat caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1129
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<210> 236

<211> 1045

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (973)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1001)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1014)

<223> n equals a,t,g, or c

<400> 236

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<210> 237

<211> 690

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (666)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (678)

<223> n equals a,t,g, or c

<400> 237

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aaaaaaaaaa aaaaaaaaaa agtttttttt aattttaagg cgggccaaaag ttttttttcc 660
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<210> 238

<211> 1873

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (568)

<223> n equals a,t,g, or c

<400> 238

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<210> 239

<211> 905

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (873)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (874)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (897)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (898)

<223> n equals a,t,g, or c

<400> 239

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ggaggacagg ggttctcctt caccacagaa cccaaacctc aggtctcacc cctgtggcct 840
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ggggg                                           905
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<210> 240

<211> 1484

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1457)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1471)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1480)

<223> n equals a,t,g, or c

<400> 240

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agatatataca atatacagat atacaaataa ggggtgaagat ggagggaatc tgataaagac 180
atcttataaa ttcaacagac acaaaagaat ttgatctccc ataagcaact gtgaaattac 240
aataacagat cctgggaagt tctacaattc taattcagtt ttttcaaggg ggaacatggc 300
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aaaggtgttc agtttcatcc ttgttaccac cgctctgaya atgggcaggg aaatttcggc 360
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ccgggtcaaa cagcaacagg tcaagatcaa gcagcttttg caggagaatg aagtccagtt 480
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ttgttcagag attttcaatg atgggtataa gctcagtga ttttacaaaa tcaaacctct 600
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aattcagaga cgatctgatg gcagtgaata cttaacaga ggatggaaa actatgaaaa 720
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tcatgataac tgttgtagt agtgcctttc attcttctca cttgcctttg ttacttaatg 1380
tgctttcagt acagcagata tgcaatattc accaaataa tgtagactgt gtttaawaaa 1440
aaacaacaaa tatgaanaaa aaaaaaaaaa nggggggctn tttt 1484

<210> 241

<211> 1521

<212> DNA

<213> Homo sapiens

<400> 241

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<210> 242

<211> 1144

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1093)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1105)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1106)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1139)

<223> n equals a,t,g, or c

<400> 242

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tcccagagga gcaggaatta gaagcttatg tagatgatat agatattgat agtgatttca 180
gaaaggatga tttttattac ttgtctcaag aagacaaaga gagacagaag cgtgagcatg 240
aagaatccaa gaggggtgctc caagaattaa aatctgtgct gggatttaaa gcttcagagg 300
cagaaaggca gaagtggaag caacttctat ttagtgatca tgtgtttctt catatagctt 360
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ccatcaatga attcagatat gggaaaagtc agtaaaaatg atactgaaga ggaaagtaat 540
aaatccgcca caacagacaa tgaaataagt aggactgagt atttatgtga aaactctcta 600
gaaggtaaaa ataaagataa ttcttcaaat gaagtcttcc cccaaggagc agaagaaaga 660
atgtgttacc aatgtgagag tgaagatgaa ccacaagcag atggaagtgg tctgaccact 720
gcccccccaa ctcccagga ctcattacag ccctccatta agcagaggct ggcacggcta 780
cagctgtcac cagattttac cttcactgct ggccttgctg cagaagtggc tgctagatct 840
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cccg 1144

<210> 243

<211> 934

<212> DNA

<213> Homo sapiens

<400> 243

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cccgaacacc atcatgtgga gacatttgca attttcctcc taaaattgcc catgggcatt 180
ataaacaatc tagttcatac agctttttca aagaagagat tatatatgaa tgtgataaag 240
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aaattgaaca actggaacta cagagagaca gcgcaagaca atccactttg gataaagaac 660
tataattttt ctcaaaagaa ggaggaaaag gtgtcttgct ggcttgctc ttgcaattca 720
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tctagaaatg ataatttgct aaagttagt gctttgagat tgtgaaatta ttaatcatcc 840
tctgtgtggc tcatgttttt gcttttcaac acacaaagca caaatttttt ttcgattaaa 900
aatgtatgta taaaaaaaaa aaaaaaaaaa tcga 934
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<210> 244

<211> 915

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (210)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (243)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (244)

<223> n equals a,t,g, or c

<400> 244

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gaccaccacc agctgcgtc actgactggc ctcatccgaa acctgtctcg gaacgctagg 180
aacaaggacg agatgtccac gaaggtggtg gagccacctg atcgagaagc tgccrggcas 240
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ccatgaacag tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaaaa aaac 915

<210> 245

<211> 1276

<212> DNA

<213> Homo sapiens

<400> 245

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acaagatgaa gcaagatgcc tcaagaaatg ctgcctacac tgtggattgt gaagattatg 180
tgcattgtgt agaatttaac ccctttgaga atggggattc aggaaaccta attgcatatg 240
gtggcaataa ttatgtggtc attggcacgt gtacgtttca ggaagaagaa gcagacgttg 300
aaggcattca gtataaaaca cttcgaacat ttcaccatgg agtcagggtt gatggcatag 360
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ctgctgatat gaaaattaga ttatttactt cagatcttca ggataaaaat gaataaagg 480
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cagctcattt tgttcttcat tctcctggca tgagtgtgtg ctggcatcct gaggagactt 660
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<210> 246

<211> 3366

<212> DNA

<213> Homo sapiens

<400> 246

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<210> 247
<211> 2148
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1259)
<223> n equals a,t,g, or c

<400> 247
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g t g a c g c a c t t a c g g c g g c a g c g t a a g t g c g t g a c g c t c g t c a g t g g c t c a g t t c a c a 120
c g t g g c g c c a g c g g a g g c a g g t g m t g t g t t g t g c t t c c t t c t a c a g c c a a t a t g a a a a 180
g g c t a a g t t a a g a a a g c a a g t a a a c g c a t g a c c t g c c a t a a g c g g t a t a a a t c c a a a 240
a a a a g g t t c g a g a a c a t c a t c g a a a a t t a a g a a g g a g g c t a a a a a g c r g g g t c a c a a g a 300
a g c c t a g g a a g a c c c a g g a g t t c c a a a c a g t g c t c c c t t a a g g a g g c t c t t c t a g g g 360
a a g c t g a g c t a a g g a a a c a g a g g c t t g a a g a a c t a a a a c a a c a g c a g a a a c t t g a c a g g c 420
a g a a g g a a c t a g a a a a g a a a a g a a a a c t t g a a c t a a t c c t g a t a t t a a g c c a t c a a a t g 480
t g g a a c c t a t g g a a a a g g a g t t t g g g c t t t g c a a a c t g a g a c a a a g c c a a g t c g g g c a 540
a a c a g a a t t c a a g a a g c t g t a c t g c c a a g a a c t t a a a a a g g t g a t t g a a g c c t c c g a t g 600
t t g t c c t a g a g g t g t t g g a t g c c a g a g a t c c t c t t g g t t g c a g a t g t c c t c a g g t a g a a g 660
a g g c c a t t g t c c a g a g t g g a c a g a a a a g c t g g t a c t t a t a t a a a t a a t c a g a t c t g g 720
t a c c a a a g g a g a a t t g g a g a g t g g c t a a a t a t t t g a a g a a g a a t t g c c a c a g t g g 780
t g t t c a g a g c c t c a c a a a a c c a a a g g a t a a g g g a a g a t a a c c a a g c g t g t g a a g g c a a 840
a g a a g a a t g c t g c t c c a t t c a g a a g t g a a g t c t g c t t t g g a a a g a g g g c c t t t g g a a a c 900
t t c t t g g a g g t t t t c a g g a a a c t t g c a g c a a a g c c a t t c g g g t t g g a g t a a t t g g t t t c c 960
c a a a t g t g g g g a a a a g c a g c a t t a t c a a t a g c t t a a a a c a a g a a c a g a t g t g t a a t g t t g 1020
g t g t a t c c a t g g g g c t t a c a a g g a g c a t g c a a g t t g t c c c c t t g g a c a a a c a g a t c a c a a 1080
t c a t a g a t a g t c c g a g c t t c a t c g t a t c t c a c t t a a t t c c t c t c t g c g c t t g c t c t g c 1140
g a a g t c c a g c a a g t a t t g a a g t a g t a a a a c c g a t g g a g g c t g c c a g t g c c a t c c t t t c c c 1200
a g g c t g a t g c t c g a c a g g t a g t a c t g a a a t a t a c t g t c c c a g g c t a c a g g a a t t c t c t n g 1260
g a a t t t t t t a c t r t g c t t g c t c a g a g a a g a g g a t g c a c c a a a a g g t g g r a t c c c a a a t 1320
g t t g a a g t g c t g c c a a a c t g c t g t g g t c t g a g t g g a c a g g g t a a g c t t t c t t t c t g t t 1380
g g c a t t t t g g t g a c c a c t a g a a t a a a c c t t c t t t t g a c a c a t c t t a t t t t t a a t a t c a g t 1440
g c c t c a t t a g c t t a c t a t t g c c a t c c c c c t a c a t c t t g g r c t c c t c t c c a t a t t t t a a t 1500
g a g a g t a t t g t g g t a g a c a t g a a a a g c g g c t t c a a t c t g g a a g a a c t g g a a a g a a c a a t 1560
g c a c a g a g c a t a a g a g c c a t c a a g g g c c c t c a t t t g g c c a a t a g a t c c t t t c c a g t c t 1620
t c c g g t c t g a c a a t g g a a t a a t a g a a g a a a g g a c a t a c a t g a a g a a t t g c c a a a a c g g 1680
a a a g a a a g g a a g c a g g a g g a g a g g g a g g a t g a c a a a g a c a g t g a c c a g g a a a c t g t t g a t 1740
g a a g a a g t t g a t g a a a a c a g c t c a g g c a t g t t t g c t g c a g a a g a c a g g g g a g g c a c t g 1800
t c t g a g g a g a c t a c a g c a g g t g a a c a g t c t a c a a g t c t t t a t c t t g g a t a a a a t c a t t 1860
g a a g a g g a t g a t g c t t a t g a c t t c a g t a c a g a t t a t g t g t a a c a g a a c a a t g g c t t t t t a 1920
t g a t t t t t t t t t a a c a t t t t a a g c a g a c t g c t a a a c t g t t c t c t g t a t a g t t a t g g t a 1980
t g c a t g a g c t g t g t a a a t t t t g t g a a t a t g t a t t a t a t a a a c c a g g c a a c t t g g a a t c 2040
c c t a a a t t c t g t a a a a g a c a a t t c a t c t c a t t g t a g t g a a g t a g t t a t c t g g a a t a a 2100
a a a a a g a a g a t a c c t a t t a a a a a a a a a a a a a a a a a a a a a a a a a a a a a a a a a a a a 2148

<210> 248
<211> 2225
<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (14)

<223> n equals a,t,g, or c

<400> 248

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tatggtttgt cgtcagtcct ttccatgcgt ccatacctct ggtggkaaga agtacatcac 180
tcaggggcag ctgcttcagt ttgtgctgac aatcatccag accagctgcg gggctcatctg 240
gccgtgcaca ttccctcttg gttggttgta tttccagatt ggatacatga tttccctgat 300
tgctctcttc acaaacttct acattcagac ctacaacaag aaaggggcct cccgaaggaa 360
agaccacctg aaggaccacc agaatgggtc catggctgct gtgaatggac acaccaacag 420
cttttcaccc ctggaaaaca atgtgaagcc aaggaagctg cggaaggatt gaagtcaaag 480
aattgaaacc ctccaaacca cgtcatctga ttgtaagcac aatatgagtt gtgcccatt 540
gctcgttaac agctgctgta actagtctgg cctacaatag tgtgattcat gtaggacttc 600
tttcatcaat tcaaaacccc tagaaaacgt atacagatta tataagtagg gataagattt 660
ctaacatttc tgggctctct gacccctgcg ctagactgtg gaaagggagt attattatag 720
tataacaacac tgctgttgcc ttattagtta taacatgata ggtgctgaat tgtgattcac 780
aatttaaaaa cactgtaatc caaacttttt tttttaactg tagatcatgc atgtgattgt 840
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aatagctctg tttagaaaaa atcaaagacc atgatttatg aaactaatgt gacataattt 1020
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aatcaagcag gctcaaactc agtggaacag tcagtttaac tttttaacag atcttatttt 1140
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acttaaatat atattctttg tcctcgagat ttttaggaag gtgtaggggt agtaggccat 1260
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ataagagaat cgagaaattt gatagaggta acttgtttaa tgtaaatcta atagtacttg 1620
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aattgttggt ttgatattta tgtaaatatc agtttaccat gctttaattt tgcacattcg 1920
tactataggg agcctatttg ttctctatta gtctgtggg ttttctgttt gaaaaggagt 1980
catggcatct gtttacattt accttatcaa acctagaatg tgtatatatta taaatgtatg 2040
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cattcaatag tgtgctgtca aagtgtgctt agctcacctg gatataccta cattgtttaa 2160
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aaaaa
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2225

<210> 249

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1197)

<223> n equals a,t,g, or c

<400> 249

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ascactcagg ctggtcctgg ggggtgggct gtaggggaaa gtgctaaagc cgctgagtga 120
agtaagaact ctgctagaga ggaaatggct gcttcatcat catcctcctc agctgggtggg 180
gtcagtgga gttctgtcac tggatctggt ttcagtgtct cagaccttgc cccaccacgg 240
aaagcccttt tcacctaccc caaaggagct ggagagatgt tagaagatgg ctctgagaga 300
ttcctctgcg aatctgtttt tagctatcaa gtggcatcca cgcttaaaca ggtgaaacat 360
gatcagcaag ttgctcggat ggaaaaacta gctggtttgg tagaagagct ggaggctgac 420
gagtggcggg ttaagcccat cgagcagctg ctgggattca cccctcttc aggttgatac 480
tgcctggatg gtcacctctg gtgcgcagca agtgcaaagc cagtggggga ctttctcaca 540
gcttacatag ccatccagag atccacagct acgtcactga attgttaatg cacatttgta 600
cttggtttct ctgtatctat tcacaggcaa caaatactta tatgtgtgat ctttcaggga 660
atgttttggt tatttgtttt taaaagtatt gggaatcaga ttaagacaat cagtttcaga 720
gaaccaggag gtttgggggt aagagatact caaaaatttt cacaagccaa gtagggcata 780
tatcagattt ggccaactga atggcgtctg tcctgtcatc catatggtgc ctggaatat 840
ttaccagtca aggtcaaggt cagcatctgt ggttaaaaat atagcattct gacctaaaaa 900
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atattctttt ttttttcccta tttttagaca tcaattctat agattctgac tttttctaac 1020
ctcttataga catgccaaat gctggcaaaa agaagtgtt tttggatatg gcagcacttg 1080
taaaaataaa gcagtaagca aaatcctttt aaacacagaa atcctgagtt cttctcattg 1140
gtggactcaa gcaattctgt agcaaataaa tcctttgaaa gagctccaaa aaaaaanaaa 1200
aaaa 1204
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<210> 250

<211> 1314

<212> DNA

<213> Homo sapiens

<400> 250

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gcaaaattgg gtccaaaacg cctttgatgg cagctgcaac tttttccgtt ggttggaaca 120
ccttcgcttg ctccagagtca ttggaaaaac cactgaactg gctacttttt aattactatt 180
tgacaacctg ccttcagtct tcagttaata agcaccgaca tatgtttgta aaacaagttg 240
atatggatca tgtcatgaag gctaaatcca tcagagagtt tgataagcga ttcacttcag 300
tcatgtttgg ataccaaaaca attgatgatt attatactga tgccagtcgg agtcctagac 360
tgaagtcagt aggaattcca gtattgtgtc taaattctgt ggatgatgtt ttctcaccca 420
gtcatgctat tccaatagaa actgctaagc aaaatcctaa tgttgctttg gtccttactt 480
cttatggagg ccatattggt tttctggagg gaatctggcc aagacagtcc acttacatgg 540
atcgtgtctt caagcaattt gtgcaagcca tggttgagca tggacatgaa ctctcttaac 600
atgtagttct ttgggtgcat tttgtctgaa ccacaattgt gaaggcagct cagcttagtg 660
cacaaatttt aactggttga tataaagcaa ataagccagc agatgggtga agagggtccag 720
aatgatatgc aaaaactact ttttagagaa acaaaacaac tttgtagcaa caaattaaat 780
atagtattag attgttactt acgtagattt tatttttact atgccttacc aagtacatcc 840
ttaaacaag tagtatgtac atgaaattgc acttaaccaa aactattgtg taaaacaaat 900
tttaattcct cagggtttta atttaaacta gtattttttt agattatttg ttttaggtga 960
```

```
tttaatggta ctttaataac tactaagaaa tattggctat ttcaatgtaa gttataaggt 1020
ggtacattcc taagggtatt tatagttgat gataacatga aaactgaaat aagataaaat 1080
acaacgtgct aaatctttta tgtattctaa ctttaaaaga caagtgcac aaagttagac 1140
tgacttctat atgtgctcct ttactctgat aatattaaat taggactaac ttatgtttta 1200
taatgattat aatttacatg cttattttta aaatagtata tggggacaca tatatatcat 1260
tatattaaaa taaattctac catttttaat tggaaaaaaa aaaaaaaaaa aaaa 1314
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<210> 251

<211> 1159

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1132)

<223> n equals a,t,g, or c

<400> 251

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ttttatatatt ttagtagaga cgggggttca ctgtgttagc caggatggtc tcgatctcca 120
ggatgggtctc gatctccagg atggtctcga tctcctgacg tcgtgatcca cccgcctcgg 180
cctcccaaaa tgctgggatt acaggtgtga gccactgtgc ccggccaaaa gaacagaaat 240
tattttatcc tgaagtaagc tgtttatatt tgggattata ctgaacctat ttgtccaata 300
acctgagttt tcaaataaatt ttagttctat aagtactata attatataaa tattaatgaa 360
ttcagattag ctgaaaggaa aaaaagtaga agcctgacta cttggtgcta actactaaag 420
attttggcag aatcaatggt ggatttggct ttccctgtccc ttcccatgac cagcccccca 480
gagtgttctg ccttgtgctg cctcccttca cckggagtgc cacaccctc tctctgccag 540
ttcagctctt cattcttcaa ggccctgacct tgtctgacct ttgtgcctct aaaccctggg 600
gccccacctc tcttgggtcc tatgtcaggt gatgtttgtg tttttggtta tgcccatctc 660
catagccaga ccaagcactc tggaagccag ggttgggtgc ttatttatct gtttgccatg 720
cagaaaatat ctgacacaaa attacctctg ttaaggaate tgaagctgaa tttagtttgg 780
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gaagttgggg ttgaggagag ccagatggct ggagtgggta tttgaaggkc tttctgtcac 1080
ctgttcagtg tggctctgcc caccctgctg gacmaagact gactgaaatg tnaaataata 1140
cagaccatct caactcaga 1159
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<210> 252

<211> 2488

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (64)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2334)

<223> n equals a,t,g, or c

<400> 252

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ccngnggacgc gtgggttgct cggcagcttg caaagcctga caacaccttg tttgtaaaca 120
gaacactttt tgatcaggtc cttgaattcc tttgtagtcc tgacgatgac tcccgacact 180
ctgaaagaca gcaggtcctt ttagaattgc tgcaggctgg aggcatagtt caatttgaag 240
agagtgcact catccggatg gcagaaaaag ctgagttcta tcaaatttgt gaattttatgt 300
atgaaagaga acaccaatat gacaaaatta ttgattgcyt cttacgtgac cctctgcgag 360
aggaagaagt ctttaattac attcacaata tcttayccat tcccgacac agtgcagagg 420
agaagcagtc tgtatggcag aaagcaatgg atcatattga ggaacycgkg kccctgaagc 480
cttgtaaagc tgcggagctg gttgccaccc acttttcttg acatattgaa acggtcatta 540
aaaaacttca gaaccagggt ttgcttttca aatttttgag gagtcttctt gacccaaggg 600
aaggatttca tgtaaatcaa gaattactgc aaatatctcc ttgtatcaca gagcagttca 660
ttgagctgtt gtgtcagttc aacccaaccc aagttataga gactctgcaa gtccttgagt 720
gctaccgtct ggaagaaact attcagatta ctgagaagta tcaacttcat gaagtcaccg 780
cttatctatt ggaagaaaaa ggagatatcc atggtgcctt cctaataatg ttagagagac 840
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<210> 253
<211> 1554
<212> DNA
<213> Homo sapiens

<220>
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<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (81)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1496)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1523)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1535)
<223> n equals a,t,g, or c

<400> 253
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cttcgcggct gctcaagatg aaccgactct tcgggaaagc gaaaccaag gctccgccgc 180
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taaaactaag gaaatggaat cttaaaagtc tatgacagtg taactctaca gtctcaaaat 1140

gacctgataa attgataaga caaagatgag attattgggg ctgttcatat tatgattcag 1200
aatcattttc tattgtggta ttataggttg gttaaagtga tggccttttt gatggggttt 1260
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aattatgaat atttcttgat atttaatgta taggacattt atttatactc aataaatatt 1440
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aggatccccc gagggggggc cangcttacg cgtgncatgc gacgtccaaa gccc 1554

<210> 254

<211> 1506

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (43)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1492)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1501)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1506)

<223> n equals a,t,g, or c

<400> 254

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gtcggcgccg ccgtaatgcy agagccgcag aagagaaccg caacaatcgc aaaatccagg 360
cctcagaggc ctccgagacc cctatggcgg cctctgtggt agcgagcacc cccgaagacg 420
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```

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<210> 255

<211> 654

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (632)

<223> n equals a,t,g, or c

<400> 255

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cgtctgccat cggcgccatc ctgcaatcta agccacaatg gtgcgcatga atgtcctggc 180
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cgaatttgaa atcattgatg accacagagc tgggaaaatt gttgtgaacc tcacaggcag 360
gctaaacaaag tgtggggtga tcagccccag atttgacgtg caactcaaag acctggaaaa 420
atggcagaat aatctgcttc catcccgcca gtttggtttc attgtactga caacctcagc 480
tggcatcatg gaccatgaag aagcaagacg aaaacacaca ggagggaaaa tcctgggatt 540
ctttttctag ggatgtaata catatattta caaataaaat gcctcatgga caaaaaaaaa 600
aaaaaaaaaa aaaaaagggg gsggtctag anggtccaag cttacgtacg cgtg      654

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<210> 256

<211> 1992

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (558)

<223> n equals a,t,g, or c

<400> 256

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gtacaactgg cagtatgtgc actgcctctt cctgtggtgc cgggtcctga gcaactgcgg 120

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ccccagcgaa scctccagcc cttggtctac ccccttgccc aagtcacatc tggctgtatc 180
aagctcatcc ccactgccc cttctacccg ctgcgaatgc actgcatccg tgcctgacg 240
ctgctctcgg ggagctcggg ggccttcac cgggtgctgc ctttcatcct ggagatgttc 300
cagcaggtcg acttcaacag gaagccaggg cgcatgagct ccaagcccat caacttctcc 360
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gagcagctgt acgacctcac cctggagtac ctgcacagcc aggcacactg catcggttc 480
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tgggagaagc tgaccggga agaggggaca cccytgacct tgtactacag ccactggcgc 720
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caccggggag gatattcggc agcccgggca gtcgcagatc ggaggatgca cctgcaggat 1920
ccccttgac ataagcgtct tcagactttt cccttccgag cggaggggagc ggcccgcgag 1980
ccccaagcgc tg 1992

<210> 257

<211> 2273

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2271)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2273)

<223> n equals a,t,g, or c

<400> 257

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cgacgtctgt ggccagggtc cagccctatt caggcaggag ctgctcttct ggggtatcgc 240
gatccactta aggatgaggc agacttggtg acaagctggt ctgagcagcg cttccagagc 300
cagaactgag ccagtgaga gcgcaccctg gggcagcctg gattcctggg gtgtccccgg 360
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gggacgctag aagggtcatg tgtaactat aatcacattt atggtttgga accatcacc 2160
caaggtaaaa aaaaaataaa aggtattccc aggtatgttt ggcaaaataa aataaaggta 2220
attaaaaacc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaattttgcn ncn 2273

<210> 258

<211> 1504

<212> DNA

<213> Homo sapiens

<400> 258

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tattcaggga tttttttaa aagtcaatca gaaaaggat actggagctt cttcatgtat 180
gtaacagcat attaaactgg agacagtgtg gaatcagcta caaaggtaat attgtattaa 240
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tgctgggtga tgaaagatta gtttttagaga gaaaatgttc atctgtgcag aggatgcatt 360
ttcttccatt aattctggaa aaaacgttca cagttatata tatggatttt tgcaaaagga 420
ctattaatag aaccttttga gatgaattaa tgtaagaata ttttttaaag aggttactg 480

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aaaa
1504

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<210> 259

<211> 1792

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (107)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (487)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1306)

<223> n equals a,t,g, or c

<400> 259

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cgggaaatccc aaagggcgtg gtgagcttca aaagtgggaa ctggggctgg gccacagccg 180
gcagcagcag catcttggcg gagtttgat ccctgcactt ggaattctta cacctcactg 240
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tgtggactag aataaaagag tttattgaat aagaaaaaaa aaaaaaaaaa aa 1792
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<210> 260

<211> 2048

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (66)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (67)

<223> n equals a,t,g, or c

<400> 260

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acccttagag gagggcgtgc gggggtctgt tttgcatgag agccaccctt ctggctgctc 180
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gagggacagg attaggcagg gtctgtcctg tggccacctg gaaagtccca ggtgggactc 1920
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<210> 261

<211> 1282

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1244)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1261)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1265)

<223> n equals a,t,g, or c

<400> 261

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cctatagcaa tggaactcag cgatgcaaat ctgcaaacac taacagaata tttaaagaaa 180
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<210> 262

<211> 599

<212> DNA

<213> Homo sapiens

<400> 262

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acgacatcct cattcgaaag kttgacaggc argggacggg gcaratcgsc ttcgacgast 540
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<210> 263

<211> 1261

<212> DNA

<213> Homo sapiens

<400> 263

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<210> 264

<211> 1020

<212> DNA

<213> Homo sapiens

<400> 264

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tcgtcactct aaagaaataa cttatgtaaa actcttagta accctgtttg tcttcaaatg 240
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<210> 265

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (557)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (565)

<223> n equals a,t,g, or c

<400> 265

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aaaatttggg ggggggnccc cgtancccat t 571

<210> 266

<211> 1350

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (204)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1313)

<223> n equals a,t,g, or c

<400> 266

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<210> 267

<211> 1319

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (61)

<223> n equals a,t,g, or c

<400> 267

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gttcaactgca ggtattgacc tgatggacat ggcttcggac atcctgcagc ccaaaggaga 480
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<210> 268

<211> 3694

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (746)

<223> n equals a,t,g, or c

<400> 268

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aatgactgct ccaggaatgt ctacattaag aagaatggct ttactttaca tcgaaacccc 240
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<210> 269

<211> 1242

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (31)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (46)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (460)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1233)

<223> n equals a,t,g, or c

<400> 269

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<210> 270

<211> 2057

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (22)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2053)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2054)

<223> n equals a,t,g, or c

<400> 270

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<210> 271

<211> 960

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (951)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (956)

<223> n equals a,t,g, or c

<400> 271

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<210> 272

<211> 1167

<212> DNA

<213> Homo sapiens

<400> 272

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<210> 273

<211> 2771

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (16)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (27)

<223> n equals a,t,g, or c

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<221> misc feature
<222> (42)
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<222> (64)
<223> n equals a,t,g, or c

<220>
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<222> (2715)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2717)
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<400> 273
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<210> 274

<211> 1889

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (15)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (57)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (87)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (113)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1676)

<223> n equals a,t,g, or c

<400> 274

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<210> 275

<211> 604

<212> DNA

<213> Homo sapiens

<400> 275

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<210> 276

<211> 1381

<212> DNA
<213> Homo sapiens

<220>
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<222> (1348)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1349)
<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

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<210> 277

<211> 1149

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (680)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1088)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1098)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1140)

<223> n equals a,t,g, or c

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<211> 811
<212> DNA
<213> Homo sapiens

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<210> 279
<211> 1260
<212> DNA
<213> Homo sapiens

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<222> (1249)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1252)
<223> n equals a,t,g, or c

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<210> 280

<211> 1668

<212> DNA

<213> Homo sapiens

<400> 280

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agtgcctttg ttagatggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1668

<210> 281

<211> 2328

<212> DNA

<213> Homo sapiens

<400> 281

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<210> 282

<211> 956

<212> DNA

<213> Homo sapiens

<400> 282

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<210> 283

<211> 1402

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (26)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (88)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (97)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (131)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1344)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1355)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1394)

<223> n equals a,t,g, or c

<400> 283

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<210> 284

<211> 675

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (20)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (520)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (560)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (618)

<223> n equals a,t,g, or c

<400> 284

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agaacctggg taccaagctn ggccaccar atgcgaaagc tcaccartaa cctgcggatt 600
ggcttcsggg catttgtnng acaagcctgt gtcaccatac atgtacctcg tgcgaatttt 660
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<210> 285

<211> 1339

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1330)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1331)

<223> n equals a,t,g, or c

<400> 285

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gtactcttgc ttaaggcaag agtttcagat ttactgttga aataaaacca actcttcatg 1260
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaaaaaan naaaaaaaaa 1339
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<210> 286
<211> 1398
<212> DNA
<213> Homo sapiens

<400> 286
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<210> 287
<211> 926
<212> DNA
<213> Homo sapiens

<220>
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<222> (20)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (917)

<223> n equals a,t,g, or c

<400> 287

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actcttgatt gcaccacccc tgtagaagat ggaatcatgg atgctgccaa ttttgagcag 180
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<210> 288

<211> 3094

<212> DNA

<213> Homo sapiens

<400> 288

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aatagttaat ggatgtgtgc acattttctg ttcagggatt aagaccagaa tatcagtgga 240
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<210> 289

<211> 1983

<212> DNA

<213> Homo sapiens

<400> 289

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<210> 290

<211> 1298

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1224)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1231)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1242)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1262)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1285)

<223> n equals a,t,g, or c

<400> 290

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<210> 291

<211> 2459

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1604)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1605)

<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (2374)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2392)
<223> n equals a,t,g, or c

<400> 291
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<210> 292
<211> 570
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (567)
<223> n equals a,t,g, or c

<400> 292
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aaaaaaaaaa raagggggcc gctctanagg 570

<210> 293
<211> 2468
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2076)
<223> n equals a,t,g, or c

<400> 293
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<210> 294

<211> 1080

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1038)

<223> n equals a,t,g, or c

<400> 294

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<210> 295

<211> 2695

<212> DNA

<213> Homo sapiens

<400> 295

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tccatatata cagaaattag acaaataata agtcttttagt tcaacttaag catatctcaa 180
atgacttctc taaattttaa gttgatcatg ataggatcat aaaagacaga aaagacttaa 240
gtaatcttgt aatgacaatt atttccattt ttgctgaact aaaaatattt aacttcataa 300
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<211> 1394

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1238)

<223> n equals a,t,g, or c

<400> 296

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<211> 998

<212> DNA

<213> Homo sapiens

<400> 297

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<210> 298

<211> 1666

<212> DNA

<213> Homo sapiens

<400> 298

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<211> 2444

<212> DNA

<213> Homo sapiens

<220>

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<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (402)

<223> n equals a,t,g, or c

<400> 299

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<210> 300

<211> 1026

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1026)

<223> n equals a,t,g, or c

<400> 300

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<211> 830

<212> DNA

<213> Homo sapiens

<400> 301

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<212> DNA

<213> Homo sapiens

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<221> misc feature

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<221> misc feature

<222> (3280)

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<211> 475

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<213> Homo sapiens

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<223> n equals a,t,g, or c

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<221> misc feature

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<221> misc feature

<222> (470)

<223> n equals a,t,g, or c

<400> 303

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<210> 304

<211> 2902

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2891)

<223> n equals a,t,g, or c

<400> 304

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<210> 305

<211> 1553

<212> DNA

<213> Homo sapiens

<400> 305

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<210> 306

<211> 1987

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (731)

<223> n equals a,t,g, or c

<400> 306

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catttcc 1987

<210> 307

<211> 785

<212> DNA

<213> Homo sapiens

<400> 307

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aaaaa 785

<210> 308

<211> 2178

<212> DNA

<213> Homo sapiens

<400> 308

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<210> 309

<211> 875

<212> DNA

<213> Homo sapiens

<400> 309

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<210> 310

<211> 756

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (613)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (638)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (684)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (756)

<223> n equals a,t,g, or c

<400> 310

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<210> 311

<211> 851

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (834)

<223> n equals a,t,g, or c

<400> 311

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<210> 312

<211> 1335

<212> DNA

<213> Homo sapiens

<400> 312

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<210> 313

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (505)

<223> n equals a,t,g, or c

<400> 313

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<210> 314

<211> 1833

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (625)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1761)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1766)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1792)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1806)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1827)

<223> n equals a,t,g, or c

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<210> 315

<211> 1354

<212> DNA

<213> Homo sapiens

<400> 315

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<210> 316

<211> 2421

<212> DNA

<213> Homo sapiens

<400> 316

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2421

<210> 317

<211> 1092

<212> DNA

<213> Homo sapiens

<400> 317

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<210> 318

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 318

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<210> 319

<211> 2612

<212> DNA

<213> Homo sapiens

<400> 319

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<210> 320

<211> 943

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (52)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (54)

<223> n equals a,t,g, or c

<400> 320

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tgggtggagt cagtccaatt caggtcagcc atatccaaaa gaccacaagt cattactaag 180
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tcagcccca cagctgctg gggaatgtg atgttctagc tctgagatgt taactgrgaa 840
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<210> 321

<211> 2959

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2948)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2956)

<223> n equals a,t,g, or c

<400> 321

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tgctgggtgt ttccacagat gccgggttcc actttgctgg agatgggaaa cttgggtggc 180
ttgttttacc aaatgatgga caatgtcacc tggaaaataa tatgtacaca atgagccatt 240
attatgatta tccttctatt gctcaccttg tccagaaact gagtgaaaat aatattcaga 300
caatttttgc agttactgaa gaatttcagc ctgtttacaa ggagctgaaa aacttgatcc 360
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atgcatacaa ttccctttcc tcagaagtca ttttgaaaaa cggcaaattg tcagaaggmg 480
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gaaaatgttc caatatttcc attggagatg aggttcaatt tgaaattagc ataacttcaa 600
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actttgagtt agtgccataa cagaccactg tatgtttact tctcaccatt tgagttgccc 2760
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tcttgactct gatgtatttt awcagggtgt gtgcatgaaa tttttataga taaagragtt 2940
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<210> 322

<211> 802

<212> DNA

<213> Homo sapiens

<400> 322

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gtggtgctcg gcgacggcgt gcagctcccg cccggggact acagcacgac ccccggcggc 180
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cacaccctcg cwgcggggg sgcaaccacc ccttccttag gttgatgtgc ttgggaaagc 720
tccttcccc tccttcccca agagaggaaa taaaagccmc ctctgccta gggccaaraa 780
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<210> 323

<211> 1724

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1590)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1650)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1701)

<223> n equals a,t,g, or c

<400> 323

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cgcgctgccg agaaagatct cagagtaaaag aagaacttaa agaaattcag atatgtgaag 180
ttgatttcca tggaacctc gtcacctct gatgacagtt gtgacagctt tgcttctgat 240

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aat t t t t g c a a a c a c g a g g c t g c a g t c a g t t c g g g a a g g c t g t a g g a c c c g c a g c c a g t g c 300
a g g c a c t c t g g a c c t c t c a g g g t g g c g a t g a a g t t t c c a g c g c g g a g t a c c a g g g g a g c a 360
a c c a a c a a a a a g c a g a g t c c g c c a g c c c t c a g a g a a t t c t g t g a c t g a t t c c a a c t c c 420
g a t t c a g a a g a t g a a a g t g g a a t g a a t t t t t g g a g a a a a g g g c t t t a a a t a t a a g c a a 480
a a c a a a g c a a t g c t t g c a a a a c t c a t g t c t g a a t t a g a a a g c t t c c c t g g c t c g t t c c g t 540
g g a a g a c a t c c c c t c c c a g g c t c c g a c t c a c a a t c a a g g a g a c c g c g a a g g c g t a c a t t c 600
c c g g g t g t t g c t t c c a g g a g a a c c c t g a a c g g a g a g c t c g t c t t a c c a g g t c a a g g 660
t c c c g g a t c c t c g g g t c c c t g a c g c t c t a c c a t g g a g g a g g a g g a g a g g a t a a g 720
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a g a a g c c g t c g t c c a g a t c a t c c g t g a c c c t c c g c a t a t a a t t c g c c c a g t g g a a g a a 840
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t c a c t g g g c t c t a c t t g t c a t c a a t g c c g t c a g a a g a c t a t t g a t a c c a a a c a a a c t g c 960
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g t g t a t t t a g c c a a a t a t c a t g g c t t t g g g a a t g t g c a t g c c t a c t t g a a a a g c c t g a a a 1200
c a g g a a t t t g a a a t g c a a g c a t a a t a t c t g g a a a t t t g c t g c c t g c c t t c t a c t t c t c a 1260
a a t c t t t c t t g t a a a g t t t c c a a t t t t t c a c t g a a a c c t g a g t t a a a a t c t t g a t g a 1320
t c a g c c t g t t t c a t a a g a a a c t c c a a t c a a g t t a a t c t t a g c a g a c a t g t g t t t c t g g a g 1380
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g a a t t t c a g a g a a g a g c c t a a a t a g c a a a n t t a c a c a a a a a c g a g t a t g a t t a g c a c t 1680
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<210> 324

<211> 2261

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1098)

<223> n equals a,t,g, or c

<400> 324

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g a a t g c g t t g a g g a a g c a t a a a g a c t t g t t g g g t a a a a g a t a c a t t g a a c t c t t c a g g a g 120
c a c a g c a g c t g a a g t t c a g c a g g t g c t g a a t c g a t t c t c c t c g g c c c c t c a t t c c a c t 180
t c c a a c c c c t c c c a t t a t t c c a g t a c t a c c t c a g c a a t t t g t g c c c c c t a c a a a t g t t a g 240
a g a c t g t a t a c g c c t t c g a g g t c t t c c c t a t g c a g c c a c a t t g a g g a c a t c c t g g a t t t 300
c c t g g g g g a g t c g c c a c a g a t a t t c g t a c t c a t c a t g g g g t c a c a t g g t t t t g a a t c a c c a 360
g g g c c g c c c a t c a g g a g a t g c c t t t a t c c a g a t g a a g t c t g c g g a c a g a g c a t t t a t g g c 420
t g c a c a g a a g t g t c a t a a a a a a a c a t g a a g g a c a g a t a t g t t g a a g t c t t c a g t g t t c 480
a g c t g a g g a g a t g a a c t t t g t g t a a t g g g g g c a c t t t a a a t c g a a a t g g c t t a t c c c c 540
a c c g c c a t g c c t g t c t c c t c c t c a c a c a t t t c c a g c t c c t g c t g c a r t t a t t c c t a c 600
a r a a r c t g c c a t t t a c c a g c c c t c t g t g a t t t t g a a t c c a c g a g c a c t g c a g c c c t y c a c 660
a g c g t a c t a c c a g c a g g c a c t c a g c t c t t c a t g a a c t a c a c a g c g t a c t a t c c c a g t g t 720
t t g a a a g a t g t a t g g t g a t c t t g a a a c c t c c a g a c a c a a g a a a a c t t c t a g c a a a t t c a g 780
g g g a a g t t t g t c t a c a c t c a g g c t g c a g t a t t t t c a g c a a a c t t g a t t g g a c a a a c g g g c 840

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ctgtgcctta tcttttgggtg gagtgaaaaa atttgagcta gtgaagccaa atcgtaactt 900
acagcaagca gcatgcagca tacctggctc tttgctgatt gcaaataaggc atttaaaatg 960
tgaatttga atcagatgtc tccattactt ccagttaaag tggcatcata ggtgtttcct 1020
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<210> 325

<211> 1213

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1213)

<223> n equals a,t,g, or c

<400> 325

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actccttggc gcctgcctga tcttccaaat caccacagga ctattcctag ccatgacta 180
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<210> 326

<211> 2764

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (372)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2128)

<223> n equals a,t,g, or c

<400> 326

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gcgcgagtgg tctggacatg gggaagatcg aggagatgga gaagatgctg aaagaggctc 840
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<210> 327

<211> 1764

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1398)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1758)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (1759)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1762)

<223> n equals a,t,g, or c

<400> 327

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<210> 328

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (535)

<223> n equals a,t,g, or c

<400> 328

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571

<210> 329

<211> 473

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (37)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (449)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (467)

<223> n equals a,t,g, or c

<400> 329

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<210> 330

<211> 1335

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (865)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1004)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1156)

<223> n equals a,t,g, or c

<220>
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<222> (1301)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1328)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1333)
<223> n equals a,t,g, or c

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<210> 331
<211> 1046
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (982)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (997)
<223> n equals a,t,g, or c

<400> 331
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<210> 332
<211> 1311
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1280)
<223> n equals a,t,g, or c

<400> 332
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<210> 333

<211> 1444

<212> DNA

<213> Homo sapiens

<400> 333

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<210> 334

<211> 1030

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

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<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (989)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1006)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1023)
<223> n equals a,t,g, or c

<400> 334
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<210> 335
<211> 2127
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (72)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2098)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (2114)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2117)

<223> n equals a,t,g, or c

<400> 335

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gggtggtggg ggcaggggac agaggccatg aaggagcaag ttttgtattt gtgacctcag 2040
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<210> 336

<211> 847

<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (291)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (829)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (847)
<223> n equals a,t,g, or c

<400> 336
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tccccactcc ttctctcacg ccaagctctg actttccgtg ctccacgac cccgcggctcc 180
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tccaccgagc cctgcgcgca gctgtccatc tcctccatcg gcgtagtggg caccgccgag 480
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caggaccgga tacttatccg ctttttcccc ttggagtcct ggcagattgg caagataggg 600
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cttcttcag agagatctct tggcagagtg agggcctgga gataaccagc tttggattat 720
ccgcgatgca acattcctgt gatcacataa tcctcttctt catcctcata tgaaataaat 780
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ttggccn 847

<210> 337
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (21)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (150)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (669)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (679)
<223> n equals a,t,g, or c

<400> 337
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aaccgcgaaa gagtaagacg gcagcggcac cctctgaaaa gaatcggggc ccaagaaaag 180
gcggtcgtgt tatcgtctcc argaaggcgc gcgtcgtgca gcagcaaaag ctcaagaaga 240
acctagaagt cggaatccgg aagaagatcg aacatgacgt ggtgatgaaa gccagcagca 300
gcctgcccga gaagctggca ctgctgaagg ccccagccaa gaagaaagg gcagctgccg 360
ccacctcttc caagacacct tcctgaggac gctggcccca gtgcaggcca acatcccacc 420
ccctacctcc atatgggacc ttgcaagtca tcccacaggc tgcaactgtca ggaagaggac 480
cctgtcccc agcactgggc ttcacctaga acttcagtgg gggccaagg tgctgagaac 540
ccagcaatga ccaggaagat acagtcacta acttcatctg tccccgtgcc ctttcccagg 600
tcctgcctcc acaggtttaa ccagacaata taaacctggc ttgtgtcaama aaaaaaaaaa 660
agggcgcgnc gtttttagang atccagctta cgtaccgtgc tt 702

<210> 338
<211> 875
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (791)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (813)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (830)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (861)
<223> n equals a,t,g, or c

<400> 338

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aaatggcaaa aaagaaaata tccttgagtt tgtaatctag ttacagaagt aaggcataca 120
cacacacaaa gataacagta cctagagaga gagtgtgtgt gagtgtgcgt gtctctgtgt 180
gtgcacgtgc acgctcatgg ccaaattgtc gcactctaca taaaggaggc aggagttcct 240
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ttccgcaaca cagaaatgac tcagaatctc agacaaaatg tattatttgt tcaattttaa 360
ttttgctact acattcataa ctcttaaatt gttaggctgt ttcatttaca tcaaagttat 420
ctcacaaaag agaaggcagg aaacgttttg tgagtgccta ttctatgtca aacactgtgt 480
tggcaccata ttttacaagt ttttttcctc ttctcacagt gatcttggtga gttagttact 540
tatattttta ttagaactca ttattctggg taccctccaa tgagaattag agaggttaaa 600
taccttttcc tagattccca cagcaggaag gtgggcatag ctgttttgtc tgacaccaga 660
acccatctca ccacactgct ttacagtctt cctgaaggga cattttgagg tggggggggg 720
ccttcaaagc tcagaggact ggggttkgaa tgggtttaat ttttgcaagg gatccatgtc 780
catgccaggg ngtttacaat tctttaactt ccntccaaa ttcgtgtgtn ccattaggga 840
catttgggtt acatccgggc nggggagggg caggg 875

<210> 339

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1427)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1432)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1440)

<223> n equals a,t,g, or c

<400> 339

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tctgttttcc atccccctca ggtccttcct cgggaggcgg cgaaggcggg ccaccctgcg 180
cgtgatcctt yatgcccggc cctgccccct ccctccgggt ggaacttccc cctcaccgcc 240
agacttaagc tgaggatcgt tggatctctg gcggggtgca gaactgagcc caggccacag 300
taccctatct acgctctgtg cttgtgccaa gggggcaatg gcggcttccct gtgttctact 360
gcacactggg cagaagatgc ctctgattgg tctgggtacc tggaagagtg agcctgggtca 420
ggtaaaagca gctgttaagt atgcccttag cgtaggctac cgccacattg attgtgctgc 480
tatctacggc aatgagcctg agattgggga ggccctgaag gaggacgtgg gaccaggcaa 540
ggcgggtgcct cgggaggagc tgtttgtgac atccaagctg tggaacacca agcaccaccc 600
cgaggatgtg gagcctgccc tccggaagac tctggctgac ctccagctgg agtatctgga 660
cctgtacctg atgactggc cttatgcctt tgagcgggga gacaacccct tccccaaaga 720
tgctgatggg actatatgct acgactccac ccactacaag gagacttgga aggctctgga 780
ggcactgggt gctaaggggc tgggtgcaggc gctgggcctg tccaacttca acagtcggca 840


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tgcttatagc cctttgggct cctctgacg tgcattggcg gatcctgatg agcctgtcct 1020
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gagagtccca agggatgcag ggcacacctc gtaccccttt aatgaccgt actgagacca 1320
cagcttcttg gcctcccttc cagctctgca gctaagtagg tcctgccaca acggaaaagag 1380
ggagttaata aagccattgg agcatccaaa aaaaaaaaaa aaaaaanayc tngsggccgn 1440
caagggaa 1448

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<210> 340

<211> 843

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (812)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (822)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (829)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (838)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (841)

<223> n equals a,t,g, or c

<400> 340

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gctgatctcc tgctgatgt ttctgtctca gagccaaggc caaggggccc agacagagtt 180
gccccaggcc cggatcagct gcccagaagg caccaatgcc tatcgctcct actgctacta 240
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gggcaacctg gtgtctgtgc tcaccaggc cgagggtgcc tttgtggcct cactgattaa 360
ggagagtggc actgatgact tcaatgtctg gattggcctc catgacccca aaaagaaccg 420
ccgctggcac tggagcagtg ggtccctggt ctctacaag tcctggggca ttggagcccc 480

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aagcagtggt aatcctggct actgtgtgag cctgacctca agcacaggat tccagaaatg 540
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gctggaaaaat acatgtctag aactgatcca gcaattacaa cggagtcaaa aattaaaccg 660
gaccatctct ccaactcaac tcaacctgga cactctcttc tctgctgagt ttgccttggt 720
aatcttcaat agttttacct accccagtct ttggaaccyt aaataataaa aataaacatg 780
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naa 843

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<210> 341

<211> 1293

<212> DNA

<213> Homo sapiens

<400> 341

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acggatatcc tctgttgggg gagaagcaac attttgtgat ttccaaaaa taaaccatgg 180
aattctatat gatgaagaaa aatataagcc attttcccag gttcctacag ggggaagttt 240
ctattactcc tgtgaatata attttgtgtc tccttcaaaa tcattttgga ctgcgataac 300
atgcacagaa gaaggatggg caccaacacc aaagtgtctc agactgtgtt tctttccttt 360
tgtggaaaat ggtcattctg aatcttcagg acaaacacat ctggaagggtg atactgtgca 420
aattatttgc aacacaggat acagacttca aaacaatgag aacaacattt catgtgtaga 480
acggggctgg tccaccctc ccaaatgcag gtccactgac acttctgtg tgaatccgcc 540
cacagtacaa aatgctyata tastgtcgag acagatgagt aaatatccat ctggtgagag 600
agtacgttat saatgtagga gcccttatga aatgtttggg gatgaagaag tgatgtgttt 660
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tccacctatt gacaatgggg acattacttc attcccgttg tcagtatatg ctccagcttc 780
atcagttgag taccaatgcc agaacttcta tcaacttgag ggtaacaagc gaataacatg 840
tagaaatgga caatggtcag aaccacaaaa atgcttacat ccgtgtgtaa tatcccgaga 900
aattatggaa aattataaca tagcattaag gtggacagcc aaacagaagc tttattygag 960
aacaggtgaa tcagytgaa ttgtgtgtaa acggggatat cgtctttcat cacgttctca 1020
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gaatcaatca taaartgcac acctttattc agaactttag tattaaatca gttctyaatt 1140
tcatttttwa tgtattgttt tactcctttt tattcatag taaaattttg gattaatttg 1200
tgaaaatgta attataagct gagaccgggtg gctctcttct taaaagcacc atattaaatc 1260
ctggaaaact aaaaaaaaaa aaaaaaaact cgc 1293

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<210> 342

<211> 1273

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (6)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (483)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1247)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1262)

<223> n equals a,t,g, or c

<400> 342

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aggaggaaga aaggaggcc acaaaggccg ggcgaggcag tatacaagcc ctgaggagat 120
cgacgcgcag ctgcaggctg agaagcagaa ggccagggaag gaagaggagc aaaaagaagg 180
tgagatggg gctgcagggtg accccaaaaa ggagaagaaa tctctagact cagatgagag 240
tgaggatgaa gaagatgact accagcaaaa gcgcaaaggc gttgaagggc tcatcgacat 300
cgagaacccc aaccgggtgg cacagacaac caaaaaggtc acacaactgg atctggacgg 360
gccaaaggag ctttcgagga gagaacgaga agagattgag aagcagaagg caaaagagcg 420
ttacatgaaa atgcacttgg ccgggaagac agagcaagcc aaggctgacc tggcccggt 480
ggncatcatc cggaacagc gggaggaggc tgcccgaag aaggaagagg aaaggaaagc 540
aaaagacgat gccacattgt caggaaaacg aatgcagtca ctctccctga ataagtaact 600
gcgacccgtg ggaggagatg ccggggacct gggccgcgct gccaggacct ctgctgtgtc 660
tcgccccacc tgtgccctgg cgccgctgca acagcccctc atggccagga gccccccatg 720
gcctggggcc tcctcttcat cttggcacag aaattgtttg ggggatgggg ggggggactg 780
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tgcccathtt cagccctacc cattgatcat ttcaagaaac ctctgtttac tgtgtggcac 1140
ccaggcaaaa catgctccac aaattcaact tgtatatttg gcagattaaa cttgacatta 1200
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gnggtttaaa tta                                     1273
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<210> 343

<211> 1793

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1251)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1267)

<223> n equals a,t,g, or c

<400> 343

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ctagtcacca tggcctgggg ccagtatggc gattatggat acccatacca gcagtatcat 120
gactacagcg atgatgggtg ggtgaatttg aaccggcaag gcttcagcta ccagtgtccc 180
caggggcagg tgatagtggc cgtgaggagc atcttcagca agaaggaggg ttctgacaga 240
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ctgcagagat ggcgctatct ttcctcctcc tgtgatgtcc tgctcccaac catttgtact 1680
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<210> 344

<211> 1672

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (95)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1667)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1668)

<223> n equals a,t,g, or c

<400> 344

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aagtctaagc gccggaagtg gtgggcattc tgggtaacga gctatttact tcctgcggtg 180
gcacaggctg tggctcgtcta tctccctggt gttcttccca tcggcgaaga tggccctgga 240
gacggtgcgc aaggacctgc ggcactctgc ggcctggttg ctgtgttcgc tggcaagac 300
tatagaccag tttgaatatg atggttgatg caattgtgat gcatactac aaatgaaggg 360
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<210> 345

<211> 2109

<212> DNA

<213> Homo sapiens

<400> 345

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<210> 346

<211> 1714

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (21)

<223> n equals a,t,g, or c

<400> 346

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<210> 347

<211> 1672

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1667)

<223> n equals a,t,g, or c

<400> 347

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<210> 348
<211> 1483
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (19)
<223> n equals a,t,g, or c

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<210> 349
<211> 1842
<212> DNA
<213> Homo sapiens

<400> 349
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<210> 350

<211> 3008

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (9)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (59)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (65)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1307)

<223> n equals a,t,g, or c

<400> 350

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<211> 2756
<212> DNA
<213> Homo sapiens

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<222> (1597)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2540)
<223> n equals a,t,g, or c

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<210> 352

<211> 1645

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (97)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1574)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1596)

<223> n equals a,t,g, or c

<400> 352

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<210> 353

<211> 1637

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (738)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (771)

<223> n equals a,t,g, or c

<400> 353

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agagtgtgtg tgccttgagg gcctgggggg atgttgctcc tcagctccct ccctcagccc 1560
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<210> 354

<211> 1119

<212> DNA

<213> Homo sapiens

<400> 354

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ccctgcgggg agtcggcccc cgaccttgcc ggcttcaccc tcctaatagcc agcagtatct 180
gttggaatg ttggccagct tgcaatggat ctgattatct ctacactgaa tatgtctaag 240
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<210> 355

<211> 738

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (654)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (689)

<223> n equals a,t,g, or c

<400> 355

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cggaaattca tcaatttgaa tgaattcaca acctatggca gcgargaaag caccaaaccg 120
gcctccgtcc gggccctgct gtttgamatc tccttctca tgctgtgcca tgtggcccag 180

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acctatggtt caraggatgat tctgtccgag tgcgcacag gagctgaggt gcccttcttc 240
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tgcttccgcc ccgactccac caaagtggag tccctggagg ccctgctcaa caactcctcg 360
gagatgaagc tagtgacgat gaagtggcat gaggcctgtc tcagcatctc agccgccatc 420
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ctggcagggc cactgttttag ygagaacacc ctgcagttct acaatgagag ggtngtgatc 660
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<210> 356

<211> 1966

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (56)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (788)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1753)

<223> n equals a,t,g, or c

<400> 356

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<210> 357

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (16)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (18)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (260)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (262)

<223> n equals a,t,g, or c

<400> 357

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tttgagggcc cagttcttga tcacaggtat tatgcagggt gatgctcccc gcattacatc 180
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<210> 358

<211> 1931

<212> DNA

<213> Homo sapiens

<400> 358

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gcctgacttt tctgtccctt gttctgcagg attagtattc tgttacagac ctctagtttt 1860
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aaaaaaaaaa a 1931
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<210> 359

<211> 869

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (869)

<223> n equals a,t,g, or c

<400> 359

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ccaaagtggg tgactgaag aagatgttgt tggatcaggg gggctttgcc ccgtgttttc 180
taggctgctt tctccactg gtaggggcac ttaatggact gtcagcccag gacaactggc 240
caaaactacg cgggattatc ctgatgccct tatcaccaac tactatctat ggcctgctgt 300
gcakttagcc aacttctacc tgggtccccc tcattacagg ttggccggtg tccaatgtgt 360
tgctgttatc tggaactcct acctgtcctg gaaggcacat cggctctaag cctgcctcac 420
tccatcgttt ccaccttgca gtgatgcagc ttgaccctgg aacgggtcaga caacctcctc 480
aaagtgggca taccagtttc cacgggggtg ggttgccggt cagagcttaa gaggactagc 540
acctgcaat gccctcttc actctaaaat gtacactgac tgctttagag cccttgataa 600
tagtcttatt cccaccacat actaggcact ccataaatat ctggtgaacc ttcattgacct 660
tatcaacttt acaccatat cccagcaaat gccactcatc cccactcttc atagacacat 720
ttgttactct aacctgcct aggttcttg tagctccagc tctttagaga ctcccgaac 780
cctttatatg gtgcctcagt aaatatgtta ttaaatatgt aatccggaaa aaaaaaaaaa 840
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 869
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<210> 360

<211> 561

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (521)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (525)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (560)

<223> n equals a,t,g, or c

<400> 360

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tctctggaga gcagcagcca tggccctacg ctaccctatg gccgtgggcc tcaacaaggg 180
ccacaaagtg accaagaacg tgagcaagcc caggcacagc cgacgccgcg ggcgtctgac 240
caaacacacc aagttcgtgc gggacatgat tcgggaggtg tgtggctttg ccccgtagca 300
gcggcgcgcc atggagttac tgaaggcttc caaggacaaa cgggcccctca aatttatcaa 360
gaaaagggtg gggacgcaca tccgcgccaa gaggaagcgg gaggagctga gcaacgtact 420
ggccgccatg aggaaagctg ctgccaagaa agactgagcc cctcccctgc cctctccctg 480
aaataaagaa cagcttgaca gaaaaaaaaa aaaaaaaaaa ntcngggggg ggcccgggtac 540
ccattcgccc tawagggggn g 561
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<210> 361

<211> 1680

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (33)

<223> n equals a,t,g, or c

<400> 361

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cgctgtttgc attaaaaggg tgggtgagtc aggaccctg gctcargagc cgyctctcct 180
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tattaactgc tcctgggcct ggagcagtat tcccaccta agattcccag catccctgtg 360
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ttggggggcg cttctctctt cttccccagg gaattctcta gcagagggag gggaccacc 480
ccagttagga agtagattgc tgcccttagc cagagacctg aactggggaa tttgaacatt 540
cctttacatt gttggagaaa tgaagccaaa gttattcaga tggttttccc aggctaaagg 600
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tctggggcca ttgacagact caggaaagga tttctacagt gttctataaa agccaaaaga 1560
gagagtgggt ttgggaagag tgagggtggt tggggagagg ggaccgatgt gcctcattgt 1620
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<210> 362

<211> 740

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (591)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (709)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (718)

<223> n equals a,t,g, or c

<400> 362

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gagagggacc ccctgcccag ccgcccgcga ctcagggcag tccgatctaa gaagcagaag 540
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camatcccct cttgggtgcc tkgatctttc tytgcccccg gggccaggac ccactgtgct 660
gttttcttgt tcagttttgt ggggaaagga accaaggttt ttgccaagna accagtttct 720
tgaaaggggt tagggaaggg 740

<210> 363

<211> 1324

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (385)

<223> n equals a,t,g, or c

<400> 363

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tagt 1324

<210> 364

<211> 2853

<212> DNA

<213> Homo sapiens

<400> 364

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<210> 365

<211> 1837

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (136)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (749)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1816)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1829)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1832)
<223> n equals a,t,g, or c

<400> 365
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aaaaaaaaa aaaacncgag ggggggccng gnaccca 1837

<210> 366

<211> 1823

<212> DNA

<213> Homo sapiens

<400> 366

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tgccaaagca ggagtcattt tccccgtggg gcggatgctg cggtagatca agaaaggcca 180
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<210> 367

<211> 898

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (25)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (30)

<223> n equals a,t,g, or c

<400> 367

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<211> 1117

<212> DNA

<213> Homo sapiens

<400> 368

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1117

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<211> 2226

<212> DNA

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<223> n equals a,t,g, or c

<220>

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<223> n equals a,t,g, or c

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<222> (36)

<223> n equals a,t,g, or c

<400> 369

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<211> 3636

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1937)

<223> n equals a,t,g, or c

<400> 370

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<211> 4039

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1085)

<223> n equals a,t,g, or c

<400> 371

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<212> DNA

<213> Homo sapiens

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gatgtatcaa attgatgcaa atttagatgt tgatacttac aataaagttt ttaatgtgtt 1560
ttaaaaaaaaa aaaaaaaaaa aaaaaaaaaa agggcggcc                                1599
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<210> 373

<211> 464

<212> DNA

<213> Homo sapiens

<400> 373

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ccttatgaat acggtaaatg tggcaaagcc tttaggcaga ggacagacct taaaaaacat 180
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actgagtgtg gggaaaccwt twgrcaaaac tcttcttttt tacaacaata aaaacctcac 360
actggagaga ttctctgaat gccttaagaa tttggttaat atggagaccc ttcccagggg 420
aaccagaagg aggatcgtga aaacctgttg actacttaga tgat 464
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<210> 374

<211> 890

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (886)

<223> n equals a,t,g, or c

<400> 374

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gagcaacatg cccaagtttt attgtgacta ctgcgataca tacctcacc c atgactctcc 180
atctgtgaga aagacacact gcagtggag gaaacacaaa gagaatgtga aagactatta 240
tcagaaatgg atggaagagc aggtcagag cctgattgac aaaacaacgg ctgcatttca 300
acaaggaaaag atacctccta ctccattctc tgctcctcct cctgcagggg cgatgatacc 360
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gatgagacct cctgcccgtc ccatgatggt gcccaactcg cccggaatga ctgcaccaga 600
cagataagga tagaggggag gccttattgt atcgggttta tattacctgt tctgcttcac 660
caggagatca tgctgctgtg atactgagtt ttctaaacag cataaggaag acttgctccc 720
ctgtcctatg aaagagaata gttttggagg ggagaagtgg gacaaaaaag atgcagtttt 780
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaanaaaa 890
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<210> 375

<211> 1874

<212> DNA

<213> Homo sapiens

<400> 375

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acagctctac aagcctggaa aaaaataatg tgctatttgg tgaaagatac ttagaaaaat 180
tttatggcct tgagataaac aaacttccag tgacaaaaat gaaatatagt ggaaacttaa 240
tgaaggaaaa aatccaagaa atgcagcact tcttgggtct gaaagtgacc gggcaactgg 300
acacatctac cctggagatg atgcacgcac ctcatgtgtg agtccccgat gtocatcatt 360
tcagggaaat gccagggggg cccgtatgga ggaaacatta tatcacctac agaatacaata 420
attacacacc tgacatgaac cgtgaggatg ttgactacgc aatccggaaa gctttccaag 480
tatggagtaa tgttaccccc ttgaaattca gcaagattaa cacaggcatg gctgacattt 540
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tggtgggttt tgcccggtga gctcatggag acttccatgc ttttgatggc aaaggtggaa 600
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aaaaaaaaaa aagc 1874

<210> 376

<211> 2018

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1997)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2012)

<223> n equals a,t,g, or c

<400> 376

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gccctgaacc cagtgcctgc agccatggct cccggccagc tcgccttatt tagtgtctct 120
gacaaaaccg gccttggtga atttgcaaga aacctgaccg ctcttggttt gaatctggctc 180
gcttccggag ggactgcaaa agctctcagg gatgctggctc tggcagtcag agatgtctct 240
gagttgacgg gatttcctga aatgttgggg ggacgtgtga aaactttgca tcctgcagtc 300
catgctggaa tcctagctcg taatatcca gaagataatg ctgacatggc cagacttgat 360
ttcaatctta taagagttgt tgcctgcaat ctctatccct ttgtaaagac agtggcttct 420
ccaggtgtaa stgttgagga ggctgtggag caaattgaca ttggtggagt aaccttactg 480
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gtggtgtcca cggagatgca gagctccgag agtaaggaca cctccttgga gactagacgc 600
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ttcaggaaac agtacagcaa aggcgtatct cagatgccct tgagatatgg aatgaacca 720
catcagaccc ctgcccagct gtacacactg cagcccaagc ttcccatcac agttctaaat 780
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attttaccac aactgtttt ttggttgcgt tatgtgtagg tgaacagtca cgcctgaac 1920
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aaaaaaaaa aaaccncgg ggggggcccc gnaccca 2018

<210> 377

<211> 818

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (818)

<223> n equals a,t,g, or c

<400> 377

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ctctggcgat cgagggggtc tagtacaccg caatcatgtc tattatgtcc tataacggag 120
gggccgtcat ggccatgaag gggaagaact gtgtggccat cgtgcagac aggcgcttcg 180
ggatccaggc ccagatggtg accacggact tccagaagat ctttcccatg ggtgaccggc 240
tgtacatcgg tctggccggg ctgcgcactg acgtccagac agttgccag cgcctcaagt 300
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tgtgtgagtc cctctgggag cccaacatgg atccggatca cctgtttgaa accatctccc 600
aagccatgct gaatgctgtg gaccgggatg cagtgtcagg catgggagtc attgtccaca 660
tcacgagaa ggacaaaatc accaccagga cactgaaggc ccgaatggac taaccctgtt 720
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aaaaaaaaa accccggggg gggcccgaa ccaaattn 818

<210> 378

<211> 2565
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1508)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2565)
<223> n equals a,t,g, or c

<400> 378
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agacctgaat gggcttgacc atctcacaaac tgctcgcgtg acgaccgcat tcgtggcagg 180
taagaagatt gctgtatcaa ctcaagaaag cagtaacttc actgtctttg tattttgaat 240
tgcaacaaca actttgatat caacaatgaa gcaatgatat ctaagaacma aagartattt 300
gccaacagtc atcataatat caagtgattg tataagcaga aacaagctgt cacagacctg 360
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atataaatca tttcaattat atctacatca aataaaataa aaatgagtga agccccaga 480
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catgcagatg aagacgatga ggaggaagat gattctycac cagaaaggca gattgtgggt 600
ggaatatgtt ccatggmaa gaaatccaaa tccaaaccaa tgaaggaaat tcttgracgg 660
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caactttatt aattacagtg attgcatttt tagcatccag ttgtaagatg aatatattaa 1800
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aacaccacaa tctgcagatg ttcaagtccc ttacataaaa tggcataagta tttatatgta 2460
acctatgcat attctcctgt atatttttaa tcatctctac attaaaatac ctgataaaat 2520
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<210> 379

<211> 1680

<212> DNA

<213> Homo sapiens

<400> 379

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aatagttaca cacaagaggg aaactggaag ccaaacactg tacagtattg ttagaagagt 180
cacctcccta ctctttttat tttacatgag tgcgtatgtg ttttggcaga tgagctttca 240
gctgaggcct gatggaaatt gagataacct gcaaagacat aacagtattt atgagttata 300
tcttagttct tgaattgtg gaatgcatga ttgacaatat atttttaatt tttatttttt 360
caagtaatac cagtactgtt taactatagc cagaactggc taaaattttt atattttcag 420
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cagataaata gaagtacagt gaggtctata gccattttat taaaatagct taaaagttag 660
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tttacagtct gtattagaca tactgttttt ataatgtttt acttctgcct taagatttag 1560
gttttttaaa tgtatttttg ccctgaatta agtgtaattt tgatggaaac tctgctttta 1620
aaatcatcat ttactgggtt ctaataaatt aaaaattaaa cttgaaaaaa aaaaaaacga 1680

<210> 380

<211> 1267

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (214)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1165)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1255)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1262)

<223> n equals a,t,g, or c

<400> 380

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atgtatatgg ctttactcaa gcaratctca tctcatgaca ggcagccacg tctcaacatg 180
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gcactgatta aaataggatt attttaarta caaaaggcat tttatatgaa ttataaactg 720
aagagcttaa agatagttac aaaatacaaa agttcaacct cttacaataa gctaaacgca 780
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atgatgcagt ttcaagtacc aaaacgttga attgatgatg cagttttcat atatcgagat 900
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taagcaaaat gccaaaaggg gtctnaattg aartgaaaat gtaattttgt ttttaaaata 1200
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anaaatt 1267
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<210> 381

<211> 1031

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1015)

<223> n equals a,t,g, or c

<400> 381

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caaaaatggt tcacttccta acagttttcc tttttccact gtgtgactga aagctcctat 180
atcattttat atttctgaat ctataaaaca aaacaaacaa gcctgamagt gtctggarga 240
rccaaagggt gcctccctgt ccccaaatat attggctata tgagagtaat ttaccctc 300
tacgtacctt aaggcaccca gttcactagt ctgtggggtc ctggagcctg tctcttcttt 360
ctggagggtt aaactgaata gcaataatta cgttacccaa agcatgtgga ggaaaagtga 420
aaccagccac ggagacgctg gccacgggc tcggcctgcg gtgtggcctg ctttgcctac 480
cagcgtcagc cgctcatttc cttctcatga agtcccatct ggtcatgggg acgagggccg 540
ggagggcacc gggtagcctt ttcacacttg gggattaggg gagtggagaa agatttgggc 600
catgcatgca aagtcaaagt ttaaaatatt atccttttca aatagatgat ataataacc 660
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tcaatctaaa ccaatgtaca ggtgtacaat gaaaaattta aatgcttagt tatttttccc 780
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gggtgggggt tgaaagtgtg tatctttaa tacatgtaca aatcgttgtc aaaagtaacg 960
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gggggggccc c 1031
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<210> 382

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1577)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1579)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1597)

<223> n equals a,t,g, or c

<400> 382

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agcggctgtc caatcgagtc gtgcgtgtgt tgggctgtaa cccgggtccc atgacctcc 180
aaggcaccaa caccaccta gtggggaccg gccccaggag aatcctcatt gacactggag 240
aaccagcaat tccagaatac atcagctggt taaagcaggc tctaactgaa ttaacacag 300
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<210> 383

<211> 175

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (95)

<223> n equals a,t,g, or c

<400> 383

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ccaaacatct actacaaggt atgagggctc ctctnacgtg gctatcctga atccagccct 120
tcttgggggtg ctctccagt ttaaattcct ggtttraggg acamctstaa catct 175

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<210> 384

<211> 2171

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2166)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2170)

<223> n equals a,t,g, or c

<400> 384

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cggacttcct gggaaagtgg ggaaggccaa ggggaaaaaa acacaaatgg ctgaagtttt 180
gccttctccg cgtggtcaaa gagtcattcc acgaataacc atagaaatga aagcagaggc 240
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tgggtgtgga ctagaaggcc taaaacaaag attagaaaag aaacagaaaa gagaaccagg 360
tacaaagaca aagaaacaaa ctacattggc atttaagcca atcaaaaaag gaaagaagag 420
aaatccctgg tctgattcag aatcagatag gagcagtgc gaaagtaatt ttgatgtccc 480
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<210> 385

<211> 2364

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (19)

<223> n equals a,t,g, or c

<400> 385

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<210> 386

<211> 2864

<212> DNA

<213> Homo sapiens

<400> 386

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aaacagatcc tctcccagac taacaccata cccatcattg gttccccctc cagcaagcgg 180
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<210> 387

<211> 2683

<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2649)
<223> n equals a,t,g, or c

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<210> 388

<211> 1446

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (35)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (37)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (57)

<223> n equals a,t,g, or c

<400> 388

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tttcccagtt tgatttcaat aaatctgtcc actcccctt tgtgggggtg aacgttttaa 1380
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aaaaaa

1446

<210> 389

<211> 723

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (705)

<223> n equals a,t,g, or c

<400> 389

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ataaaaactg acttgtaatc caggctatgt ctcttttttag cttcgtaatc tttggcaagg 180
ccattggatt cttcagctgt acaattagga gactcgatca ggtgattgcc tttctcagct 240
gtcagttctc taatttcagg cttggtagct tgttaggaact gaaattgcaa ttaaaacctt 300
tataaactca aactaaatca tgaattacag aaaaagtcca ttcttccaaa acttgatggt 360
accacactta caagttttaa atatgaagtc gactgtttta aggattctgc atatattcta 420
gtgtgcacat tcagaaacat ttttcttgga aaaagtaccc aacatttttt ataactgcac 480
atattaattt attgccagaa taaattgcat tgcattgctaa ataaagtcag ataattcaaa 540
tccatttgct tttatgtagt ttttcttcta aatgtcaaca ttttggattt aaaatgttta 600
tggttttata tgagggtagg aaatcttaac tgctttgggg ggtattgttt ataggctttt 660
tgttatgggg ccggtagtgt tttaataggg ggattgcccc tttcnaccgt ttgggggccc 720
ggg 723
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<210> 390

<211> 1046

<212> DNA

<213> Homo sapiens

<400> 390

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ccgacctgct ggtgccactc tggaaagggc caagactctc tccccaggga agaattgggt 180
cgtcaaagac gtttttgcct ttgggggtgc cgtggagaac cccgagtact tgacacccca 240
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tcaagagggt ggagggccct ccgaccactt ccaggggaac ctgccatgcc aggaacctgt 540
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gcgacccatt cagagactgt ccctgaaacc tagtactgcc ccccatgagg aaggaacagc 840
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<210> 391
<211> 699
<212> DNA
<213> Homo sapiens

<400> 391
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atttggtgtg ctgttgaagg ggggagacta gagaaatggc agggaaacctc ttatccgggg 180
caggtaggcg cctgtgggac tgggtgcctc tggcgtgcag aagcttctct cttggtgtgc 240
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aacgttgtat ccgaaagagg aaaatggttg gaagtagaat gttcgtgat gacctgcaca 480
accttaataa acgcacccgc tatctctaca aacactttaa ccgacatggg aagtttcgat 540
agaagagaaa gctgagaact tcggaaaagg ctcatctgtc accctggaga agggaaactg 600
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gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagtcgacc 699

<210> 392
<211> 1545
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (58)
<223> n equals a,t,g, or c

<400> 392
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ccggactcgg acgcgtggta gccccaggat gggtaggttc aacgagaaga agacaacatg 120
tggcaccgtt tgccetcaagt acctgctgtt tacctacaat tgctgcttct ggctggctgg 180
cctggctgtc atggcagtg gcatctggac gctggccctc aagagtgact acatcagcct 240
gctggcctca ggcacctacc tggccacagc ctacatcctg gtgggtggcgg gcactgtcgt 300

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caagcgctac caccagccgg gccatgaggg tgtgaccagc gctgtggacc agctgcagca 540
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caaccatccc tgccacatac aggtgctcaa taaacacttg tagagcagaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1545
```

<210> 393

<211> 749

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (490)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (748)

<223> n equals a,t,g, or c

<400> 393

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tgaaccggyc caggtcggaa acggagcagt tttccttgag cggagattca ggtttttcag 180
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cgcaaaaggg cccctcgtag caaggtcccg cgcacacgag actttcacat caatctcttc 300
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gactgcctcg ctgccccacc tcccgtcctt tggcctgtcc ccagattcct tccctggttg 600
acttgactca tgcttgtttc actttcacat ggaatttccc agttatgaaa ttaataaaaa 660
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aaaaaaaaaa aaaaaaaaaa aaaaaaana 749
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<210> 394
<211> 611
<212> DNA
<213> Homo sapiens

<400> 394
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agccggaaga gcgtttccca aagtgtattc tgcggaacta gcacctactg tgttctcaac 180
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aatttaattt ctttttttaa ttttggtgta caagctgtaa catttcatct ttcaaagtgt 480
aacacgctga tttcctcaaa tagagatacc cctttgagtg ataaatttgc aaaatgctgt 540
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tccttttaaa a 611

<210> 395
<211> 1856
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1851)
<223> n equals a,t,g, or c

<400> 395
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gagcccgccg cggccaggcc ctgccgctca tggtgccagc ccagagaggg gccagcccg 180
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agaaccagga gttaagacag cgcttgggga tggatgccct ggttgctgaa gaggaggcgg 480
aagcaagggg aatgaagtga ggccagtggc cgggtctgct gagtccgcag cactcagact 540
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caatactgtt gcccttttcc ttgactatta cactgcctgg aggatagcag agaagcctgt 1260

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gtagcttctg aaagggtgctt tctccattta tttaaaacta cccatgcaat taaaagggtac 1800
aatgcaaaaa aaaaaaaaaa aaaaaaaccc ggggggsgcc ccggaaccaa nttccc 1856
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<210> 396

<211> 2651

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (45)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (47)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2642)

<223> n equals a,t,g, or c

<400> 396

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gagccgaaga tggcagtgaa cgtatactca acgtcagtga ccagtataa cctaagtcga 180
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<210> 397

<211> 2507

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2489)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2496)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2504)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2505)

<223> n equals a,t,g, or c

<400> 397

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<213> Homo sapiens

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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<400> 398
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<212> DNA
<213> Homo sapiens

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<211> 1522

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (479)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1471)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1481)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1487)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1501)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1508)

<223> n equals a,t,g, or c

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<210> 401

<211> 1370

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1223)

<223> n equals a,t,g, or c

<400> 401

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<210> 402

<211> 1412

<212> DNA

<213> Homo sapiens

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<222> (51)

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<221> misc feature

<222> (1406)

<223> n equals a,t,g, or c

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<210> 403

<211> 1750

<212> DNA

<213> Homo sapiens

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<220>

<221> misc feature

<222> (40)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (44)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (70)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (107)

<223> n equals a,t,g, or c

<400> 403

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<210> 404
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<212> DNA
<213> Homo sapiens

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<222> (150)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1330)
<223> n equals a,t,g, or c

<400> 404
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gattgttaan ctgcctctt 1339

<210> 405
<211> 482
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (440)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (469)

<223> n equals a,t,g, or c

<400> 405

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ctgctctaca ccagtgaata atttacctc taataggggg tggttaactat aaagatgata 420
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gg 482
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<210> 406

<211> 1413

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (9)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (24)

<223> n equals a,t,g, or c

<400> 406

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taattcattt gaatttgaaa aacgtagaaa tgaacctatc aaataccagc gagagctatg 360
gaataaaaact attgatgcga tgaagagagt tgaagaaatc aaacagaagc gccaaagctaa 420
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cagtgtcaga tatttttatt ttagtatttc ctgttttggg ttatttgcac cttagaagag 1080
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<210> 407

<211> 1693

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1548)

<223> n equals a,t,g, or c

<400> 407

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tcgagacagt tct 1693

<210> 408

<211> 1342

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (107)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1332)
<223> n equals a,t,g, or c

<400> 408
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aaaaaaaaaa anaaaaaaaa ca 1342

<210> 409
<211> 2417
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (107)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (680)

<223> n equals a,t,g, or c

<400> 409

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aggaagcggc tctgctgagg ttcaaggggc cccagcacag tgtggcatcc gttcagcttt 180
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<210> 410

<211> 1401

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1394)

<223> n equals a,t,g, or c

<400> 410

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tgatcccaaa atgcaaactg acaaaccttt tgaccagacc acaattagtc tgcagatggg 180
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tmaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
aaaaaaaaaa gggnggccgt t 1401
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<210> 411

<211> 3016

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (399)

<223> n equals a,t,g, or c

<400> 411

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<210> 412

<211> 958

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (930)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (934)

<223> n equals a,t,g, or c

<400> 412

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gctaatttag ccgaagaagc ctgggaatca agtttgaaac aaagattaat aaagttcctt 840
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggnggccgt tttaaaggaa ccaggttt 958
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<210> 413

<211> 500

<212> DNA

<213> Homo sapiens

<400> 413

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gtgaaatcta gagtaaaacc aagctggccc aaggtgtcct gcaggctgta atgcagttaa 360
atcagagtgc catttttttt tttgttcaa tgattttaat tattggaatg cacaattttt 420
ttaatatgca aataaaaagt ttaaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 480
gcggccgctc gaattaagcc 500
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<210> 414

<211> 3397

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3081)
<223> n equals a,t,g, or c

<400> 414
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 3397
```

<210> 415

<211> 2880

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<400> 415

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tatggacaat tggaaagtga ctggtatttt gaaaggtaat gggagcccag tcaatgggag 480
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cccagcgccg tttgacctct cccaagatac accagcagcc tgcttactac taaacgcaat 720
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```

<210> 416

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (12)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1610)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1611)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1616)

<223> n equals a,t,g, or c

<400> 416

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```

<210> 417

<211> 1815

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (270)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1184)

<223> n equals a,t,g, or c

<400> 417

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<210> 418

<211> 1966

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (15)

<223> n equals a,t,g, or c

<400> 418

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<220>

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<222> (2843)

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<210> 420

<211> 2705

<212> DNA

<213> Homo sapiens

<400> 420

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<211> 1901

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1828)

<223> n equals a,t,g, or c

<400> 421

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<210> 422

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 422

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<211> 777

<212> DNA

<213> Homo sapiens

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<222> (759)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (764)

<223> n equals a,t,g, or c

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<210> 424

<211> 1649

<212> DNA

<213> Homo sapiens

<400> 424

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<210> 425

<211> 1608

<212> DNA

<213> Homo sapiens

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<222> (1598)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1600)
<223> n equals a,t,g, or c

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<210> 426
<211> 1794
<212> DNA
<213> Homo sapiens

<220>
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<222> (1789)
<223> n equals a,t,g, or c

<220>
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<222> (1790)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1793)

<223> n equals a,t,g, or c

<400> 426

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<210> 427

<211> 770

<212> DNA

<213> Homo sapiens

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<220>

<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (97)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (618)
<223> n equals a,t,g, or c

<400> 427
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taaaaaatag aaattatctc actacttaaa tcccattttt ttcacttcat atgaaagaac 180
atattgatag tatattctat attatttcat agatctgtct gaaagagatt gggaacaaaa 240
atatctaatt gagatattct ttaatttttt acatagcagc tttatttttt ttattctgta 300
gtatcagcga aatcagtcac gtttatacct tgaatataaa tatcaggaat catgcaatta 360
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aggatattaa aaaacatttg aaaaagagaa aaagaaaaat cagtgtttag aaatgttgat 540
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tttatagaac aaggtggnca ggtggggagc cctttaccct tctggtgaag ttaaaccata 660
ggaagtttac aatttgccct tcacaaacat tagcagtcct gggcatggtg gctgragcct 720
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<210> 428
<211> 512
<212> DNA
<213> Homo sapiens

<220>
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<222> (18)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (484)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (491)

<223> n equals a,t,g, or c

<400> 428

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ggactgtacc tgcacgggg ctgggcgagg gagaataagc tgtaccatcg caaaccgctg 180
ccatgaagg ggtcagtcct acaagattgg tgacacctgg aggagaccac atgagactgg 240
tggttacatg ttagagtgtg tgtgtcttgg taatggaaaa ggagaatgga cctgcaagcc 300
catagctgag aagtgttttg atcatgctgc tgggacttcc tatgtggtcg gagaaacgtg 360
ggagaagccc taccaaggct ggatgatggt agattgtact tgccctgggag aargcagcgg 420
acgcatcact tgcacttcta gaaatagatg caacgwtcag gacacaagga catctataga 480
attngagaca ncttgagcaa gaaggataat cg 512
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<210> 429

<211> 1470

<212> DNA

<213> Homo sapiens

<220>

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<222> (1346)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1347)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1357)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1387)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1415)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (1454)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (1462)

<223> n equals a,t,g, or c

<400> 429

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ttgggtgggg ggccgctgaa ctgacaagcg acatttcagc tcctttcacc cgccggaacc 180
ccggagccgg ggcccgctca gccggcgta ccatgaccaa ggccggtagc aagggcggga 240
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tcccggtgaa ggagctggct gcccttccaa aggccaccat cctggatctg tcttgtaata 360
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<210> 430

<211> 434

<212> DNA

<213> Homo sapiens

<400> 430

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gaatccccag cccggaagct ctcccagtc ttccgcttc ctgttacggg aggcactggt 180
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gcctcaacaa cctc 434
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<210> 431

<211> 1823
<212> DNA
<213> Homo sapiens

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<222> (1804)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1805)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1815)
<223> n equals a,t,g, or c

<400> 431
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<210> 432
<211> 3391
<212> DNA
<213> Homo sapiens

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<222> (33)
<223> n equals a,t,g, or c

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<222> (114)
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<210> 433

<211> 2553

<212> DNA

<213> Homo sapiens

<220>

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<222> (2510)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2516)

<223> n equals a,t,g, or c

<400> 433

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<210> 434

<211> 2532

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (2470)

<223> n equals a,t,g, or c

<400> 434

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<210> 435

<211> 1822

<212> DNA

<213> Homo sapiens

<400> 435

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<210> 436

<211> 1030

<212> DNA

<213> Homo sapiens

<400> 436

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<210> 437

<211> 1632

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (14)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1602)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1616)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1617)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1628)

<223> n equals a,t,g, or c

<400> 437

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<210> 438

<211> 1016

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (27)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (993)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (994)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (995)

<223> n equals a,t,g, or c

<400> 438

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<210> 439

<211> 594

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (476)

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<220>

<221> misc feature

<222> (519)

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<220>

<221> misc feature

<222> (530)

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<220>

<221> misc feature

<222> (531)

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<220>

<221> misc feature

<222> (539)

<223> n equals a,t,g, or c

<400> 439

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aaggaaaaac aggtcttcat cgaatctact aattccacac cttttaaaaa tttttnggga 480
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<210> 440

<211> 1580

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (873)

<223> n equals a,t,g, or c

<400> 440

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<210> 441
<211> 1082
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<223> n equals a,t,g, or c

<220>
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<222> (1074)
<223> n equals a,t,g, or c

<400> 441
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<210> 442

<211> 1241

<212> DNA

<213> Homo sapiens

<400> 442

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<210> 443

<211> 968

<212> DNA

<213> Homo sapiens

<400> 443

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acaagttctg aaataatagc acaatttcaa agaagagact ctttgcaaag ttgataacat 240
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375

<210> 444
<211> 1360
<212> DNA
<213> Homo sapiens

<220>
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<222> (114)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (302)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (330)
<223> n equals a,t,g, or c

<400> 444
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gcccgccttg gggaacaggc cgtcgcgggc cctgcccctc gactgtcccc agcagtacca 240
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caggatgata tcgaagagct ggagaccaag gccgtgggaa tgtctaacga tggccgcttt 420
ctcaagtttg acatcgaaat cggcagaggc tcctttaaga cggctctaca aggtctggac 480
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<210> 445
<211> 1835
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (326)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1229)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1738)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1747)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1758)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1801)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1806)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1831)
<223> n equals a,t,g, or c

<400> 445
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gaaagaactt tccaaagtga gggaatatgt ccaattaatt agtgtgtatg aaaagaaact 420
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<210> 446

<211> 1355

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (55)

<223> n equals a,t,g, or c

<400> 446

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gaawaaaaaa aaaaaaaaaa amawaaaaaa aaaaa 1355

<210> 447

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (153)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (313)

<223> n equals a,t,g, or c

<400> 447

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tcctgtgctt tgnctcctgg gtgatttctc ttcaagtcag ttgtgggagg tgcctaggaa 360
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<210> 448

<211> 1393

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1360)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1383)

<223> n equals a,t,g, or c

<400> 448

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aanaaaaaaa aaa 1393
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<210> 449

<211> 1663

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (57)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (180)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (621)

<223> n equals a,t,g, or c

<400> 449

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gccagcaaag ccctcagagg ccacctcaga ccggtcagag ggcagcagcc gggacgcagn 180
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gaactggctg aatcagactc cgactgcgtc cctgcagagg ctggccaggc ctagacaggg 360
aagtctgtta gaactgctgt gctgatcaac gggacgctcc gtctttgaag aaagaagaga 420
tggtctctcc ccagccatgg gccacccttg ccagtractc caagtggaaac tacttagctc 480
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ttataaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1663

<210> 450

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 450

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cttctagacg acaaaatgca aaaaaggagg ccaaagactt ttggaatgga tatgaaagca 180
tacctgagat ctatgatccc acatctggaa tctggaatga aatcttccaa gtccaaggat 240
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gagttctggc tggcttgtga agactataag aaaacagagt ctgatctttt gccctgtaaa 420
gcagaagaga tatataaagc atttgtgcat tcagatgctg ctaaacaaat caatattgac 480
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<210> 451

<211> 926

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (687)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (865)

<223> n equals a,t,g, or c

<400> 451

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<210> 452

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (147)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (150)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1608)

<223> n equals a,t,g, or c

<400> 452

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aaaaaaaaaa aaaaaaaaaa aa 1642

<210> 453

<211> 2254

<212> DNA

<213> Homo sapiens

<400> 453

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gagtttgatt ataaaaaaaa aaaaaaaaaa aaaa 2254

<210> 454

<211> 1931

<212> DNA

<213> Homo sapiens

<400> 454

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<210> 455

<211> 771

<212> DNA

<213> Homo sapiens

<400> 455

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<210> 456

<211> 1169

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1164)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1167)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1169)

<223> n equals a,t,g, or c

<400> 456

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<210> 457

<211> 3249

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3234)

<223> n equals a,t,g, or c

<400> 457

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tccacaact 3249

<210> 458

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1895)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1902)

<223> n equals a,t,g, or c

<400> 458

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cttagactat tgtgcagtaa acctaaaagg tagtgagagaa ttgcttcctg ctagcaggaa 180
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ggtataatgc ccttccatca cacaacagga caccacccca gttttgtttt ctgggtttct 420
tccccctttg taggaatcag ataccttttg tagaaaaaaa tggcttatgc cacgtaaagg 480
tgaattttta gaaaccacct tctaggcgtt tttggaaccc ttactgaaat ccctccctt 540
gttacagatg gcgtagaagt cacaaagctg ttaattggac tgttgcttct ttgcctgttc 600
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attttacttt aaaaatgaaa tctggtgtta ctgtatttta tcgttttcaa taaaacttct 1860
taagtgtttt ggaaaaaaa aaaaaaaaaa aattnctgcg gncgcgaagg gaattc 1916
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<210> 459

<211> 2773

<212> DNA

<213> Homo sapiens

<400> 459

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gcaaggaggc ggcggcggcc agcgagtggc gagtagtga aacgttgctt ctgaggggag 180
cccaagatga ccggttctaa cgagttcaag ctgaaccagc caccgagga tggcatctcc 240
tccgtgaagt tcagcccaa cacctccag ttctgtcttg tctcctctg ggacacgtcc 300
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gtcctggact gcgccttcta cgatccaacy catgcctgga gtggaggact agatcatcaa 420
ttgaaaatgc atgatttgaa cactgatcaa gaaaatcttg ttgggacca tgatgcccc 480
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atcagatgtg ttgaatactg tccagaagt aatgtgatgg tcaactggaag ttgggatcag 540
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aaggtatata ccctctcagt gtctggagac cggctgattg tgggaacagc aggccgcaga 660
gtgttggtgt gggacttacg gaacatgggt tacgtgcagc agcgcaggga gtccagcctg 720
aaataccaga ctcgctgcat acgagcgttt ccaaacaagc agggttatgt attaatctct 780
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ctttttgtaa tatactctaa acctgttatt tctgtgctaa taaacgagat gcagaacct 2700
tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gsgggccgct 2760
cgcgatctag aac 2773

<210> 460

<211> 2031

<212> DNA

<213> Homo sapiens

<400> 460

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tttcttcaat cacatctgaa taaatcactt gaagaaagct tatagcttca ttgcaccatg 180
tgtggcattt gggcgctggt tggcagtgat gattgccttt ctgttcagtg tctgagtgct 240
atgaagattg cacacagagg tccagatgca ttccggtttg agaatgtcaa tggatacacc 300

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aactgctgct ttggatttca ccggttggcg gtagttgacc cgctgtttgg aatgcagcca 360
attcgagtga agaaatatcc gtatttggg ctctgttaca atggtgaaat ctacaacccat 420
aagaagatgc aacagcattt tgaatttgaa taccagacca aagtggatgg tgagataatc 480
cttcattctt atgacaaagg aggaattgag caaacaattt gtatgttgga tgggtgtgtt 540
gcatttgttt tactggatac tgccaataag aaagtgttcc tgggtagaga tacatatgga 600
gtcagacctt tgtttaaagc aatgacagaa gatggatttt tggctgtatg ttcagaagct 660
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gttaaatatc atcactgtcg ggatgaaccc ctgcacgccc tctatgacaa tgtggagaaa 840
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taggtggtct ttatgctgta atgtgaaagc aaatatttct tcgtgttgga tggggactgt 1920
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gtcctaaatc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2031

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<210> 461

<211> 1839

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1496)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1832)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1839)

<223> n equals a,t,g, or c

<400> 461

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gcccaggccg agcacgatgc cccctaaaaa gggaggtgat ggaattaaac caccccaat 180
cattggaaga tttggaacct cactgaaaat tggattgtt ggattgcaa atgttgaggaa 240
atctactttc ttcaatgtgt taaccaatag tcaggcttca gcagaaaact tcccgttctg 300
cactattgat cctaattgaga gcagagtacc tgtgccagat gaaaggtttg actttctttg 360
tcaataccac aaaccagcaa gcaaaattcc tgcctttcta aatgtggttg atattgctgg 420
ccttgtgaaa ggagctcaca atgggcaggg cctggggaat gcttttttat ctcattatag 480
tgcctgtgat ggcattcttc atctaacacg tgcttttgaa gatgatgata tcacgcacgt 540
tgaaggaagt gtagatccta ttcgagatat agaaataata catgaagagc ttcagcttaa 600
agatgaggaa atgattgggc ccattataga taaactagaa aaggtggctg tgagaggagg 660
agataaaaaa ctaaacctg aatatgat atgtgcaaa gtaaaatcct gggttataga 720
tcaaaagaaa cctgttcgct tctatcatga ttggaatgac aaagagattg aagtgttgaa 780
taaacactta tttttgactt caaaaccaat ggtctacttg gtaaatctt ctgaaaaaga 840
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gacaaacaaa ttatttttat ttgttttaaa attaaaatac tgtgtacccc ccccccncyc 1500
atgaaatgca ggttcactaa atgtgaacag ctttgctttt cacgtgatta agaccctact 1560
ccaaattgta gaagcttttc aggaaccata ttactctcat gatacttcat taatctccat 1620
catgtatgcc aagcctgaca catttgacag tgaggacaat gtggcttgct cctttttgaa 1680
tctacagata atgcatgttt tacagtactc cagatgtcta cactcaataa aacatttgac 1740
aaaacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1800
aaaaaaaaaa aaaaaaaacc ccgggggggg gncccaan 1839
```

<210> 462

<211> 779

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (26)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (731)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (737)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (759)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (762)

<223> n equals a,t,g, or c

<400> 462

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gggagtggag aggcccgagg ccaggaaagc agagacagac aaagcgtag gagaagaaga 120
gaggcagggg agacaagcca ggcacgatgg ccaccttccc accagcaacc agcgccccc 180
agcagccccc aggcccgagg gacgaggact ccagcctgga tgaatctgac ctctatagcc 240
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gaggggctac caggaaagcg cctccaaccc tagcaaaagt gcaagatggg gagtgagagg 600
ctgggaatgg agggcagagc cagggaagatc cccagaaaa gaaagctaca gaagaaactg 660
gggctcctcc aggggtggcag caacaataaa tagacacgca cggcarccam aaaaaaaaaa 720
aaaagggsgg nccggancca attggcctaa agggggggnt tncaattaat gggccgggt 779
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<210> 463

<211> 1717

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (27)

<223> n equals a,t,g, or c

<400> 463

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ttctcatgg actgctactt catggatgat agcttcattg ctttgggtag ggatttaagg 180
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atcttgttts tttcgtgaga gatctcgcca tggcagcatc ttgtaaagta agtgtaattg 540
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cacatgcaca aaagacttaa ctagctttac atttagcagt cagttgggta gattaggttt 600
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cgtggattcc atttgaccca gtttactatc agttcagttc aggtagattt ggttcaactt 720
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gattttagc tacctactgt gcctgacttg gtgcctgtgt gaggattaag cccttagtct 1620
gctcttgcaa ttattcaaat gacaaattaa atttgctttt gtaataacaa taaaagtgtg 1680
catcttcct tttgaaaaaa aaaaaaaaaa aaaaaag 1717

<210> 464

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (787)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (819)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (827)

<223> n equals a,t,g, or c

<400> 464

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ggcggcggag gctgaccccc taggacgctt cacgtgtccc gtgtgcttag aggtgtacga 120
gaagccggta caggtgccct gcggacacgt cttttgctct gcatgcctgc aggaatgtct 180
gaagccgaag aagcctgtct gtgggtgtgt tcgcagcgt ctggcacctg gcgtccgagc 240
cgtggagctc gagcggcaga tcgagagcac agagacttct tgccatggct gccgtaagaa 300
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catggaaggt gtgaaggcca ccattaagga tgcattctct cagccaagga atgttccaaa 420
ccgttacacc tttccttgct cttactgtcc tgagaagaac tttgatcagg aaggacttgt 480
ggaacactgc aaattattcc atagcacgga taccaaactc gtggtttgtc cgatatgtgc 540

ctcgatgccc tggggagacc ccaactaccg cagcgccaac ttcagagagc acatccagcg 600
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gaatcaggtg ttgcagcgt ccatcatcga ccagtgaagc gagtccgtgc ttgctatctg 720
tctcatgtta cagagcttcc attacatatt aaacgtgaaa tctatgaaaa aaaaaaagg 780
ggggggnccc ggttacccca atttcggccc tattaggtna agtcgtna 828

<210> 465

<211> 1173

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (137)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1166)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1168)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1171)

<223> n equals a,t,g, or c

<400> 465

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gcggttcagg cccttgntca ctcaatgacc tccagttctt tagatacaac agtaaagaca 180
ggaagtctca gcccatggga ctctggagac aggtggaagg aatggaggat tggagcagg 240
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agtattacaa cgacagtaac gggctctcag tattgcaggg aaggtttggg tgtgagatcg 360
agaataacag aagcagcgga cattctggaa atattactat gatggaaagg actacattga 420
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gaagtgggag gcagaaccag tctacgtgca gcgggccaag gcttacctgg aggaggagt 540
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1173

<210> 466

<211> 521

<212> DNA

<213> Homo sapiens

<400> 466

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<210> 467

<211> 1428

<212> DNA

<213> Homo sapiens

<400> 467

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<210> 468

<211> 3463

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1187)

<223> n equals a,t,g, or c

<400> 468

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<210> 469

<211> 621

<212> DNA

<213> Homo sapiens

<400> 469

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aaaaaaaaaa aaaaaaaaaa a 621
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<210> 470

<211> 1833

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (126)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (386)

<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (524)
<223> n equals a,t,g, or c

<220>
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<222> (1798)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1812)
<223> n equals a,t,g, or c

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<210> 471
<211> 3202
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3160)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3180)

<223> n equals a,t,g, or c

<400> 471

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<210> 472

<211> 941

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (927)

<223> n equals a,t,g, or c

<400> 472

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<210> 473

<211> 1279

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1144)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1273)
<223> n equals a,t,g, or c

<400> 473
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gaaccaagtt tantttggg 1279

<210> 474
<211> 3209
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (427)
<223> n equals a,t,g, or c

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aaaaaaaaa aaaaaaama mgcgtccgc 3209

<210> 475
<211> 833
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (58)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (73)
<223> n equals a,t,g, or c

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gaggaatggg atttaatgac ctttgatgcc aaccatgatg acagcgtgaa aaaaatcaaa 180
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caccttacct tgaaagtggg gaagcccagt gatgaggagc tgcccttggt tcttgtggag 360
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gtgaaagcaa tgatcgagac taagacgggt ataatccctg agaccagat tgtgacttgc 480
aatggaaaga gactggaaga tgggaagatg atggcagatt acggcatcag aaagggaac 540
ttactcttcc tggcatstta ttgtattgga gggtgaccac cctgggcatg ggggtgtggc 600
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tttactaatg tattactgag actagtaaataa aaatttttaa ggcaaaatag agc 833

<210> 476
<211> 1141
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature

<222> (11)

<223> n equals a,t,g, or c

<400> 476

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tgacagcggt taacaaagct tagagaaacc tccaggagac tgctatcatg gcagagaagc 180
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cagctggagt agagtttgaa gagaaattta taaaatctgc agaagatttg gacaagttaa 300
gaaatgatgg atatttgatg ttccagcaag tgccaatggg tgagattgat gggatgaagc 360
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acataaagga gagagccctg attgatatgt atatagaagg tatagcagat ttgggtgaaa 480
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gatctgatgt gaattcagat ttccaatctt ctctagcca accattttcc tggaattaaa 1080
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g 1141
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<210> 477

<211> 1102

<212> DNA

<213> Homo sapiens

<400> 477

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<210> 478

<211> 4201

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4077)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4161)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4186)

<223> n equals a,t,g, or c

<400> 478

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<210> 479

<211> 787

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (780)

<223> n equals a,t,g, or c

<400> 479

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tgagaggtgt agtaccgccc ccagagccaa ttttccactt ccgcktccgg cgctgcggca 180
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aagtatatgg gaccttaagc tcaccttctt tacttgatc aaatgatgac tggatactg 660
gtctcccatc cctttgcttg tggcaggaga tggcttaaat aaataactta aayttaaaaa 720
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaactn 780
ggggccg                                           787
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<210> 480

<211> 731

<212> DNA

<213> Homo sapiens

<400> 480

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ctgggcccct gactcaaaaa agtggttttg accagagagg cccagatgga ggctgttc 660
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aaaaaaaaaa a                                           731
```

<210> 481

<211> 1119

<212> DNA

<213> Homo sapiens

<400> 481

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ccccagtcct cccacccgc gcgtggcggc gccggctccc tagccaccgs ggccccaccc 180
tcttcgggc tcagctgtcc gggtgcttt cgcctccgcc tgtggatgct gcgcctctcc 240
gaacgcaaca tgaaggtgct ccttgccgcc gccctcatcg cggggtccgt cttcttcctg 300
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ggaaagactg ttccaaaaac agtggataat tttgtggcct tagctacagg agagaaagga 480
tttggttaca aaaacagcaa attccatcgt gtaatcaagg acttcatgat ccagggcgga 540
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gagaacttca aactgaagca ctacgggcct ggctgggtga gcatggccaa cgcaggcaaa 660
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tgtaacaaac tcctaccaac actgaccaat aaaaaaaaat gtgggttttt ttttttttta 1080
ataaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagg 1119
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<210> 482

<211> 2056

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (137)

<223> n equals a,t,g, or c

<400> 482

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ggaggccacg ggcgatgnat cttcgggtcc tgggtggggc tgcctccct gccatgctac 180
tggctgcccc accacccatc aacaagctgg cactgttccc agataagagt gcctgggtgcg 240
aagcaagaac atcacccaga tcgtgggcca cagcggctgt gaggccaagt ccatccagaa 300
cagggcgtgc ctaggacagt gcttcagcta cagcgtcccc aacaccttcc cacagtccac 360
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gcactgtagc tgcaggccct gcggcaagga gcctagtcac gaggggctga gcgtctatgt 540
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aaamaggggg gggccc                                     2056
```

<210> 483

<211> 887

<212> DNA

<213> Homo sapiens

<400> 483

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attaatttca agaaaaatat cttgagtttt aagaaataaa catctccaga aaaggagaaa 180
gtcgatttta taaaatgtcg caactctcca acatttgggg tagtgactcc ttttttgta 240
ggacatttga aactagcaag cagccattgt ttctaaagaa ttctggcttc acattgactc 300
atgtttcttt cactccattt tgaaatagct aaaaatcatt aaaactgtaa atattttgtt 360
gcttgggtaa gcatcttctg ggaactttgt atctatggta tataatcata gaattttata 420
ttttcatata aagctaattt ttttctagtt tcaactccgt catagtkttt tttccttttt 480
gtgggtggata tgtgaattca actttctgtg tattgaagta gcaaaaacca tctttacatt 540
ccaaaagaat ccaacatgtg ttatttcttt gaggcagtga ttgtgaaagt tgggttttct 600
ttttaattcc attgaccatt tgtgcaatag gaattagaca taattagtca ctgaaaacat 660
tcgtcacatt gaccatttgc gaaaaagtgt gctttttttt tttttttaa tttgttcagg 720
gggaggggtt ttgtaacctg aaatttttcc ctttttcttc tgtttaaact atatcaaac 780
attctattat agtggtattt aatatgtaaa ttgtattgct atacataaaa taaagtatgg 840
tttttgatgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aataaaa 887
```

<210> 484

<211> 1878

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1446)

<223> n equals a,t,g, or c

<400> 484

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gaagccgctc accgtcggaa gctgcgggag ctgaaactgc gccatcgtca ctgtcggcgg 180
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agtggttatt gcaggcctct gtctcctcat accatctatt cagagacgta gctgaagtca 420
```

cagccttccg agggagcctg ctaagctggt acgaccaaga gaaacgggac ctacatgga 480
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gtctcaccatc tccactgatg cacacagcct caacagtgca gccagtgac acctctgaaa 1800
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aaaaaaaaa aaaaaaaa 1878

<210> 485

<211> 1566

<212> DNA

<213> Homo sapiens

<400> 485

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tagcaaaactt caggagagct actttctatc caaataattt aaaaaacact tttcacctac 120
tcctttcatg gttataacac attggcagac tttttgctgg ctctgggagc catgatttta 180
atcacattct gcaagggtgac aaatgtcata cattccacat tgtgtggtag ccatctcttt 240
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agaaccctct cacaccagag acagttcttc tctgttcagt ttccaatccc cgataatttg 360
ctaaaaataac attgtacatc caagagaggg aagaagagta tgtcagtata ttatgcagaa 420
gatagataca gccttttcag aagatctcca ctagtttttg ttccaaaaat tcaagtttat 480
gggagaaaac tcaattagcc accttttcac agttgtgtgg atataacatt tgggggatct 540
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cattctgtaa tcaactgagc tagttccaat aaagttaagc aggttttaaat ccactttgtg 1500
cctatctttt cactgacaat aaagttagct attttaaaat gcaaaaaaaaa aaaaaaaaaa 1560
aaaatt 1566

<210> 486

<211> 3046

<212> DNA

<213> Homo sapiens

<400> 486

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atggataaca gactgatgga actctttcct gccataaagc aaagtgttga acacttcaca 780
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<210> 487

<211> 1904

<212> DNA

<213> Homo sapiens

<400> 487

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1904

<210> 488

<211> 827

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (826)

<223> n equals a,t,g, or c

<400> 488

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 827

<210> 489

<211> 1926

<212> DNA

<213> Homo sapiens

<400> 489

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<210> 490

<211> 1461

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1432)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1452)

<223> n equals a,t,g, or c

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<211> 805

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (20)

<223> n equals a,t,g, or c

<400> 491

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<210> 492

<211> 2269

<212> DNA

<213> Homo sapiens

<400> 492

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<210> 493

<211> 4108

<212> DNA

<213> Homo sapiens

<400> 493

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<211> 2209

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (352)

<223> n equals a,t,g, or c

<400> 494

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<210> 495

<211> 1677

<212> DNA

<213> Homo sapiens

<400> 495

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<210> 496

<211> 1702

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1691)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1701)

<223> n equals a,t,g, or c

<400> 496

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cagaggctaa gaccatccc gtatctgctc tcctgaaata attctggagt catgcctgaa 180
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<210> 497

<211> 2376

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (6)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2354)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2375)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2376)

<223> n equals a,t,g, or c

<400> 497

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cccacaagca gaccgggctg tatggcatca ccacggccct gtctcagtgt ccgcaagcca 180
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2376

<210> 498

<211> 840

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (840)

<223> n equals a,t,g, or c

<400> 498

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catgaccctg cagtcgcaga agttccagat aggagattac ttggacatag caattacccc 480
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ttattgcoat taagccttta aattctaaac aaattataat gcatacatcta tttaggagtt 660
agatttggat gtgctattgt atgattacga atagtctgta tgtttcaagc ctttctgtaa 720
aatatgaaga aaagtgtctt tagcattctg tgtaaaactg tactgtttaa tatatgtgtg 780
taatcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840

<210> 499

<211> 461

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (452)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (455)

<223> n equals a,t,g, or c

<400> 499

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cgccatgtct tctcacaaga ctttcaggat taagcgattc ctggccaaga aacaaaagca 120
aaatcgccc attccccagt ggattcggat gaaaactgga aataaaatca ggtacaactc 180
caaaaggaga cattggagaa gaaccaagct ggtctataa ggaattgcac atgagatggc 240
acacatattt atgctgtctg aaggtcacga tcatgttacc atatcaagct gaaaatgtca 300
ccactatctg gagatttcga cgtgttttcc tctctgaatc tgttatgaac acgttggttg 360
gctggattca gtaataaata tgtaaggcct ttcyttttta aaaaaaaaaa aaaaacyyrr 420

ggggggggccc gggtcccaat ccccccctatt tnaanccct t

461

<210> 500

<211> 2782

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2620)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2641)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2643)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2712)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2742)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2759)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2779)

<223> n equals a,t,g, or c

<400> 500

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<210> 501

<211> 1249

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (36)

<223> n equals a,t,g, or c

<400> 501

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tgagtattta tctttttatt ttttattttt ttttttgaaa gaatgtcttg gaatgcgcaa 360
gtctcccttt agagccgtct tttgcaggga gcgggaagtg acaagagctc agatctccct 420
cccgatctcc ctccccacct ccgaagtctc ctccgtggac cacagggtga tctttgtgcg 480
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<210> 502

<211> 1358

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1334)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1347)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1349)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1351)

<223> n equals a,t,g, or c

<400> 502

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tggggcgggt ggtcgggtca agatagcagc agcagggtgc agggctcaag acaccacccc 180
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<210> 503

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (457)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (492)

<223> n equals a,t,g, or c

<400> 503

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ccaactgcag atctaagaga atgctggcta ttaaaagatg caagcatttt gaactgggag 360
gagataagaa gagaaagggc caagtgatcc agttctaagt gtcacttttt attatgaaga 420
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<210> 504

<211> 2011

<212> DNA

<213> Homo sapiens

<220>
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<222> (1941)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1961)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1974)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1976)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2002)
<223> n equals a,t,g, or c

<400> 504
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agaatcattg agggcttatt ttgtatacca actgctaaac tagatgcttc atacattgtt 180
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cattgcttta tcacgkrta cctgggttgc tattacataa agagcaatct ttctaaaatg 1860
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<210> 505

<211> 1989

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1917)

<223> n equals a,t,g, or c

<400> 505

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agcagctgca gctctcgccg ctgaaggggc tcagcttggc cgacaaggag aacacgccgc 180
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agaaggcaga ggcttccctt tggaccgccg aggaggtgga cctctccaag gacattcagc 420
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gggacaaaaga ggtacacctt ggtgaacgtg ttgtagcctt tgctgcagtg gaaggcattt 780
tcttttccgg ttcttttgcg tcgatatctt ggtcaagaa acgaggactg atgcctggcc 840
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tagtcagttg gtgccagata gaagacaggt tgtgttttta tcctgtggct tgtgtantgt 1920
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agggggcct 1989

<210> 506

<211> 1085

<212> DNA

<213> Homo sapiens

<400> 506

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ggaatgacat cttacgcaaa aagggatatct tccccccaa ggaaagtctg aaagaattgg 180
aagaggaggc agaagaggag cagcgcatcc tccagcagtc agtggtgaaa acatatgaag 240
atatgacttt ggaagagctg gaggatcatg aagacgagtt taatgaggag gatgaacgtg 300
ctattgaaat gtacagacgg cggagactgg ctgagtgga agcaactaaa ctgaagaata 360
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gcgaggggctt gtgggtcatc ttgcacctt acaacaagg aattcccctc tgtgccctga 480
taaatacagca cctcagtga cttgccagga agtttcctga tgtcaaattt atcaaagcca 540
tttcaacaac ctgcataccc aattatcctg ataggaatct gccacgata tttgtttacc 600
tggaaggaga tatcaaggct cagtttattg gtcctctggt gtttggcggc atgaacctga 660
caagagatga gttggaatgg aaactgtctg aatctggagc aattatgaca gacctggagg 720
aaaaccctaa gaagccgatt gaagacgtgt tgctgtcctc agtgcggcgc tctgtcctca 780
tgaagaggga cagcgattcc gaggtgact gaggtacag cttctatcac atgccgaact 840
ttcttgtgac aaattgtctg gatTTTTTaa aaaaggaaa agcaagaatg aatccttgtg 900
gttttttagtt ttgtataaat tatgtttcaa atctttacat tttggaaata atcattgctg 960
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aaaattaaaa ccagccattt gtatggcaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1080
aaaaa 1085

<210> 507

<211> 1485

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (570)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1475)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1476)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1485)

<223> n equals a,t,g, or c

<400> 507

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accgtagagc gcaggaacgg gtgggtaatt ctagagacaa aagccaatta aagtccattt 1440
cagacctgcg gaaaaaaaaa aaaaaaaaaa aaacnngggg ggggn 1485
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<210> 508

<211> 1930

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (30)

<223> n equals a,t,g, or c

<400> 508

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acaaaatttg ttagggtcat tcatgaaaac tttaatacta aaagcacttt ccattatata 180
ctttttaaa gtctagataa ttttgaaacca atttattatt gtgtactgag gagaaataat 240
gtatagtaga ggacagcctt ggtttgtaaa gctcagttcc actagttcat ggttttgtgc 300
aacttctgag cctcagtttt ctcccttgca aattaataat tacatacctt tatagatttt 360
gaaattaatt taaatattag tatttggtac atgaaggctt aatgttaagt ttcctttaat 420
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gatccacaat aatccctttg atcacgttaa tctaaatcta gatgtctttg tctaattttt 480
tttgaatagc agttataaat gtaaaggact caaagttaa gtaaaaagt atactccacc 540
ttgtgtttca aagaatttag ttccacctct tcataccagt ttaacactta atatatattca 600
ttggatttta gacagggcaa aaggaagaac aggggcctct ggaggccctt ggttatttaa 660
atcttggatt atttgtgata gtaatcacaa atttttggct aatttttaac ctgaggtttt 720
gttttttttt taaaggaaat gcagcctagt cttgagaaca taattttata taatcaatta 780
ctaaatgtta aactattacc acacagccca taaaacagca tttgcgttta ttgagagaga 840
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<210> 509

<211> 1134

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (895)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1041)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1064)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1090)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1106)

<223> n equals a,t,g, or c

<400> 509

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ggcagcgcgg ctgaggagaa aggcggattg gtatctgatg cctatgggga ggatgacttt 180
tctcgtctag ggggtgatga agatggttat gaagaagaag aagatgagaa cagtagacag 240
tcggaagatg acgattcaga gactgaaaaa cctgaggctg atgacccaaa ggataataca 300
gaagcagaaa agcgagaccc ccaggaactc gtggcctcct tttctgaaag agttcggaac 360
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<210> 510

<211> 1382

<212> DNA

<213> Homo sapiens

<400> 510

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gttcagcgtg ccggccatcc tgaagggtg gatggatagg gtgctgtgcc agggctttgc 780
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<210> 511

<211> 1741

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1696)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1710)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1715)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1717)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1720)

<223> n equals a,t,g, or c

<400> 511

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<211> 1530

<212> DNA

<213> Homo sapiens

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<222> (1342)

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<220>

<221> misc feature

<222> (1444)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1488)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1508)

<223> n equals a,t,g, or c

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<210> 513

<211> 2999

<212> DNA

<213> Homo sapiens

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<222> (243)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2606)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2996)

<223> n equals a,t,g, or c

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<210> 514

<211> 2048

<212> DNA

<213> Homo sapiens

<400> 514

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<210> 515

<211> 3300

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (126)

<223> n equals a,t,g, or c

<400> 515

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<210> 516

<211> 3425

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (402)

<223> n equals a,t,g, or c

<400> 516

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ggggc 3425

<210> 517

<211> 1358

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1346)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1356)

<223> n equals a,t,g, or c

<400> 517

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taaatacata tagctctttc atgtctaaaa ccattttatg atattgccaa aatgtgatag 240
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ctgaagataa tactcttaat tgagttgtat tgtacttctt aggcaaaagca gtgtaaaact 360
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gaatctgctg cttgttggtt cagtgtttct tatgaacaag agccacagta cagagcttca 480
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<210> 518

<211> 1368

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1225)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1311)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1333)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1335)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1347)

<223> n equals a,t,g, or c

<400> 518

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tctggaagat caagaagctc attaagagct tggaggcggc ccgcggcaat ggcaccagca 240
tgatatcatt gatcattcct cccaaagacc agatttcacg agtggcaaaa atgttagcgg 300

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ttgtatactg tggaacaatt gtaacagaag aaggaaagga aaagaaagtc aacattgact 480
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<210> 519

<211> 933

<212> DNA

<213> Homo sapiens

<400> 519

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cattagagat ttcttctgga aaactggaaa caagataggg tttaaaccag caggaggcat 180
ccgcagtgca aaggattccc ttgcttggct ctctcttgta aaggaggagc ttggagatga 240
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gcagatttac catcatgtga ctggaagata tgcagcttat catgatcttc caatgtctta 360
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taattgctaa aattatttaa ttaaaaaatt gggcagtagg taactggcat tcctctcttt 480
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agtttctcct aaaaacttta agtaaaatgt taatggtagc ttgataaca tcaaattcta 660
agggagaaaa aaacaatatt aaaccgcca agcagtgtgc ctagcagag gaaaatgcaa 720
catctcgcaa gcgctgctgt aacgacttca ggagtcactg attcagcact aatttcctgc 780
tgtgaaaact catctttcat tttgcccgt gataggcgt tttattaatt gttgtcctaa 840
tgaaaattct gacattgtca tatacacga tgaatatcat taaaattttt aaaataaaaa 900
aaaaaaaaa aaaaaactcg agggggggcc cgg 933
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<210> 520

<211> 1430

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (104)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (105)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1428)
<223> n equals a,t,g, or c

<400> 520
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c t g t c t c a g g a g a t g a a t t g a t g a c c t g g c t c a t a a a c a c a t n n t c a a g a c t g t g g a t t 120
t c a c g c a g g a t a g t a a t t a t t g t g t t a a c c g g g g a c a g g a t a a a c t g t t a c g c a t a t a t g 180
a a g c t c t g t g t g c a g t g a g a c a g a a c c t a a g g a a t t a g t g g t c a t a c t t c t g g t a t a a a a 240
a a g c t c t g t g t g c a g t g a g t g a g a t a a c a g a t t c t t c t g c t g a t g a c a a a a c t g t t c g a c 300
t t t g g g a t c a t g c t a c t a t g a c a g a a g t g a a a t c t c t a a a t t t a a t a t g t c t g t t a g t a 360
g t a t g g a a t a t a t t c c t g a g g g a g a t t t g g t t a t a a c t a t g g a c g a t c t a t t g c t t 420
t t c a t a g t g c a g t a a g t t t g g a c c c a a t t a a a t c c t t t g a a g t c c t g c a a c c a t c a a t t 480
c t g c a t c t c t t c a t c c t g a g a a g a a t t t c t g t t g c a g g c g g t g a a g a t t t a a a c t t t 540
a t a a g t a t g a t t a t a a t a g t g g a g a a g a a t t a g a a t c c t a c a a g g g a c a c t t t g g t c c t a 600
t t c a c t g t g t g a g a t t t a g t c c t g a t g g a g a a c t c t a t g c a g t g g t t c a g a a g a t g g a a 660
c a t t g a g a c t a t g g c a a a c t g t g g t a g g a a a c g t a t g g c c t t t g g a a a t g t g t g c t t c 720
c t g a a g a a g a t a g t g g t g a g c t g g c a a a g c a a a g a t t g g t t t t c c a g a g a c a a c a g a a g 780
a g g a g c t a g a a g a a t t g c t t c a g a g a a t t c a g a t t g c a t c t t c c t t c a g t c c t g a t g 840
t t a a g g c c t g a g c g t c a a t c a t a t g t t g c a g t t a g t a t a c a a c t g a c t a a a a c a a g c a a g 900
c a g a g a a a a g c a t c a g c c t t c c a g a g t t a c t g t c t g c t t a a g g c a g a a a c a g c a g t a a a t 960
a a t g a g g a a a a t g a a t t a g c t c c a g t g c t g g a a c a a c t a a c t a a c t t g g t g t t a c c t g t a 1020
a g t g a a a a c t c a a g t g t c a g a t g a a g g g a g g t g g a g t t a t c c t c t t a t a g t a c a g t g g c c 1080
t g t t a t c t t t t a a t g a a t a t a c a a g c c a a c a t c c a a t t t c t a t t a t t a c a a t t a g g g 1140
t t c t t g t a g c t g t t a t g t t a a t a t g g a g a g a a a a c t a t a t t g g c t g a t t t t t c t g a t 1200
c t t a a a g c a g a a t g c c t t t t c t t t t t t g c t t c a g t t g t a a g a a g a g g g a a t a c a t g a t 1260
a a a g t a a c t g g t t t g a t t t c t c g t t c a t t g t a c a c t g c c t c t g a a c a t c t a a t t g t t t t t 1320
a g t t g t c t a a a t a a a a t g c c t c t a a a a c a a a a a a a a a a a a a a a a a a a a a a a a a a a a 1380
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<210> 521
<211> 1169
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1159)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1166)
<223> n equals a,t,g, or c

<400> 521

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gagggggcct tggtgaccgt ggtggtcgtg gaggccgagg gggctttggc gggggccgag 180
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<210> 522

<211> 2162

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (169)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2133)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2136)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2139)

<223> n equals a,t,g, or c

<400> 522

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cgcccacagc cgcccagcgg cgcccagaga gcgcgcgccc cgcagccccc cgcctagccc 120
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<210> 523

<211> 799

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (443)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (758)

<223> n equals a,t,g, or c

<400> 523

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ccatcaagct acaaatratc ttacaaatgg aacctcaaat gagctcagct cagggttct 600
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gaggtgcccc attgggttt 799
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<210> 524

<211> 1722

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (13)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (36)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (40)

<223> n equals a,t,g, or c

<400> 524

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ttccacgcgt ttnagagaag ggaactccca cagcanaggn cataaaacca tccagggcag 60
tctggggcgg ctcaattctg cgtgtccagg gagtgaggag gagctcagcc ccgtcccaaa 120
yacagatggg accatgaact ccggacacag cttcagccag accccctcgg cctccttcca 180
tggtgcggga ggtggtctgg gccggcccag gagcttcccc agggctccca ccgtccatgg 240
cggtgcgggg ggagcccga tctccctgtc cttcaccacg cggagctgcc cccccctgg 300
aggttcttgg ggttctggaa gaagcagccc cctactaggc ggaaatggga aggccaccat 360
gcagaatctc aacgaccgcc tggcctccta cctggagaag gttcgcgccc tggaggaggc 420
caacatgaag ctggaagacc gcacacctga atggcaccag cagagagatc ctggcagtaa 480
gaaagattat tcccagtatg aggaaaacat cacacacctg caggagcaga tagtggatgg 540
taagatgacc aatgtctaga ttattcttct cattgacaat gccaggatgg cagtggatga 600
yttcaacctc aagwtgaaa atgaacctc ctttaaaaaa gacttggaag ttgaagtcsa 660
gggcctccga aggaccttag acaacctgac cattgtcaca acagacctag aacaggagggt 720
ggaaggaatg aggaagagc tcattctcat gaagaagcac catgagcagg aaatggagaa 780
gcacatgtgt ccaagtgact tcaatgtcaa tgtgaagggt gatacagggt ccagggaaga 840
```

```

tctgattaag gtcctggagg atatgagaca agaatatgag cttataataa agaagaagca 900
tcgagacttg gacacttggt ataaagaaca gtctgcagcc atgtcccagg aggcagccag 960
tccagccact gtgcagagca gacaaggga catccacgaa ctgaagcgca cattccaggc 1020
cctggagatt gacctgcagr cacagtacag cacgaaatct gctttggaaa acatgttatc 1080
cgagacccag tctcgktact cctgcaagct ccaggacatg caagagatca tctcccacta 1140
tgaggaggaa ctgacgcagc tacgccayga actggagcgg cagaacaatg aataccaagt 1200
gctgctgggc atcaaaaccc acctggagaa ggaaatcacc acgtaccgac ggctcctgga 1260
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tgaaatccaa aagcacgcat gagaccaatg aaagtttccg cctgttgtaa aatctatttt 1440
cccccaagga aagtccttgc acagacacca gtgagtgagt tctaaaagat acccttgga 1500
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ctttcctact gcagccttca gattctcatc attttgcac tattttgtag ccaataaaac 1680
tccgcactag caaaaaaaaa aaaaaaaaaa aaaaagtctg ac 1722

```

<210> 525

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (515)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (526)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (557)

<223> n equals a,t,g, or c

<400> 525

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tcccgggccc gagggcatca gacggcggct gattagctcc ggtttgcatc acccggaaccg 60
ggggattagc tccggtttgc atcacccgga ccgggggatt agctccggtt tgcatacccc 120
ggaccggggg cggggcgcgc acgagactcg cagcgggaagt ggaggcggct ccgcgcgcgt 180
ccgctgctag gaccggggca ggctggagc tgggctggga tcccagctc ggagcagcg 240
cagcggggcg gccacactgc tgggtccctg gargetctga gcccggcg cgccggggcc 300
cacgcggaac gacggggcga gatgcgagcc accctctg ctgctcctgc gggttccctg 360
tccaggaaga agcgggttga gttggatgac aacttagata ccgagcgtcc cgtccagaaa 420
cgagctcgaa gtgggcccc gcccagactg ccccctgccc tggtgcccct gagcccact 480
actgctccag atcgtgcaac tgctgtggsc actgntccc gtyttnngsc ctatgtccty 540
ctkgaagccc gaagaanggc gg 562

```

<210> 526

<211> 2023

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (12)

<223> n equals a,t,g, or c

<400> 526

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taaatgttaa tgaagttaaa ccataaaca aaggtgaaga acaaattggg tttgagctag 120
tggagaaatt atttcaaggt cagctggtat taaggacgcg ttgcttggaa tgtgaaagt 180
taacagaaag aagagaagat tttcaagaca tcagtgtgcc agtacaagaa gatgagcttt 240
ccaaagtaga ggagagttct gaaatttctc cagagccaaa aacagaaatg aagaccctga 300
gatgggcaat ttcacaattt gcttcagtag aaaggattgt aggagaagat aaatatttct 360
gtgaaaactg ccatcattat actgaagctg aacgaagtct tttgtttgac aaaatgcctg 420
aagtataac tattcatttg aagtgtttg ctgctagtgg tttggagttt gattgttatg 480
gtggtggact ttccaagatc aacactcctt tattgacacc tcttaaattg tcactagaag 540
aatggagcac aaagccaact aacgacagct atggattatt tgcggttggt atgcatagt 600
gcattacaat tagtagtggg cattacactg cttctgttaa agtactgac cttaacagt 660
tagaactaga taaaggaaat tttgtggtg accaaatgtg tgaaataggt aagccagaac 720
cattgaatga ggaggaagca aggggtgtgg ttgagaatta taatgatgaa gaagtgtcaa 780
ttagagttgg tggaaataca cagccaagta aagttttgaa caaaaaaat gtagaagcta 840
ttggacttct tggaggacaa aagagcaaa cagattatga gctatacaac aaagcctcta 900
atcctgataa gggtgctagt acagcgtttg ctgaaaatag aaattctgag actagtata 960
ctactgggac ccatgaatct gatagaaaca aggaatccag tgaccaaaca ggcattaata 1020
ttaagtggatt tgagaacaaa attcatacag tagtgcaaag cttaaaggag tatgagggga 1080
agtgggtgct ttttgatgat tctgaagtca aagttactga agagaaggac tttctgaatt 1140
ctctttcccc ttctacatct cctacttcta ctccttactt gctattttat aagaaattat 1200
agagtgaagt tattttcctt gtgtatatat taaacacacc catacaaca ttggtaaaagt 1260
tgattacatc aaagaatctt tagcttatct tttgaagcta ctggatatta ttggtctctc 1320
taggttttta tataaatagt gaaatytgaa ttactgaaaa ccatgttaat ttttagaact 1380
cattttcctc agtagagact agtgatgcat tagcttctgg gaacaaactt gtatcggttc 1440
ttaattaaat tatccaaac ggaggcattt aaacacttgg atttacacca gtcttttggt 1500
tttgcttttt aaaataaagt gctcgatttt gtattctcca tttttggag taattatcta 1560
catgatgttt atagttcctg tggtttttca cccaagaagc agaatctcat tcagtacatt 1620
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atgtgtgtat tcacaatggt gtatgtacat tttgtgcctt gattcactta gaagtgtctc 1740
agaaaacctg gacagttcgc ttctacacaa gaattttata tgtatttatg aagatgattc 1800
tgtaccctag tatatctttt tgggcatgga ctaatttgta tctgtttaac tcatattctg 1860
cacgactgtg atatagtaca tcaaacttag aggtgtgacc ttaaatttaa ctttttttaa 1920
aaactgggag gtcaataaaa tttaaactgc ttaactatgt atatgaatat ttgaattttt 1980
tacttgata tttttataaa tacagctgag ttttcttaaa gcg 2023
```

<210> 527

<211> 2847

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (286)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (290)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2842)

<223> n equals a,t,g, or c

<400> 527

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ggcacaggtt attctgtgtc ttctcatagta gaaaccttaa tgatcgggtct gttgtagtga 60
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tgtaaatggt cttttaatta attaaaaaga aattagtcag ctacaagcat gaacatgtgg 180
aacgcttacc tttgtactag gcgtttttgt ttttgttta atggcctttg gaatattata 240
gtattaacat ctgaaaaact aggtaaattt atcttagaat taagtnttn gctcctttt 300
tgcagaaaaa gaacagcaag aagcgattga acacattgat gaagtacaaa atgaaataga 360
cagacttaat gaacaagcca gtgaggagat tttgaaagta gaacagaaat ataacaact 420
ccgccaacca ttttttcaga agaggtcaga attgatcgcc aaaatcccaa atttttgggt 480
aacaacattt gtcaaccatc cacaagtgtc tgcactgctt ggggaggaag atgaagaggc 540
actgcattat ttgaccagag ttgaagtga agaatttgaa gatattaaat caggttacag 600
aatagatttt tattttgatg aaaatcctta ctttgaat aaagttctct ccaaagaatt 660
tcatctgaat gagagtgtg atccatcttc gaagtccacc gaaatcaaat ggaaatctgg 720
aaaggatttg acgaaacgtt cgagtcacaa gcagaataaa gccagcagga agaggcagca 780
tgaggaacca gagagcttct ttacctggtt tactgacct tctgatgcag gtgctgatga 840
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cgatatggat gatgaagaag gagaaggaga agaagatgat gatgatgatg aagaggagga 960
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tgatgaaggg gaggaaggag aggaggatga aggagaagat gactaaatag aacactgatg 1080
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ctactccatg gttctcaatt tatttggggg gaaatacctt gaggagaata caatgggaaa 1260
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cctcctttct ctgtatattg ggctcagaga gtacactgtg tctctatgtg aatatggaca 1500
gttagcattt accaaccatg atctgtctac tttctctgt ttaaaaaaag aaaaaaaac 1560
ttaaaaaaat ggggttatag aaggctagca aagggtgggt ttgagatgtt tgggtgggtt 1620
aagtgggcat ttgacaaca tggcttctcc tttggcatgt ttaattgtga tatttgacag 1680
acatccttgc agtttaagat gacactttta aaataaattc tctcctaagt atgacttgag 1740
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tctattgtaa tttgttcct gtttattttt aaattttctt tttgtttcac tggaaaggaa 1860
agatgatgct cagttttaaa cgttaaaagt gtacaagttg ctttgttaca ataaaactaa 1920
atgtgtacac aaaggatttg atgcttttct ctgagcatag gtatgcttac tatgacctc 1980
caagtttgac ttgtataaca tcaactgcaa actttgtcac cctaacttcg tattttttga 2040
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gtattaatat tcctcatagct gggaaacgtg ggttcaattt gccattgggt tctgaaagta 2160
ttcacatcat ttgggatacc agatagctca atactctctg agtacattgt gcccttgatt 2220
tttatctoca agtggcagtt tttaaaattg gccttttacc tggatataaa ttaattgtgc 2280
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tgccatgtct tcattggcta tataaaatgt ggccaagaag ataggctctc agtaagaagt 2400
ctgatgggtga gcagtaactg tccctgcttt ctggtataaa gctctcaaat gtgaccatgt 2460
gaatctgggt gggataatgg actcagctct gtctgctcaa tgccattgtg cagagaagca 2520
ccctaatagca taagcttttt aatgctgtaa aatatagtcg ctgaaattaa atgccacttt 2580
ttcagagggtg aattaatgga cagtctggtg aacttcaaaa gctttttgat gtataaaact 2640
tgataaatgg aactattcca tcaataggca aaagtgtaac aacctatcta gatggatagt 2700
atgtaatttc tgcacaggtc tctgtttagt aaatacatca ctgtataccg atcaggaatc 2760
ttgctccaat aaaggaacat aaagatttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aaaaaaaaaa aaaaaaaaaa anaaaaaa 2847
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<210> 528

<211> 816

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (22)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (94)

<223> n equals a,t,g, or c

<400> 528

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aaaacgantg tgtaattaac anaggctgtg cgcatgaacg ttgccgttat ggttcgcgaa 60
ttttccccgg cgcccaatgc gagggagacg aaantatgta aatgagtgga ttctggctga 120
gctatcctat tggctatcgg gacaaaattt gcttgagcca atccaaagtg ctccgtggac 180
aatcgccggt ctgtctataa aaaggtgaag cagcggcggt ttcggcgact ttcccgatcg 240
ccaggcagga gtttctctcg gtgactacta tcgctgtcat gtctggtcgt ggcaagcaag 300
gaggcaaggc ccgcgccaag gccaaagtcg cgtcgtcccg cgctggcctt cagttccccg 360
taggcgagtg catcgctctg cgcaaaggca actacgcgga gcgagtgggg gccggcgcg 420
ccgtctacat ggctgcggtc ctcgagtatc tgaccgccga gatcctggag ctggcgggca 480
acgcggctcg ggacaacaag aagacgcgca tcatccctcg tcacctccag ctggccatcc 540
gcaacgacga ggaactgaac aagctgctgg gcaaagtcac catcgcccag ggcggcgtct 600
tgctaatac ccaggccgta ctgctcccta agaagacgga ggtcaccac aaggcaagg 660
gcaagtgagg ctgacgtccg cccaagtggc ccagcccggc ccgcgtctcg aaggggcacc 720
tgtgaactca aaaggctctt ttcagagcca cccacgtttt caaataaaa agttgttaat 780
gctggcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 816
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<210> 529

<211> 885

<212> DNA

<213> Homo sapiens

<400> 529

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cccgcggtct tctctgcaaa tgggtccgt ggcctagcgc ccccgctccc gccacccgtg 120
atcgtgcgcc gagggccgcg aggggtcgcc gccagatcc caccagccag caagctaaag 180
catggcggcc atccctcca gcggtcgtc cgtggccacc cacgactact accggcgccg 240
cctgggttcc acttcagca acagtcctg cagcagtacc gagtgcctcg gggaagccat 300
tccccacccc ccaggtctcc ccaaggctga cccgggtcat tggtaggcca gcttctttt 360
cggaagtcc accctccgt tcatggccac ggtgttgag tccgcagagc actcgaacc 420
tccccaggcc tccagcagca tgaccgctg tggcctggct cgggacgcc cgaggagca 480
ggccggcggt cagtccagca cagccagcgc tgggccccg tcctgacctg agcggttacc 540
accagcccca ggctgcgga ggcgctagtc caccagagcc cctycccgcc cctctcccca 600
ctcgcctcc ctcgcccccc tccccacctc ccaccccca ccctgtaaac taggcggctg 660
cagcaagcag acctcgcat caacacagca gacacaaaa accagtgaga gccccgctct 720
ctaccgcccg gccccagcac tcgctagctt tcctgacacc tggaactgtg cacctggcac 780
caagcggaat ataaactcca agcagccagt agccccgatg gtgtgtgcct gagctgtgtg 840
gcccgaggtt ccaaaaaaaaa aaaaaaaaaa aaaaaaaaa aaaaa 885
```

<210> 530

<211> 742

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (693)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (695)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (715)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (730)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (741)

<223> n equals a,t,g, or c

<400> 530

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ggtacctgac agtaccggtc ggaattcccg ggtcgacca cgcgtccgct gctgctctta 60
aaggtagagg cctcagggtc cctgctgtag acggggcggg ggagagtacg atgggtgggg 120
```



```

cgtggtgggt cgtaggcgcc tcgagatgga gccccagct tccttgatgg atcgcggggc 180
gcgagtggcc tagacaagcc ggagctggga ccggcaatcg ggcgttgatc cttgtcacct 240
gtcgcagacc ctcatccctc ccgtgggagc cccctttgga cactctatga ccctggaccc 300
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cgcattggaa gaacgcggtg ggcttctggc tgctgggcct ttgcaacaac ttctcttatg 480
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gccatgtgga cccaggccca acgccgatcc cccacaacag ctcatcacga ttgactgca 600
actctgtctc tacggctgct gtgctcctgg cggacatcct cccacactc gtcacaaat 660
tggtggstyc tyttggsctt cacctgctgc ccnaccgt tgaggatgct gtgantctct 720
gtgctttatn ggggacagct ng 742

```

<210> 531

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (502)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (510)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (523)

<223> n equals a,t,g, or c

<400> 531

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gtcggcattc ccgggtcgac ccacgcgtcc gggcccgttt ccggcggcgt cgcgcgtttg 60
cgarccctcg gtggtcctca gggagggtct ctcggccaga acacgtggat gccacccac 120
cactgagcct catggagggtg gtaacatttg gcgatgtggc tgtgcacttc tctcgggagg 180
agtggcagtg tctggaccct ggccagaggg ccccttacag ggaagtgatg ctggagaacc 240
acagcagtggt ggctggacta gcaggaattcc tggttttcaa gcctgagctg atctctcggc 300
tggagcaggg agaagagcca tgggtcctcg acctgcargg agcagagggg acagaggcac 360
caargacctc caagacaggt gaggtctaga tccatcgca gagaagccct ggggtgarga 420
gaaactkcar gaggggctca caactgtrgg tagcttagg tgartcgcg gggctacact 480
kggatgcctg ggaatgctac tnggggaaan cagcatccaa canct 525

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<210> 532

<211> 1925

<212> DNA

<213> Homo sapiens

<400> 532

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gtggtctgag gccggtacag ctgcgcgtct gcgggaatag gtgcagcggg cccttggcgg 60
gggactctga gggaggagct ggggacggcg accctaggag agttctttgg ggtgactttc 120

```

aagatggact ctactctaac agcaagtga atccggcagc gatttataga tttcttcaag 180
aggaacgagc atacgtatgt tcaactcgtct gccaccatcc cattggatga cccactttg 240
ctctttgcc atgcaggcat gaaccagttt aaaccattt tcctgaacac aattgacca 300
tctcacccca tggcaaagct gagcagagct gccaatatccc agaagtgcac ccgggctggg 360
ggcaaacata atgacctgga cgatgtgggc aaggatgtct atcatcacac cttcttcgag 420
atgctgggct cttgggtctt tggagattac ttttaaggaat tggcatgtaa gatggctctg 480
gaactectca cccaagagtt tggcattccc attgaaagac tttatgktac ttactttggc 540
ggggatgaag cagctggctt agaagcagat ctggaatgca aacagatctg caaaatttgg 600
gaaatgattc tggggacat tctgaccaca tgcattacta tcagggtaaa aaatatttcc 660
gagataggag gggaggtggc agaaattcag actggtcttc agatacaaat cgacaaggac 720
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gattacctga ggaagaagag atcaaggaaa aaaaaccac cagtcaagga aagtcaagta 900
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gagaacgaga gggaaagttt aaaggaagag gaaatgatcg cagggaaaag ctccagtctt 1440
ttgactctcc agaaaggaaa cggattaagt actccaggga aactgacagt gatcgtaaac 1500
ttgttgataa agaagatatc gacactagca gcaaaggagg ctgtgtccaa caggctactg 1560
gctggaggaa agggacaggc ctgggatatg gccatcctgg attggcttca tcagaggagg 1620
ctgaaggccg gatgaggggc ccagtggtg gagcctcagg aagaaccagc aaaagacagt 1680
ccaacgagac ttaycgagat gctgttcgaa gagtcagtgt tgctcgatat aaagaactcg 1740
attaagaaag gagacaagtt ccatgggata caacctccct cttgttttgt ttgtctctcc 1800
ttttcttttg ttactgttct tgctgctaga acttttttaa ataaactttt tttcaatgtg 1860
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggg 1920
ggggg 1925

<210> 533

<211> 502

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (469)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (482)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (487)

<223> n equals a,t,g, or c

<400> 533

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cgggatagcc ggggggtctgg caggaatggg agcatccaga acgagaagga gaccatgcaa 360
aagctgaacg accgcctggc ctcttacctg gacaaaatga aggagcctgg agaccgagaa 420
accggagggt ggaagcaaa aaccgggag cactttggag aagaagganc ccaggtcaga 480
gnctggnagc cattaattca ag                                     502
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<210> 534

<211> 1800

<212> DNA

<213> Homo sapiens

<400> 534

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<210> 535

<211> 2497

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2467)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2487)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2493)

<223> n equals a,t,g, or c

<400> 535

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ccgctgctgc tgctgggagg atggaagcgc tggcgccggg ggcgggcccgc ccggcatgta 120
gtagcggtgg tgctgggcga cgtgggcccgc agcccccgta tgcagtacca cgcgctgtcg 180
ttggccatgc acggcttctc ggtgaccctc ctgggggttct gcaactccaa accccatgat 240
gagctcttgc agaacaacag aattcagatt gtgggggttga cagaacttca gagtcttgca 300
gttgggcccc gaggttttcca gtacggagtc aaagttgtac ttcaggctat gtacttgctg 360
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cctagcattg ctgtctgctg gttcgtgggc tgcctttgtg gaagcaagct cgtcattgac 480
tggcacaact atggctactc catcatgggt ctggtgcatg gcccacaacca tccccctcgtt 540
ctgctggcca agtggtacga gaagttcttt gggcgccctgt cccacctgaa cctgtgtgtt 600
accaatgcta tgcgagaaga cctggcggat aactggcaca tcagggtgtg gaccgtctac 660
gacaagcccc catcttttctt taaagagaca cctctggacc tgcagcaccg gctcttcatg 720
aagctgggca gcatgcactc tccgttcagg gcccgctcag aacctgagga ccagtcacg 780
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<210> 536

<211> 4090

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (42)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (528)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (535)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2475)

<223> n equals a,t,g, or c

<400> 536

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<210> 537

<211> 586

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (56)

<223> n equals a,t,g, or c

<400> 537

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<210> 538

<211> 1250

<212> DNA

<213> Homo sapiens

<400> 538

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<210> 539

<211> 1350

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1305)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1344)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1349)

<223> n equals a,t,g, or c

<400> 539

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aaaaggggcg ccgccccaga gganccccng 1350

<210> 540

<211> 2509

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (38)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (367)

<223> n equals a,t,g, or c

<400> 540

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ggccgcacgg cctcggcagc gatggcactg aaggactacg cgctagagaa ggaaaaggtt 180
aagaagttct tacaagagtt ctaccaggat gatgaactcg ggaagaagca gttcaagtat 240
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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 541

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<210> 542

<211> 2210

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (40)

<223> n equals a,t,g, or c

<400> 542

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<210> 543

<211> 1715

<212> DNA

<213> Homo sapiens

<400> 543

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<210> 544

<211> 3109

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1011)

<223> n equals a,t,g, or c

<400> 544

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<210> 545

<211> 1176

<212> DNA

<213> Homo sapiens

<400> 545

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<210> 546

<211> 1735

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

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<223> n equals a,t,g, or c

<400> 546

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<210> 547

<211> 1048

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1043)

<223> n equals a,t,g, or c

<400> 547

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<220>

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<211> 1816

<212> DNA

<213> Homo sapiens

<400> 550

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<211> 2610

<212> DNA

<213> Homo sapiens

<400> 551

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<211> 4021

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4000)

<223> n equals a,t,g, or c

<400> 552

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<212> DNA

<213> Homo sapiens

<400> 553

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<211> 3713

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<213> Homo sapiens

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<222> (3006)

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<400> 554

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<211> 1997

<212> DNA

<213> Homo sapiens

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<222> (1887)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1951)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (1980)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (1992)

<223> n equals a,t,g, or c

<400> 555

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<211> 906

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<222> (879)

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<221> misc feature

<222> (906)

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<400> 556

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<210> 557

<211> 3484

<212> DNA

<213> Homo sapiens

<400> 557

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<210> 558

<211> 790

<212> DNA

<213> Homo sapiens

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<220>

<221> misc feature

<222> (9)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (788)

<223> n equals a,t,g, or c

<400> 558

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<210> 559

<211> 558

<212> DNA

<213> Homo sapiens

<400> 559

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<211> 534

<212> DNA

<213> Homo sapiens

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<222> (16)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

<400> 560

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tgtgctgaag cggccacatg tggacgagtt cctccagagg atggggcagc ttttgaatgt 480
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<210> 561

<211> 3043

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3038)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3039)

<223> n equals a,t,g, or c

<400> 561

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<210> 562

<211> 1386

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (480)

<223> n equals a,t,g, or c

<400> 562

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acctcgctga ggtgaagcct ttggtggaga aaggggagac catcacccgc ctctgcaag 240
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<210> 563

<211> 2638

<212> DNA

<213> Homo sapiens

<400> 563

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<210> 564

<211> 691

<212> DNA
<213> Homo sapiens

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<222> (569)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (575)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (581)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (619)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (650)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (653)
<223> n equals a,t,g, or c

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tgaagaattc cgatatggnt tactcttaat tacaacaagt ggctggccgn atnttcaggt 660
tcgagtggat tggaacactt caagccccc a 691

<210> 565
<211> 1967
<212> DNA
<213> Homo sapiens

<400> 565

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atgttttaaa gacttagttg tcagtattaa ataactcttg cattataggg aaaaaacctc 180
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaggg gggggag 1967
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<210> 566

<211> 1334

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1253)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1307)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1309)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1312)
<223> n equals a,t,g, or c

<400> 566
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<210> 567
<211> 1610
<212> DNA
<213> Homo sapiens

<400> 567
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gaaagcacta ggtttcttgc attcaaagag taaagattct gctgaaaagc taaaagcact 180
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<210> 568

<211> 1412

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1018)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1037)

<223> n equals a,t,g, or c

<400> 568

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<210> 569

<211> 1125

<212> DNA

<213> Homo sapiens

<400> 569

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gagaagggtg ccgaggcccg caaaagaaag aaccggaggc tgaagcaggc caaagaagaa 240
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<210> 570

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1899)

<223> n equals a,t,g, or c

<400> 570

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<210> 571

<211> 1253

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1205)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1207)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1212)

<223> n equals a,t,g, or c

<400> 571

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<210> 572

<211> 2013

<212> DNA

<213> Homo sapiens

<400> 572

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<210> 573

<211> 669

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (445)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (631)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (638)

<223> n equals a,t,g, or c

<400> 573

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taaacggga 669

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<210> 574

<211> 2432

<212> DNA

<213> Homo sapiens

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<221> misc feature

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<220>

<221> misc feature

<222> (2326)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2367)

<223> n equals a,t,g, or c

<400> 574

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<210> 575

<211> 1372

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (71)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1335)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1338)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1370)

<223> n equals a,t,g, or c

<400> 575

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<210> 576

<211> 2020

<212> DNA

<213> Homo sapiens

<400> 576

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<210> 577

<211> 3161

<212> DNA

<213> Homo sapiens

<400> 577

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3161

<210> 578

<211> 2046

<212> DNA

<213> Homo sapiens

<400> 578

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<210> 579

<211> 302

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (226)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (241)

<223> n equals a,t,g, or c

<400> 579

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<210> 580

<211> 3067

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (626)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1808)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2945)

<223> n equals a,t,g, or c

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<211> 1574

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (457)

<223> n equals a,t,g, or c

<400> 581

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<211> 960

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (924)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (937)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (939)

<223> n equals a,t,g, or c

<400> 582

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<210> 583

<211> 541

<212> DNA

<213> Homo sapiens

<400> 583

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541

<210> 584

<211> 2968

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (454)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1437)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2961)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2964)

<223> n equals a,t,g, or c

<400> 584

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<210> 585

<211> 2608

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (84)

<223> n equals a,t,g, or c

<400> 585

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<210> 586

<211> 1893

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1184)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1865)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1883)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1887)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1893)

<223> n equals a,t,g, or c

<400> 586

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cgccgcgccg cttcgagggc gccccaggcc gcgccatggg gaaggtgacg ttcaactccg 240
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<210> 587

<211> 2463

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2413)

<223> n equals a,t,g, or c

<400> 587

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<210> 588

<211> 1945

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1240)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1939)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1945)

<223> n equals a,t,g, or c

<400> 588

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<212> DNA

<213> Homo sapiens

<400> 589

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<211> 2307

<212> DNA

<213> Homo sapiens

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<210> 592
<211> 1078
<212> DNA
<213> Homo sapiens

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<210> 593

<211> 2492

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2113)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2452)

<223> n equals a,t,g, or c

<400> 593

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<210> 594

<211> 1904

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1878)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1893)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1895)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1903)

<223> n equals a,t,g, or c

<400> 594

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<210> 595

<211> 337

<212> DNA

<213> Homo sapiens

<400> 595

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<210> 596

<211> 1288

<212> DNA

<213> Homo sapiens

<220>

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1285)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1287)

<223> n equals a,t,g, or c

<400> 596

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<210> 597

<211> 1052

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (937)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (943)

<223> n equals a,t,g, or c

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<222> (995)

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<222> (1004)

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<221> misc feature

<222> (1009)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (1040)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (1051)

<223> n equals a,t,g, or c

<400> 597

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gaaggagaat aaaaccattg tttttgtgga aacccaaaaga agatgtgatg agcttaccag 420
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<210> 598

<211> 2093

<212> DNA

<213> Homo sapiens

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<222> (969)

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<220>

<221> misc feature

<222> (1422)

<223> n equals a,t,g, or c

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<222> (1425)
<223> n equals a,t,g, or c

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<400> 598
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taaaagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2093

<210> 599
<211> 562
<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (383)

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<221> misc feature

<222> (437)

<223> n equals a,t,g, or c

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<222> (445)

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<222> (549)

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<221> misc feature

<222> (561)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (562)

<223> n equals a,t,g, or c

<400> 599

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cgagggtctca ctatgccag gttggtctca aactcctgtg ctcaagcaat cctcccatct 180

tggtcccta agtgctggga ttatagcat gagccaccgt gcccgccctc atgtctgeat 240
gttaaaagtt ctgagaattc ctatggaaaa taaatttgac tttgcttaat gcagttcctc 300
taaaacttact taattccttt ttcttttttt ctttactatt tattaattnt tctcttttct 360
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tgcaagggct tctgaangac agcangetga gaaaggccga tcctaacact tanctctttg 480
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<210> 600

<211> 528

<212> DNA

<213> Homo sapiens

<220>

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<223> n equals a,t,g, or c

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<222> (2)

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<222> (8)

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<222> (104)

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<222> (417)

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<222> (458)

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<221> misc feature

<222> (493)

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<221> misc feature

<222> (507)

<223> n equals a,t,g, or c

<400> 600

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ctggagtgca gtggtgtgat ctgggtcac tgcaacctct gcctcccagg ttccagcaat 180
tctcctgcct cagcctccct agtggctggg atgacaggcg cctgccatca tgcctgacta 240
gtttttgtat ttttagtaga gacggcggtt caccatgttg gccaggctgg tctcaaaactc 300
ctgacctcag gtgatccgcc tacctcagcc tcccaaagtg ctgggattac aggcgtgac 360
caccacacct ggcccttgca atcttctact ttaagggttg cagagataaa ccaatanatc 420
cacaccgtac atctgcaata tganttcaag aaaggaanta gtaccttcaa tacttaaaaa 480
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<210> 601

<211> 475

<212> DNA

<213> Homo sapiens

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<222> (160)

<223> n equals a,t,g, or c

<220>

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<222> (172)

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<222> (174)

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<222> (212)

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<221> misc feature

<222> (250)

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<221> misc feature

<222> (297)

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<221> misc feature

<222> (302)

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<221> misc feature

<222> (306)

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<221> misc feature

<222> (341)

<223> n equals a,t,g, or c

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<220>
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<222> (450)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (468)
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ctgccattaa ggtgtggtggc cgaanatatg ctcattgtggn gttgaggaaa gnanacattg 180
acctnaccaa nagggcggnna gaactcactg angatgangt ggaacgtgtg atcaccatta 240
tgcagaatcn acgccagtac aagatcccag actgggttctt gaacagacag aatgatngta 300
angatnaatc tacttcaagc taacatgcta tcatttctac nttgagtact gctaagggtt 360
ctttccacaa cttgtacaca atgtttattna ctgcccagtt tataatttcc ctnttggttc 420
ccattttaag acttatttaa ttantatgcn ttttaaattt ttgagacntg ataga 475

<210> 602
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (84)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (100)
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<400> 602
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ggaattaacc cgagcaggca tggaggcctc tgctctcacc tcatcagcag tgaccagtgt 180
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<210> 603
<211> 432
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (365)
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<220>
<221> misc feature
<222> (408)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (416)
<223> n equals a,t,g, or c

<220>
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<222> (421)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (425)
<223> n equals a,t,g, or c

<400> 603
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gacttggtgt gggactgctg ataggaagat gtcttcagga aatgctaaaa ttgggcaccc 120
tgcccccaac ttcaaagcca cagctgttat gccagatggt cagtttaaag atatcagcct 180
gtctgactac aaaaggaaaa tatgttgtgt tcttctttta ccctcttgac ttcacctttg 240
tgtgccccac ggagatcatt gctttcagtg atagggcaga agaatttaag aaactcaact 300
gccaagtgat tgggtcttct gtggattctc acttctgtca tctagcatgg gtcaatacac 360
ctaanaaaca aggaggactg ggacccatga acattccttt ggtatcanac ccaacncaca 420
nttgntcagg at 432

<210> 604
<211> 371
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (282)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (291)
<223> n equals a,t,g, or c

<400> 604
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aacaaaatga ctgaagcaca ggaagatggc cagtcaactt ctgatttgat tggccagttt 180
ggtgtcgggt tctattccgc cttccttgta gcagataagg ttattgtcac ttcaaaacac 240
aacaacgata cccagcacat ctgggagtct gactccaatg anttttctgt naattgctga 300
cccaagaggg aaacactcta ggacggggga acgacaattt acgtggagta tggaccaatt 360
tccttattaa g 371

<210> 605
<211> 392
<212> DNA
<213> Homo sapiens

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<222> (292)
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<221> misc feature
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (330)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (331)
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<220>
<221> misc feature
<222> (342)
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (363)

<223> n equals a,t,g, or c

<400> 605

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ggattcggat gaaaactggg aaataaaatc aggtacaact ccaaaaaggag acattggaga 180
agaaccaagc tgggtctatg aaggaattgc acatgagatg gcacacatat ttatgctgtc 240
tggaagggtgc acgatccatg ttaccatatg caagctggaa aatgtgcacc antatctggg 300
agattttcga cgtgtttttc cncctctggan nctgtttatg gnacaagggt ggtttggttt 360
ggntccatta aattaaatta ggtaaaggcc cc 392
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<210> 606

<211> 442

<212> DNA

<213> Homo sapiens

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<221> misc feature

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<220>

<221> misc feature

<222> (312)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (368)

<223> n equals a,t,g, or c

<400> 606

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agcgggcccc gcctgcggag gtgggcggca tgcagctccg ctttgccccg ctctccgagc 120
acgccacggc cccacccggg ggctccgcgc gcgcccgggg ctacgacctg tacagtgcct 180
atgattacac aataccacct atggagaaaag ctgttggtgaa aacggacatt cagatagcgc 240
tcccttcttg gtgtnatgga agagtggctc cacggtcagg cttggctgca aaacacttta 300
ttgatgtagg antggtgtca tagatgaaga ttataagagg aatgttggtg ttgtactgtt 360
taattttngg caagaaagtt tgaagtcaaa aaagggtgatc gaattgcaca gtcatttgca 420
acggattttt tatccagaaa ta 442
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<210> 607

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

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<220>

<221> misc feature

<222> (124)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (132)

<223> n equals a,t,g, or c

<400> 607

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agaaagtggg tgatccattt ttaagaaag attggtatga tgtgaaagca cctgctatgt 120
tcantataag anatattgga aagacgctcg tcaccaggac ccaaggaacc aaaattgcat 180
ct 182
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<210> 608

<211> 673

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (561)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (569)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (603)

<223> n equals a,t,g, or c

<220>

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<222> (604)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (627)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (630)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (652)

<223> n equals a,t,g, or c

<400> 608

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atcaccacag gactattcct agccatgcac tactcaccag acgcctcaac cgccttttca 180
tcaatcgccc acatcactcg agacgtaaaat tatggctgaa tcatccgctg ccttcacgcc 240
aatggcgccct caatattctt tatctgcctc ttcctacaca tcgggcgagg cctatattac 300
ggatcatttc tctactcaga aacctgaaac atcggcatta tcctcctgct tgcaactata 360
gcaacagcct tcataggcta tgcctcccg tgaggccaaa tatcattctg agggggccaca 420
gtaattacaa acttactatc cgccatccca tacattggga cagacctagt tcaatgaatc 480
tgaggaggct actcagtaga cagtcccacc ctcacacgat tctttacctt tcaacttcac 540
ttgcccttca ttattggcag ncctacagna ctcacctcta ttttttgccg aaacgggggat 600
canncaaccc ccttagggaa tcacctnccn tttccgataa aaatcaacct tncacccttt 660
actacacaat cat 673
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<210> 609

<211> 553

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (377)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (449)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (497)

<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

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gacagtgtag aagaattcct gagtgaaaag ttggaacgca tataaatctt gcttaaattt 180
tgtcctatcc ttttgttacc ttatcaaatg aaatattaca gcacctagaa aataatttag 240
ttttgcttgc ttccattgat cagtctttta cttgaggcat taaatatcta attaaatcgt 300
gaaatggcag tatagtccat gatattctaa gagttggcaa gcttaacaaa acccattttt 360
tataaatgtc catcctnctg catttggtga taccactaac aaaatgcttt gtaacagact 420
tgcggttaat tatgcaaatg atagtttgng ataattgggg ccaagtttta cgaacaacag 480
atttctaaat tagaganggt taccaggaca gatgatacta tgcctaaggg ctgggngccc 540
ttttnaagga aga 553

<210> 610
<211> 458
<212> DNA
<213> Homo sapiens

<220>
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<220>
<221> misc feature
<222> (18)
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tgactacttt ggcgaatggg acattagttg cattccgagg tcattatttc tggatgctaa 120
gtccattcag tccaccatct ccagctcgca gaattactga agttttgggg aatcctttcc 180
cccattgata ctgttttact aaggggaatt tttcnagaaa aggtngcagc attcagcagt 240

atatttataa acaggaacct gtacagaagt gcccttgga naaggcctgc tctaaaatta 300
tccagtggta tngngnaacg acacaggtta agagacgtcg cttnaacgtg ctaaaaggac 360
ctttccaana cacaccatca gaatccataa tcacctgcca aatgggggtat cnagaccaag 420
gggcctccan aaggagttaa gnggttaccg tggggngg 458

<210> 611

<211> 565

<212> DNA

<213> Homo sapiens

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<222> (471)

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<220>

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<222> (534)

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ctctagaact agtgatccc ccgggctgca ggaattcggc acgaggttgc agtgagccga 120
gatcgacca ttgcactcca gtctgggcaa cagagtgaga ttccgtctca aaaaaaaaaa 180
gaaaaggaaa aaaaaatagc attatacctc ttccttgtct caaccgccat gaaaattctg 240
aacactccaa attcagttga ataatccaaa acaaaattta taagtataaa ataattttac 300
ttcttatagt aatagtatac tttaaaaagc ctcagggtat attatcttct aaacagctac 360
aattcagtc agctacatta accaactatg ttctctagtt gaggaacaac taggcctatt 420
tactgctgt gtagcctcag tgcctaacat gggcgccaaa taaatatng nggattacac 480
tgaattgtaa aaaccattcg tttttgttta caattgccaa aaatctcaaa agnccctgta 540
tttatgtaat tctttgaaat tatta 565

<210> 612

<211> 442

<212> DNA

<213> Homo sapiens

<220>
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gtcggccacg tcgtccttcg gaggcctggg cggcggtcc gtgcgtattg ggccgggggt 120
cgcttttcgc gcgccagca ttcacggggg ctccggcggc cgcggcgat ccgtgtcctc 180
cgcccgcttt gtgtcctcgt cctcctcggg gggctacggc ggcggctang gcggcgctcct 240
gaccgcgtcc gangggctgc tggcgggcaa cgagaagcta accatgcaga actnaangac 300
cgcttggtt ctactggana agttcgcncc tgnaggggca aagggaacta aaagttaa 360
ccgcnattgt acaaaacagg gcttggcctt cccggataaa gcattataaa gancntcagg 420
aattggggaa aaatttttgn nc 442

<210> 613
<211> 306
<212> DNA
<213> Homo sapiens

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<220>

<221> misc feature
<222> (190)
<223> n equals a,t,g, or c

<220>
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<222> (192)
<223> n equals a,t,g, or c

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<222> (199)
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<220>
<221> misc feature
<222> (213)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (237)
<223> n equals a,t,g, or c

<220>
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<222> (272)
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<220>
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<222> (299)
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<220>
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<222> (302)
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cttccgaacc aagtttgaga cggaacaggc tctgcgcatg ancgtggagg ccgacatcaa 120
cggcctgcnc aggtgctgga tgagctgacc ctggcccaga accgaccttg gngatgcagt 180
tcgancctn angaagagnt ggcctaccta agnaggaccc tgagggggaa tcaattncgt 240
taaggggcca atgggaggcc attaatTTTg anttggttcc ttccggacct tttggccant 300
cntggt 306

<210> 614
<211> 555
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

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<222> (497)
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<220>
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<222> (545)
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accattgaga actccaggat tgtcctgcag atcgacaatg cccgtctggc tgcagatgac 120
ttccgaacca agtttgagac ggaacaggct ctgcgcata gctggaggc cgacatcaac 180
ggcctgcgca ggggtgctgga tgagctgacc ctggccagga ccgacctgga gatgcagatc 240
gaaggcctga aggaagagct ggcctacctg aagaagaacc atgaggagga aatcagtacg 300
cttaggggcc aagtgggagg ccagggtcagt gtggagggtg attccgctcc gggcaccgat 360
ctcgccaaga tcctgagtga catgcgaagc cnatatgagg tcatggccna gcagaaccgg 420
aaggatgctt aancctggtc accagcccgg actgaagaat tgaaccggga ggtcgcttgc 480
cacacggagc aacttcngat gagcaggtcc aagggttactg acctgcggcg caacccttaa 540
ggncntgaga atgaa 555

<210> 615
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<212> DNA
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<222> (28)

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<222> (57)

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<221> misc feature

<222> (173)

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<400> 615

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ctctagaact agtggatccc ccgggctgca ggaattcggc acgaggctaa ggctgcgttg 120
gggtgaggcc ctcaacttcat ccggcgacta gcaccgcgtc cggcagcgcc agncctacac 180
tcgcccgcgc catggcctct gtctccgagc tcgcctgcat ctactcggcc ctcattctgc 240
acgacgatga ggtgacagtc acggaggata agatcaatgc cctcattaaa gcagccggtg 300
taaatgttga gccttttttg cctggcttgt ttgcaaaggc cctggccaac gtcaacattg 360
ggagcctcat ctgcaatgta ggggccggtg gacctgctcc agcagctggt gctgcaacca 420
gcaggaggtc ctgccccctc cactgctgct gctccagctg aggagaagaa agtggaagca 480
aagaaagaag aatccgagga gtctgatgat gacatgggct ttggtctttt tgactaaacc 540
tcttttataa catgttcaat aaaaagctga acttt 575
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<210> 616

<211> 346

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (139)

<223> n equals a,t,g, or c

<400> 616

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gtcgcctcct acctgctggc tgccctaggg ggcaactcct cccccagcgc caagggnatc 120
aagaagatct tggacaacnt gggatcgcag gcggacgcag accggctcaa caaggttatc 180
agtgcgctga atggaaaaaa cattgaagac gtcattgccc aggggtattgg caagcttgcc 240
agtgtacctg ctgggtggggc tgtagccgtc tctgctgccc caggctctgc agccccgtct 300
gctggttctg cccctgctgc agcagaggag aagaaagatg agaaga 346
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<210> 617
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<212> DNA
<213> Homo sapiens

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<222> (388)
<223> n equals a,t,g, or c

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<222> (397)
<223> n equals a,t,g, or c

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<222> (408)
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tcccgttccg ctgcccgcgc tgccaccatg acggaacagg ccatctcctt cgccaaagac 120
ttcttgccg gaggcacgc cgccgccatc tccaagacgg ccgtgggtcc gatcgagcgg 180
gtcaagctgc tgcgtcaggt ccagcacgcc agcaagcaga tcgccgccga caagcagtac 240
aagggcatcg tggactgcat tgcgcgcatc cccaaggagc agggcggtgt gtccttctgg 300
aggggcaacc ttgccaacgt cattcgctac ttcccactc aagccctcaa cttcgncttc 360
aaggataagt acaagcagan cttcctgngg ggcgtgnaca agcacacnc 409

<210> 618
<211> 473
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (9)
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<222> (322)
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<223> n equals a,t,g, or c

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<220>
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<222> (368)
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<220>
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<222> (446)
<223> n equals a,t,g, or c

<220>
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<222> (470)
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<400> 618
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gagagggggc gactattata caagtggca agttgatcaa agaagctgcc gggaaaagca 120
atctgaagag ggtgaccctg gagcttgag gaaagagccc ttgcattgtg ttagctgatg 180
ccgacttgga caatgctgtt gaatttgac accatggggt attctaccac cagggccagt 240
nttgatatgc cgcattncagg atttttgtg aagaatcaat ttatgatgag ttgttgcga 300
ggagtgttga gcgggttaag antatatacct tggaantcc ttgacccca gnagttcann 360
caagnccntc agattgacaa ggaccatttg gtaaatactt gacccattg agagtnggaa 420
gaaagaaggg gccaanaggga tntggnggag gccctggggg ataaagggtan ttg 473

<210> 619
<211> 604
<212> DNA
<213> Homo sapiens

<220>
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<222> (440)

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<222> (492)

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<220>

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<222> (500)

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<222> (537)

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<222> (554)

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<222> (584)

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<222> (587)

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<222> (593)

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aatggcgag actaccaccc aagggttga tgggctgtct gagcgctgtg cccagtacaa 180
gaaggacgga gctgacttcg ccaagtggcg ttgtgtgctg aagattgggg aacacacccc 240
ctcagccctc gccatcatgg aaaatgccaa tgttctggcc cgttatgcc a gtatctgcca 300
gcagaatggc attgtgccc a tcgtggagcc tgagatcctc cctgatgggg accatgactt 360
gaagcgcttg ncagtatgtg accgaaaagg tgcttggtt gctgctacaa ggctcttgag 420
tgaccaccac atctacctgn aaggcacctt gctgaagccc aacatggtcc cccaggccat 480

gcttgcactc anaagttttn ttatgaagga gattgcccacat ggcgaacccg tctcaancgc 540
tgtgcccgcga caantgcccc cccgcttgtc acttgggatc aacnttncct gtnttggaag 600
gccca 604

<210> 620
<211> 312
<212> DNA
<213> Homo sapiens

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<220>
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<222> (311)
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<220>
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<222> (312)
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cccaacactc caggccctgc cccctcccac tcttgaagag gaggccgcct cctcggggct 180
ccaggctggc ttgcccgcgc tctttcttcc ctcgtgacag tgggtgtgtg tgctcgtctgt 240
gaatgctaag tccatcacc tttccggcac actgccaaat aaacagctat ttaaggggga 300
aaaaaanann nn 312

<210> 621
<211> 248
<212> DNA
<213> Homo sapiens

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<220>
<221> misc feature
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<220>
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<222> (207)
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<220>
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<222> (246)
<223> n equals a,t,g, or c

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ggttgcacga aacacactgg ggaatggagc aaaacagtct ttgaatatcg aacacgcaag 120
gctgtgagac tacctattgt ngatattgca ccctatgaca ttggtggtcc tgatcaagaa 180
tttggtgtgg acntnggncc tgtttgnntt ttataaacca aactctatct gaaatcccaa 240
caaaanaa 248

<210> 622
<211> 344
<212> DNA
<213> Homo sapiens

<220>
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<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (19)

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<222> (31)

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<222> (283)

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<222> (297)

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<222> (303)

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<222> (310)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (312)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (342)

<223> n equals a,t,g, or c

<400> 622

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gtatgggaaa tgccatgttt gtcaaagagc aactcagtct gctggacagg ttcacggagg 120
atgccaagag gctgtatggc tccgaggcct ttgccactga ctttcaggac tcagctgcag 180
ctaagaagct catcaacgac tacgtgaaga atggaactcg agggactata acctgaacga 240
catacttctc cagctgaagt acacaggcaa tgnccagcna ctnttcaccc tgccgtntca 300
ngncaagatn gnggaagtgg aagccatgtt ggttttcaga gncc 344
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<210> 623

<211> 316

<212> DNA

<213> Homo sapiens

<220>

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<223> n equals a,t,g, or c

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<222> (286)

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<221> misc feature

<222> (294)

<223> n equals a,t,g, or c

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<222> (308)

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<221> misc feature

<222> (313)

<223> n equals a,t,g, or c

<400> 623

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cggctctgaag ggtctggctg gtgagccagg ttttaaaggc agccgagggg accctgggcc 120
cccaggacca cctcctgtca tcctgccagg aatgaaagac attaaaggag agaaaggaga 180
tgaagggcct atggggctga aaggatacct gggcgcaaaa ggtatccaag gaatgccagg 240
catccccangg ctgtcaggaa tccctgggct gcctgggagg cccggncaca tcanaggaa 300
caaggganac atngga 316
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<210> 624
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<212> DNA
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<220>
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<222> (172)
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<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

<220>
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cccgntncca gccccccagt ggcagttctc cctgctccac tncaagttcc atctgtgaca 240
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gccatgaagg ggcttgccac cgacgaagat gccatcatca gcgtcctcgc ctaccgcaac 300
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atacctcana ctgctgctgg actcacttcg aaaagcccag ggnaattgac aacgtcctcg 180
tcattcttag ccatgaacttc tggtcgaccg agatcaatca gctgatcgcc ggggtgaatn 240
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tactttgagt gctgtctcca tgtttgatgt atctgagcag gntgctccac aggtagctct 300
agcagggctg gcaacttann aggtggngag cagagaattc tcttatccaa catcaacatc 360
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gcccggtcct ttcgtttctt cccttccttt ctgcgccagt tcgccggntt tccccgtnaa 420
gctntaaatn gggggctncc tttanggttc cgattaangn ttacggggac cttngaccca 480
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cgtcgtgact gggaaaaccc tggcgntacc caacttaatc gccttgtagc acatccccct 180
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ccctggcggt acccaactta atcgccctgc agnacatccc cntttcgcca gctggcgtaa 240
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aagngcttta cgggaccttn gncccaaaa aaacttgatt agggnggatg gntcacngta 540
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<212> DNA
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<212> DNA
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atccaggcca naaagttcac agtcaaattg ggaggggtat tcttnatgca ggagacccca 180
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243

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<212> DNA
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<400> 635
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ccgctccttt cgctttcttc ccttcctttc tcgccacgtt cgccggcttt ccccgctcaag 480
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aaaaacttga ttaggggat gggtcacgta gtgggccatc gcctgataga cggttttcgc 600
ctttgacgtt ggagtcacgt cttaatagg actcttgtn aaactggaac aacactnaac 660
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tcgtgactgg gaaaaccctg gcgttaccce acttaatcgc cttgcagcac atcccccttt 180
cgccagctgg cgtaatagcg aagaggcccg caccgatcgc ccttcccaac agttgcgcag 240
cctgaatggc gaatgggacg cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt 300
tacgcgcagc gtgaccgcta cacttgccaa gcgccctaag cgcccgttcc tttcgctttc 360
ttcctttctt ttttngccac gttcggccgg cttttccccc taaagcttta aatcnggggg 420
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acgtcgtgac tgggaaaacc ctggcggttac ccaacttaat cgccttgag cacatcccc 180
tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat cgccttccc aacagttgcg 240
cagcctgaat ggcgaaatggg acgcgccctg tagcgcgcca ttaagcgcg cggtgtggt 300
ggttacgcgc agcgtgaccg ntacacttgc cagcgcccta gcgcccgntc ctttcgcttt 360
cttccttctt tctcggcacg gtcgnccggc tttncgccgnc aagctntaaa tcgggggggt 420
tcnntttagg ggttccgaat taagggttt accgggaacc ntngaacccc caaaaaactt 480
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acgtcggtgac tgggaaaacc ctggcggttac ccaacttaat cgccttgag cacaatcccc 180
tttcgccagc tggcataata gcgaagaggc ccgnaccgat cgcccttccc aacagttgag 240
cagcctgaat ggcgaatggg acncgccctg tagcggcgca ttaagcgagg cgggtgtngt 300
ggttacgcgc agcgtgaccg ctacacttgc agcnccctag cgcccgctcc tttnntttt 360
ttnccttcct ttntngcacg tttnacggct ttcccgtaa gctctanac gggggctcct 420
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gaaggnattc ctctgaatn cagcagagaa ctgaatcttt gcctgggncaa gcagctggga 180

aggatgggac gttactttgt gctgaactta caatatttca aaaggggttc ttactttctn 240
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accattccca ggaaggntta ggcccagggn aaagganggt ttaagntggt tgtncncgaa 360
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acacatgacc ccagccctct acagcggtaa ggtgaggac ccacattncc cctgccctct 180
gagacttngg gggacgttgc cccctgana tgcagnnngg gcctgaatat gtgaaccagc 240
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ttggtgccac tctggnaagn ggccaagaat ctnttcccca gggaagaatt gggtcgtcaa 360
aagnggtttt tgcnttttgg gggttccggt gagaancccg agtangttta caacccaag 420
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<212> DNA

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 tatttgacaa agatggtgat ggaactataa caacaaagga attgggaact gtaatgagat 180
 ctcttgggca gaatcccaca gaagcagagt tacaggacat gattaatgaa gtagatgctg 240
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 acacagacag tgaagaagaa attagagaag cattccgtgt gtttgataag gatggcaatg 360
 gctatattag tgctgcagaa cttcgccatg tgatgacaaa ccttggaaga gaagttaaca 420
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 ctatgaagag tttgtaccaa atgatgacag caaaagtgaag agaccttttn ccagaatggg 540
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 gcgcgccagc acagaaacag aggagagtcc cagagcagga ggcccctggc ccagcgggcc 180
 ctccacaca caccacaca ctcgccgcc cactgtcctg ggccgctgg aagccggcgg 240
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 gtgattggaa aaaccaccca acttgaanc nactctttt cctgggtcct tctctccagg 420
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cctgctggac ggctccgagc ggctgggtga gcagaacttc cacaaggccc ggcgcttcgt 180
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<222> (194)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (207)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (245)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (258)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (297)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (301)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (316)
<223> n equals a,t,g, or c

<400> 648
gcncagatgg gcatgctgaa ggggcctctt cttaacaaat ttctgaccac agccaaagat 60
aagaaccgct gggaggacnc tggtaagcag ctctacaacg tggaggccac atcctatncc 120
ctcttngccc tactgcagct aaaagncttt gactttgtnc ctcccgtogt ncnttngctc 180
aatgnacaga gatnctacgg tgggtgntat ggctctaccc aggccacctt catgggtgttc 240
caagncttag ctcaatanca gaaggacggc cctgaccacc aggcactgaa ccttgangtg 300
nacctccaaa tgctcng 317

<210> 649
<211> 575
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (501)
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (509)

<223> n equals a,t,g, or c

<400> 649

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gtaggaacac cctcatcatc tacctggaca aggtctcaca ctctgaggat gactgtctag 60
ctttcaaagt tcaccaatac tttaatgtag agcttatcca gcctggagca gtcaagggtct 120
acgcctatta caacctggag gaaagctgta cccggttcta ccatccggaa aaggaggatg 180
gaaagctgaa caagctctgc cgtgatgaac tgtgccgctg tgctgaggag aattgcttca 240
tacaaaagtc ggatgacaag gtcaccctgg aagaacggct ggacaaggcc tgtgagccag 300
gagtggacta tgtgtacaag acccgactgg caaggttcaa gctgtccaat gactttgacc 360
gagtacatca tggccattga gcagaccatc aagtcaggct cggatgaggt gcaggttggg 420
cagcagcgca cgttcatcag ccccatcaag tgcagagaag ccctgaagct tgaggagaag 480
aaacactact tcattgtggg nctctctnc caattctggg gagagaagcc caaccttagc 540
tacatcatcg ggaaggacac ttgggtggag cactg 575
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<210> 650

<211> 277

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (186)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (243)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (256)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (265)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (267)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (269)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (276)

<223> n equals a,t,g, or c

<400> 650

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tcgacccacg cgtccggcat tgtctatcat tgcactggag atccaagcac agaagtgtgt 60
agagttaaca gaaggaatag aatgtcttca gacacattcc aagataaatg gcagagattt 120
gaccttcttg caagaacttg tatccaagtg ttttaactgaa tattcatcta agcaaagtgg 180
ttccanacca aatgttccag aagtttgaaa atggatttgt tcctggacgt actgcacggc 240
aanctgaagc acaggntact aacngntna acccanc 277
```

<210> 651

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (9)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (13)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (86)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (89)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (97)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (100)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (106)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (175)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (221)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (289)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (299)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (321)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (324)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (355)
<223> n equals a,t,g, or c

<400> 651
ggcacaggnt ccngggtgga gctggctgag tcgcgcgctc tgetccaccc gggggggctg 60
ttttttcttg gctggctcg cggcgcnacng agatggnagn gcagtnggac gaggccgtga 120
agtaatacac cctaggagga gattcagaag cacaaccaca gcaagagcac ctggnctgat 180
cctgncacca caagggtgtac gaatttgacc aaatttctgg nagaggcatc cctgggtggg 240
gaggaagttt taaggggaac aagcttgag gtgacgctac ttgaggaant tttgagggnt 300
gttcggggca cttttaccag ntgncccaag ggaaaattgt tcccaaaaac atttnca 357

576

<210> 652
<211> 190
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (138)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (146)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (148)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (172)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (180)
<223> n equals a,t,g, or c

<400> 652
ggacgctact tccctatca tagaagagct tatcaccttt catgatcacg ccctcataat 60
cattttcctt atctgcttcc tagtcctgta tgcccttttc ctaacactca caacaaaact 120
aactaatact aacatctnag acgctnanga aatagaaacc gtctgaacta tntgcccgn 180
catcatccta 190

<210> 653
<211> 603
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (415)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (600)
<223> n equals a,t,g, or c

<400> 653

```

gcttcgaccc cgccggagga ggagacccca ttctatacca acacctattc tgatttttcg 60
gtcaccctga agtttatatt cttatccctac caggcttcgg aataatctcc catattgtaa 120
cttactactc cggaaaaaaa gaaccatttg gatacatagg tatgggtctga gctatgatat 180
caattggctt cctaggggtt atcgtgtgag cacaccatat atttacagta ggaatagacg 240
tagacacacg agcatatttc acctccgcta ccataatcat cgctatcccc accggcgtea 300
aagtatttag ctgactcgcc aactccacg gaagcaatat gaaatgatct gctgcagtgc 360
tctgagccct aggattcatc ttcttttca ccgtagggtg cctgactggc attgnattag 420
caaactcatc actagacatc gtactacacg acacgtacta ccgttgtagc ccacttcac 480
tatgtcctat caataggagc tggatttgcc atcataggaa ggcttcattc actgatttcc 540
ctattctcag gctacaccct agaccaaac tacgcaaaa atcatttcac tatcataatn 600
cac 603

```

<210> 654

<211> 356

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (198)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (270)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (302)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (328)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (340)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (347)

<223> n equals a,t,g, or c

<400> 654

```

ggtttttttc ttcgcaggat ttttctgagc cttttaccac tccagcctag cccctacccc 60
ccaattagga gggcactggc cccaacagg catcaccccg ctaaattccc tagaagtccc 120

```

actcctaaac acatccgtat tactcgcatc aggagtatca atcacctgag ctcaccatag 180
tctaatagaa aacaaccnaa accaaataat tcaagcactg cttattacaa ttttactggg 240
tctctatfff accctcctac aaagcctcan agtacttcga gtctcccttc accatttccg 300
anggcatacta cggctcaaca ttttttgnag cccaggcttn cacgganttt cacgtc 356

<210> 655

<211> 682

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (660)

<223> n equals a,t,g, or c

<400> 655

gcgcaagtag gtctacaaga cgctacttcc cctatcatag aagagcttat cacctttcat 60
gatcacgccc tcataatcat ttctcttata tgcttcctag tcctgtatgc ccttttcccta 120
acactcacaa caaaactaac taatactaac atctcagacg ctcaggaaat agaaaccgtc 180
tgaactatcc tgcccgccat catcctagtc ctcacgcccc tcccatccct acgcatcctt 240
tacataacag acgaggtcaa cgatccctcc cttaccatca aatcaattgg ccaccaatgg 300
tactgaacct acgagtagac cgactacggc ggactaatct tcaactccta cataacttccc 360
ccattattcc tagaaccagg cgacctgcga ctccttgacg ttgacaatcg agtagtactc 420
ccgattgaag cccccattcg tataataatt acatcacaaag acgtccttgca ctcatgagct 480
gtccccacat taggcttaaa aacagatgca attcccggac gtctaaacca aaccactttc 540
accgctacac gaccgggggt atactacggg caatgctctg aaatctgtgg agcaaaccac 600
agtttcatgc ccacgggcct agaattaatt ccctaataaa tctttgaaat aagggcccg 660
atttacccta tagcaccct ct 682

<210> 656

<211> 520

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (429)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (442)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (449)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (483)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (485)

<223> n equals a,t,g, or c

<400> 656

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gagaagagct tatcaccttt catgatcacg ccttcataat cattttcctt atctgcttcc 60
tagtcctgta tgcccttttc ctaacactca caacaaaact aactaatact aacatctcag 120
acgctcagga aatagaaacc gtctgaacta tcctgcccgc catcatccta gtcctcatcg 180
ccctcccatc cctacgcacg ctttacataa cagacgaggt caacgatccc tcccttacca 240
tcaaatcaat tggcaccaat ggtactgaac ctacgagtac accgactacg gcggactaat 300
cttcaactcc tacatacttc cccattatt cctagaacca ggcgacctgc gactccttga 360
cggtgacaat cgagtagtac tcccgattga agccccattc gtataataat tacatcacia 420
gacgcttgna ctcaagagct gncacacant aggcctaaaa acaggatgca atttccgggc 480
ggntnaaaca aaacaatttt accggtacac gaacggggggg 520
```

<210> 657

<211> 353

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (227)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (340)

<223> n equals a,t,g, or c

<400> 657

```
gcactttctg ccaaagaaat ctctcctttt gcttctagca ccgactagat ttccttcagc 60
tgatgattga ctcccagaat tcgaaagaaa ctgagtccca caaagctctg tctgatctgg 120
agctcgcagc ccagtcataa atcttcattt ttgtgggcta tgaaaccacc agcagtgttc 180
tttcttcac tttatatgaa ctggccactc accctgatgt ccagcnaaaa ctgcaaaagg 240
gagattgatg cagttttgac caataaggca ccacctacct atgatgccgt ggtacagatg 300
gattaccttg acatggtggt gaatgaaacc tcaaattatn cccgttggtg tta 353
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<210> 658

<211> 362

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (203)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (215)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (240)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (262)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (310)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (321)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (333)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (338)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (362)
<223> n equals a,t,g, or c

<400> 658
ggcanaggcc accaccatcc tgcattgccc actttacttg gccttctcct ggctctaact 60
caggcagcca agaccctcc cacttccttc ttggcctcc ctctcctcag gtatgaaaat 120
gaagctggcc ctgcgcccag gcgtttgaag gctgacatca acggcttgcg ccgagtcctg 180
ggatgagctg accctggcca ggnctgacct ggagntgcag atcgagggcc tgaatgagg 240

agctagcctt acctgaagtg gnaccacgaa ggagggagat ggaaggagtt tcagcagcca 300
gttgcccggn caagttcaat nttggagatg ggncgganca ccgggtgtgg gacctgaccc 360
gn 362

<210> 659

<211> 447

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (33)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (47)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (100)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (147)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (168)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (175)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (202)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (204)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (228)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (240)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (247)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (286)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (294)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (353)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (445)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (446)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (447)
<223> n equals a,t,g, or c

<400> 659
gcttctnccg tccttctagg atctccgcct ggntcggccc gcctgcntcc actcctgcct 60
ctaccatgtc catcaagggtg acccagaagt cctacaaggn gtccacctct agcccccg 120

ccttcagcag ccgctcctac acgaatnggc ccggttcccg catcaacncc tcgancttct 180
cccgaatagg cagcagcaac tntngcagtg gcctgggcgg cggctatngt ggggccagcn 240
gcatggnagg catcacgcga gttacggtca accagagcct gctganccccc cttntcctgg 300
aggtggaccc caacatccag gccgtgcgca cccaggagaa ggagcagatc aanaccctca 360
acaacaagtt tgctcttca tagacaaggt aggttcctgg agcagcagaa caagatgttg 420
gaaaccaagt agagctcctt ggcnnn 447

<210> 660

<211> 295

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (10)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (55)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (70)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (73)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (82)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (86)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (95)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (121)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (131)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (144)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (168)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (173)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (229)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (241)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (257)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (270)
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (284)

<223> n equals a,t,g, or c

<400> 660

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ggnacgagcn aaggcctgca ccattctcct ccgggggggct agcaaagaaa ttctntcgga 60
agtagaacgn gancctccag gntgcnatgc aagtntgtcg caatgttctc ctgggaccct 120
nagctggtgc naggggggtgg ggcntccaaa atggctgtgg cccatgcntt ganagaaaaa 180
tccanggccca tggactggtg tgggaacaat ggccatacag ggctgttgnc cagggcccta 240
naggttcatt cctcgtnacc ctggatccan aaactgtggg gggncagcca ccatt      295
```

<210> 661

<211> 212

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (207)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (210)

<223> n equals a,t,g, or c

<400> 661

```
gttggcgtgc tgggcctgga cctctggcag gtcaagtctg gcaccatctt tgacaacttc 60
ctcatcacca acgatgaggc atacgctgag gagtttggca acgagacgtg gggcgtaaca 120
aaggcagcag agaaacaaat gaaggacaaa caggacgagg agcagagggt taaggaggag 180
gaagaagaca agaaacgcaa agaggangan ga                                212
```

<210> 662

<211> 130

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (13)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (20)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (35)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (48)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (74)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (123)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (129)

<223> n equals a,t,g, or c

<400> 662

aaaatacatt ganatacatn atgaaggcca ctatnaccct ccttctgntt gcacaacttt 60
cctgggctgg accntttcat cagacaggct tattagactc tatgctagaa catgaagctt 120
atnggatcng 130

<210> 663

<211> 232

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (9)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (10)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (21)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (138)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (139)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (195)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (205)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (216)
<223> n equals a,t,g, or c

<400> 663
gnctcatnnn gactgttctg ncccgattgt tgctgctggt gttggtgaat ttgaagctgg 60
tatctccaag aatgggcaga cccgagagca tgcccttctg gcttacacac tgggtgtgaa 120
acaactaatt gtcggtgna acaaaatgga ttccactgag ccaccctaca gccagaagag 180
atatgaggaa attgntaagg aagtnagcac ttaccnttaa gaaaaaactg gg 232

<210> 664
<211> 296
<212> DNA
<213> Homo sapiens

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caccacgtcc cgaattctca gacgacacct ggagactgtc ccgacactcc cctgagaggt 180
ttctggggcc cgctgcggtc acgagggggg gcccggttac ccaattcgtc ctatagtgat 240
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<210> 665
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cgggcaagtc caccactact ggccatctga tctataaatg cgggtggcatc gacaaaagaa 180
ccattgaaaa atttgagaag gaggtgctg agatgggaaa gggctccttc aagtatgcct 240
gggtcttgga taaactgaaa gctgagcgtg aacgtggtat cnccattgga tatctccttg 300
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tccccgggtcc ttcgagctcc ttgtgcgcgc tggtgggtgct gctgctgctg ctgacgcagc 180
caggggcccat cgccagcgct ggtcctgccg ntgctgtgtt ganagagctg cgttgccgtt 240
tgtttacaga ccacgcaagg agtccatccc aaaaatgatc agtaatntgc aagtgtncgc 300
cataggccca acagtgcctc aangngggaa gn 332

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ggancgtntc atgtccttgn atccanacaa attgtgccga cgacgccatg gaccctggta 180
ctaaaganag agcttggtgc gcatttggaa ttgcaccatg cacgggcctg accttctggg 240
naccgccagct gtgtaggcag aggacagggt gacaattttg tctttgcgca tggcntaatg 300
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ttgcacacgc ctgaaaagt ggtgaggttc aagtacccaa agctcatctc ctattcctac 180
atggttcgtg ggggccactt tgcggccttt gaggagccgg agctgctcgc ccaggacatc 240
cgcaagttcc tgcggtgct ggagcggcat gnanccaccc ctctcccccc gcttgccact 300
tccccccaca atgccctcca ggnnttcttg ggggaagata accntttctg aggatgantt 360
tgccctccgtc ccntgnccag ttggganccc agttcaaccc ctnaaccttc nagttaattc 420
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gcttcctcc aagaggaccc cgggggtccc gaggggaacc ctctggagga ggaaacgtcc 180
agcaccgagc tggagactgg cagtgtccca atccttcaat tgggtgatttc tgctgtgatg 240
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gtggtggccg gggcatggac cgaggtggct ttngtgagg aagacgaggt ggccctgggg 480
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gaaaa 545

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gctacagtca acatcttgat ntcaactgtgc caactgcggt gcctgccctt canagccctg 180
cactttgttt tntccccctgg cttcatcnac tacatcagtg gcacccctca tgctctgatt 240
gtgcgtcgct acctctccct gctggacacg gccgtggagc tgganctccc aagataccgg 300
ggccccgcgc ttccccgaan gcagtaagtg cccatctttc cccaacctct cntcaccgac 360
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<210> 671
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gtgtggccct gatggtgtc tgtgagaccc accgcgccc catggtcaa caccactgt 240
gcccgggctg cggctacttc tgcacggcgg gcaccttcct ggagtggcac cctgacttcc 300
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<212> DNA

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tttngacctg agaacagctt cctatgntaa tgccattgng aangtcttca aagtgtacan 180
tgaagctggg gtgaccttca catngatgga ncatggetga cttncncaact atcctcttca 240
catgtaactt ntgcagacct atcanaagtt tacatgtaac cacagnnntc cctttctctn 300
ctgactnatt aataatggct accattctta acangttaat ccaagtncaг cncgtttaag 360
ggngnaaagg antcaagggt nggcgggttc atntncaagn tgcgtgtggn agtagtaatt 420
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tnatcttggt gttgcagnct ttnc 504

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<212> DNA
<213> Homo sapiens

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cctgctcggc gaccagaaca ccttcaccca tgaccacctc agcaagttcc cacttaaata 240
aaggcatcaa gcagggtgtac atgtccctgc ctgagggtga gaaagtccag gccatgtata 300
tctggatcga tggtagtgga gaaggactgc gctgcaagac ccggaccctg gacagtgagc 360
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<210> 674
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<212> DNA
<213> Homo sapiens

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aaggcgaggt agccctctgt tgattggtgt acggagtga cataaacttt ctactgatca 180
cattcctata ctctacagaa caggcaaaga caagaaagga agctgcaatc tctctcngt 240
ggacagcaca acctgccttn tcccggngga agaaaaagca gnggagtatt actttgcttc 300
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gcagcaagna 370

<210> 675
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<212> DNA
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<220>
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<222> (325)
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<220>
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<222> (329)
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<400> 675
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gtggtgatgg tgactcacca gagcagtgcg cggctggctg gagggcgtga ggctctcaga 180
cggggagcga ggctggtttc ctgtgacagc nntgngagtt catttccaac ccagaggtcc 240
gtgacacaga acctgaaggg aagcttcacg gagtgcaaga cttgccaaac tacagctngt 300
gggaacagca agcctnantt ttctnctgna gaaggagttt tcgtgagctg gaagaacaag 360
ttg 363

<210> 676
<211> 441
<212> DNA

<213> Homo sapiens

<220>

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<222> (214)

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<220>

<221> misc feature

<222> (353)

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<220>

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<222> (404)

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<222> (413)

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<222> (440)

<223> n equals a,t,g, or c

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<222> (441)

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<400> 676

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agaatctggt aaaagcacca ttgtgaagca gatgaggatc ctgcatgtta atgggtttaa 180
tggagacagt gagaaggcaa ccaaagtgc gganatcaaa aacaacctga aagaggcgat 240
tgaaaccatt gtggccgccca tgagcaacct ggtgcccccc gtggagctgg ccaaccccga 300
aaaccagttc agagtggact acatcctgag tgtgatgaac gtgcctgact ttnacttccc 360
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cgaacgctcc aacgaatacn n 441
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<210> 677

<211> 550

<212> DNA

<213> Homo sapiens

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<222> (487)
<223> n equals a,t,g, or c

<220>
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<222> (523)
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<220>
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gggagcgcaa cgtgctcatc tttgacctgg gcgggggcac ctctgacgtg tccatcctga 180
cgatcgacga cggcatcttc gaggtgaagg ccacggnccg ggacacccac ctgggtgggg 240
aggactttga caacaggctg gtgaaccact tcgtggagga gttcaagaga aaacacaaga 300
aggacatcag ccagaacaag cgagccgtga ggcggctgcg caccgctgcg agagggccaa 360
gaggaccctg tcgtccagca cccaggccag cctggagatc gacttccttg ttttgagggc 420
atcgacttnt acacgttcat caccagggcg aagggttcgaa ggagctgtgc ttccgacctt 480
gntnccnaaa cacccttggg aaccccgctg gaaaaaaggc ttnttgcgcc gaaaggccca 540
ancttggggac 550

<210> 678
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<212> DNA

<213> Homo sapiens

<220>

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<223> n equals a,t,g, or c

<220>

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<222> (55)

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<220>

<221> misc feature

<222> (134)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (295)

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<220>

<221> misc feature

<222> (330)

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<220>

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<222> (333)

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<220>

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<220>

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<220>

<221> misc feature

<222> (385)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (401)

<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>
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<222> (435)
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atggaggata tggntacac tggttacaac aactactatg gatatggtga ttatagcaac 180
cagcagagtg gttatgggaa ggtatccagg cgaggtggtc atcaaaatag ctacaaacca 240
tacttaaatt attccatttg caacttatcc ccaacagggtg gtgaagcata ttttnccatt 300
tgaaggttcc tttgaggggg gctccgccc ngncttaatt ggcnttccaa ctaaattttt 360
gggtatccag tccccnatgg gagtntgcgg tggggccccc nggagtttaa ttcgggggtcc 420
ccntaaagga ttttn 435

<210> 679
<211> 390
<212> DNA
<213> Homo sapiens

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<220>
<221> misc feature
<222> (217)
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<220>
<221> misc feature
<222> (287)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (330)
<223> n equals a,t,g, or c

<220>
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<222> (333)
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<220>
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<222> (371)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (390)
<223> n equals a,t,g, or c

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tccctggaag ctccctgcatg gcagctctga cagtgcact gatggtgctg aactccccac 120
tggctttggc tggggacacc cgaccacgtt tcttgagca ggtnaaacat gaatgtcatt 180
tcttcaacgg gacggaacgg gtgcggttcc tggacanata cttctatcac caagaagaat 240
acgtgcgctt cgacagcgac gtgggggaat accgggcggt gacgganctg gggcggccta 300
actccgaata ctggaacagc cagaaagacn ccngggacag aagcgggccg cggcggacac 360
ctactgcaga nacactacgg ggttggtgn 390

<210> 680
<211> 343
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
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<223> n equals a,t,g, or c

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<220>
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<222> (18)
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<220>
<221> misc feature
<222> (121)
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<220>
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<222> (175)
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<220>
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<222> (272)

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<220>

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<222> (278)

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<220>

<221> misc feature

<222> (292)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (331)

<223> n equals a,t,g, or c

<400> 680

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cagattatgc cattgccagg cgcatagtag atttgcattc agaattgag gaatcaattg 120
nnaatatcta tncctcgcgat gatatcagaa gatatctncn ctatgcaaga aagtntaaac 180
ccaagaattc caaagantca gnggacttca ttgtggagca atntaaacat ctccgcccgn 240
aagatggggt ctggagtagc ccagtcttca tngagggntn cagttgcggc cncattgagg 300
gccttggtac cgtctctctt ggaagccaat ngctccgggt gcc 343

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<210> 681

<211> 523

<212> DNA

<213> Homo sapiens

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<220>
<221> misc feature
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gacccacgcg tncgcccaat ttaccaatc tatcacccta tagaagagct aatgttagta 120
taagtaacat gaaaacattc ncctccgcat aagcctgcgt cagattaaaa cactgaactg 180
acaattaaca gcccaatatc tacaatcaac caacaagtca ttattaccct cactgtcaac 240
ccaacacagg catgtcata aggaaaggtt aaaaaaagta aaaggaactc ggcaaatctt 300
accccgctg tttacaaaaa acatcacctc tagcatcacc agtattagag gcaccgcctg 360
cccagtgaca catgtttaac ggcgcggta ccctaaccgt gcaaaggtag cataatcact 420
tggtccttaa ttagggacct gnatgaatgg ctccacgagg gtcagctggc tcttactttt 480
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<210> 682

<211> 713

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (423)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (583)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (595)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (605)

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<220>

<221> misc feature

<222> (626)

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<222> (633)

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<222> (640)

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<221> misc feature

<222> (646)

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<222> (660)

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<400> 682

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aaatcttacc cgcctgttt accaaaaaca tcacctctag catcaccagt attagaggca 120
ccgcctgccc agtgacacat gtttaacggc cgcggtaccc taaccgtgca aaggtagcat 180
aatcacttgt tccttaaata gggacctgta tgaatggctc cacgaggggt cagctgtctc 240
ttacttttaa ccagtgaat tgacctgccc gtgaagaggc gggcatgaca cagcaagacg 300
agaagaccct atggagcttt aatttattaa tgcaaacagt acctaacaaa cccacaggtc 360
ctaaactacc aaacctgcat taaaaatttc gggtggggcg acctcggagc agaaccacac 420
ctnccagcag tacatgctaa gacttcacca gtcaaagcga actactatac tcaattgatc 480
caataacttg accaacggaa caagttaccc tagggataac agcgcaatcc tattctagag 540
tccatatcaa caatagggtt tacgaacctc gatgtttgat cangacattc ccatngtgca 600
gccnctatt taaaagggtc gttggntcac gantaaaggn cctacntgaa ctgagttcan 660
aaccggagta aattccaagg cgggttttta tctaccttaa aattcccccc tgg 713
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<210> 683

<211> 289

<212> DNA

<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (15)

<223> n equals a,t,g, or c

<220>

<221> misc feature

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<223> n equals a,t,g, or c

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<222> (237)
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<221> misc feature
<222> (252)
<223> n equals a,t,g, or c

<220>
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<222> (287)
<223> n equals a,t,g, or c

<400> 683
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accccccggtt gcggctcggg cctgctctgc taccgcgccg gaggggtgga gaagcccctg 180
cacacactga tgcacgggca aggcgtgtgc atggagctgg cgganatcga ggccatncan 240
gaaagcctgc anccctctga caaggacgag ggtgaccacc ccaacanca 289

<210> 684
<211> 464
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (353)
<223> n equals a,t,g, or c

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agaactcacc atggaatttg ggctgagctg gctttttctt gtggctattt taaaaggtgt 120

ccagtgtgag gtgcaattgg tggagtctgg gggaggcttg gtacagcctg gggggtcctt 180
gagactctcc tgtacagtct ctggattcac ctttcgcaac tatgccatga gttgggtccg 240
ccagggtcca ggggaagggg tggaatgggt ctcagcaatt gacggtagtg gttataaacac 300
atactacgag aggtccctgc agggccgctt tagtgtctcc agagacaatt ccnagaacac 360
actatatctg caaatgaaca gcctgggagc cgaggacacg gccatctatt attgtgcgaa 420
gacagaacgt atgggtactg gctggtacgg acgaaatgac tact 464

<210> 685

<211> 545

<212> DNA

<213> Homo sapiens

<220>

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<222> (6)

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<220>

<221> misc feature

<222> (10)

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<222> (428)

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<222> (438)

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<222> (442)
<223> n equals a,t,g, or c

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<222> (456)
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<220>
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<222> (457)
<223> n equals a,t,g, or c

<220>
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<222> (505)
<223> n equals a,t,g, or c

<220>
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<222> (509)
<223> n equals a,t,g, or c

<220>
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<222> (536)
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cggcctccat ctccctgcagg tctagtcaga ccctcctgca tgtcaatgga cacaactatt 180
tggattggta catgcagaag ccagggcagc ctccacagct cgtgggtctat aggggttcca 240
atcgggcctc cggggtccct gacaggttca gtggcgggtg atcaggcaca gattttacac 300
ttagaatcac cacggtggag gctgangatg ttggcgttta ttactgcatg caagctctac 360
aaagtccgta cacttttggc caggggacca agctggagat caaacgaact gtgggctgca 420
ccatctgnct tcatcttncc gncatctgat gaacanntga aatctggaac tgcctctggt 480
gggggcctgc tgaataactt ctatnccana gagggccaaa gtaccagtgg aaaggnggga 540
taacg 545

<210> 686
<211> 496
<212> DNA
<213> Homo sapiens

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<220>

<221> misc feature

<222> (417)

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<222> (460)

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<222> (472)

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<221> misc feature

<222> (481)

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<220>

<221> misc feature

<222> (488)

<223> n equals a,t,g, or c

<400> 686

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gcctggattc cacagcttcg cgccgtgtac tgtcgccccca tccctgcgcg cccagcctgc 180
caagcagcgt gccccggttg caggcgatcat gcagcgggcg cgacccacgc tctgggcegc 240
tgcgctgact ctgctggtgc tgctccgcgg gccgcgggtg gcgcgggctg gcgcgagctc 300
ggggggcctt ggtcccgtgg tgcgctgcga accgtgcgac gcgcgtgcac tggcccantg 360
cgcgcccttc gccgcggtg tgccgcccga cttggtgcgc caagccgggc ttgcggnatg 420
tgcctgacgt gcgcactgag cgaaggggcca gccgtgcggn atctacaccg ancgtgtgg 480
nttccggnct tcgttg                                     496
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<210> 687

<211> 476

<212> DNA

<213> Homo sapiens

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<222> (7)

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<220>

<221> misc feature

<222> (10)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (56)

<223> n equals a,t,g, or c

<400> 687

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tcacacgact gcagctggag acagagatcg aggctctcaa ggaggagctg ctcttcatga 180
agaagaacca cgaagaggaa gtaaaaggcc tacaagccca gattgccagc tctgggttga 240
ccgtggaggt agatgcccc aaatctcagg acctcgccaa gatcatggca gacatccggg 300
cccaatatga cgagctggct cggaagaacc gagaggagct agacaagtac tggctctcagc 360
agattgagga gagcaccaca gtggtcacca cacagtctgc tgaggttga gctgctgaga 420
cgacgctcac agagctgaga cgtacagtcc agtccttga gatcgacctg ggactt 476
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<210> 688

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<400> 688

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anantaaccc tcactaaagg gaacaaaagc tggagctcca ccgcggtgag gccgctctag 60
aactagtga tccccgggc tgcaggaatt cggcacgagc aggttcccgc ccggaagaag 120
cgaccaaagc gcctgaggac cggcaacatg gtgcggtcgg ggaataaggc agctgttgtg 180
ctgtgtatgg acgtgggctt taccatgagt aactccattc ctggtataga atccccattt 240
gaacaagcaa agaaggtgat aaccatgttt gtacagcgac aggtgtttgc tgagaacaag 300
gatgagattg ctttagtcct gtttgggtaca gatggcactg acaatcccct ttctgggtgg 360
gatcagtatc agaacatcac agtgcacaga catctgatgc taccagattt tgatttgctg 420
gaggacattg aaaagcaaaa tccaaccagg ttctcaacag gctgacttcc tgggatgcac 480
taa 483
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<210> 689

<211> 339

<212> DNA

<213> Homo sapiens

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<222> (236)

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<222> (337)

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<220>

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<222> (338)

<223> n equals a,t,g, or c

<400> 689

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gagattgaaa ggcgaggagc agaagctgct gagaaacgcc agaagatgnc agaagatggc 120
ttgtcagatg acagnaaacc attcaagtgt ttcantccta aaaggttcat ctcttcaaga 180

tagaagagcg agcagat ttt tgattaagtc tgtgcagaaa agcagtgggtg ttcaantcga 240
cccttcaagc agcattagtn ttccaagttt gacagcagan tggagcatnt taccatggca 300
tttgagggga ccaaaagcag ccaaaacctt aaaaaanna 339

<210> 690
<211> 594
<212> DNA
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<220>
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<223> n equals a,t,g, or c

<220>
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<222> (473)
<223> n equals a,t,g, or c

<400> 690
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acaaagagaa gggggagaaa acctagcaga ccaccatgtg ctatgggaag tgtgcacgat 120
gcatcggaca ttctctgggtg gggctcgccc tcctgtgcat cgcggtaat attttgcttt 180
actttcccaa tggggaaaca aagtatgcct ccgaaaacca cctcagccgc ttcgtgtggt 240
tcttttctgg catcgtagga ggtggcctgc tgatgctcct gccagcat ttcgttcattg 300
ggctggaaca ggatgactgc tgtggctgct gtggccatga aaactgtggc aaacgatgtg 360
cgatgctttc ttctgtattg gctgctctca ttggaattgc aggatctggc tactgtgtca 420
ttgtggcagc ccttggctta gcagaaggac cactatgtct tgattccctc ggncagtggg 480
actacacctt tgccagcacc gagggccaag taccttctgg ataccttcac atgggtccgag 540
tgcactgaac ccaacacatt ggggaatgga atggatctct ggtttctatc ctct 594

<210> 691
<211> 538
<212> DNA
<213> Homo sapiens

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<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (55)

<223> n equals a,t,g, or c

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ctagaactag tggatccccc gggctgcagg aattcggcac gagcgcatga ctttgtcttc 120
tccgcacgac tggtacagag gtctccagag cttctctct cctgtgcaa atggcaactc 180
ttaaggaaaa actcattgca ccagttgcgg aagaagaggc aacagttcca aacaataaga 240
tactgtagt ggggtgttga caagttggta tggcgtgtgc tatcagcatt ctgggaaagt 300
ctctggctga tgaacttgct cttgtggatg ttttggaaga taagcttaaa ggagaaatga 360
tggatctgca gcatgggagc ttatttcttc agacacctaa aattttggca gataaagatt 420
attctgtgac cgccaattct aagattgtag tggtaactgc aggagtccgt cagcaagaag 480
gggagagtgc gctcaatctg gtgcagagaa atgttaatgt cttcaaattc attattcc 538

<210> 692

<211> 201

<212> DNA

<213> Homo sapiens

<220>

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<220>

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<222> (143)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (161)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (165)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (183)

<223> n equals a,t,g, or c

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aagtccaata tggcaactct aaaggatcag ctgatttata atcttctaaa ggaagaacag 120
accnccaga ataagattac agntgttggg gttggtgctg ntggnatggc ctgtgccatc 180
aanatcttaa tgaaggactt g 201

<210> 693
<211> 589
<212> DNA
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<222> (377)
<223> n equals a,t,g, or c

<220>
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<222> (401)
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<220>
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<220>
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<222> (551)
<223> n equals a,t,g, or c

<220>
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<222> (571)
<223> n equals a,t,g, or c

<220>
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<222> (572)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (576)
<223> n equals a,t,g, or c

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ccgggggtgt taacttggtt attgcagctt ataatggta caaataaagc aatagcatca 120
caaatcttcac aaataaagca tttttttcac tgcattctag ttgtgggttg tccaaactca 180
tcaatgtatc ttatcatgtc tggatcgatc ctgcattaat gaacggccaa cgcgcgggga 240
gaggcggttt gcgtattggc tggcgtaata ncgaaaagcc cgcaccgatc gcccttccca 300
acagttgccc ancctgaatg gcgaatggga cgcgccctgt ancggcgcat taancgcggc 360
gggtgtggtg gttaccncaa cgtgaccgct acacttgcca ncgccctaac gcccgctcct 420
ttcnccttct tcccctncct ttctcccca cgttcgcgcg gggttncccc gtcaaaactct 480
aaatccgggg ntccccttta agggttccca atttaattgc ttaacggcac ctccaacccc 540
aaaaaaactt naataagggg tgaatggttc nnctanttgg gccaccccc 589

<210> 694
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<212> DNA
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<222> (135)
<223> n equals a,t,g, or c

<220>
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<222> (149)
<223> n equals a,t,g, or c

<220>
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<222> (370)
<223> n equals a,t,g, or c

<220>
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gagatctgcc ctgccggcca cggtacacc tacgcgagct ccgacatccg cctgtccatg 120
aggaaagccg aggangaaga actggcaang cccccaaggg agcaagggca gangagcagc 180
tgggcactgc ccgggccaac ananaagcag cccctccggg ttcgtcacgg acacctggt 240
tgangccggg accatccctg acaaggttga ctctcaagct ggccagggtca cgaccagtgt 300
cactcatgca cctgcctggg tcacanggaa atgccacaan cccaccaat gcctgaacag 360
ggaattgcnn aaaattccgg aanaaa 386

<210> 695
<211> 475
<212> DNA
<213> Homo sapiens

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<222> (231)
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<222> (278)
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<222> (423)
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<220>
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<222> (463)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (465)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (466)
<223> n equals a,t,g, or c

<400> 695
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aagcagtgtc aagacagtaa ggattcaaac catttgccaa aaatgagtct aagtgcattt 120
actctcttcc tggcattgat tgggtggtacc agtggccagt actatgatta tgattttccc 180
ctatcaattt atgggcaatc atcaccaaac tgtgcaccag aatgtaactg ncctgaaagc 240
taccacaagt ccatgtactg tgatgagctg aaattganaa gtgtaccaat ggtgcctcct 300
ggaatcaagt atctttacct taggaataac cagattgacc atattgatga aaaggccttt 360
gagaatgtaa ctgatctgca gtggctcatt ctagatcaca accttctaga aaactccaag 420
atnaaaggga gagttttctc taaattgaaa caactgaana agntnntata accac 475

<210> 696
<211> 444
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (402)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (410)
<223> n equals a,t,g, or c

<400> 696
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ggaaatgaaa cttctctttg ggactgcaag aactggcaat ggggtggact tacctgtgat 120
cactatgaag aagccaaaat tacctgctca gccacaggg aaccagact ggttgagggg 180
gacattccct gttctggacg tgttgaagtg aagcatggtg acacgtgggg ctccatctgt 240
gattcagact tctctctgga agctgccagc gttctatgca ggggaattaca gtgtggcaca 300
gttgtctcta tcctgggggg agctcacttt ggagagggaa tggacagatc tgggctgaag 360
aattccagtg ttgagggaca tgaatcccca tctttcatct tncagtagn aaccccgccc 420
aaaaggaact tgtagccaca gcaa 444

<210> 697
<211> 411
<212> DNA

<213> Homo sapiens

<220>

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<222> (104)

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<220>

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<222> (305)

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<222> (338)

<223> n equals a,t,g, or c

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<222> (370)

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<222> (375)

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<222> (391)

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<222> (410)

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<400> 697

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ccagacgaca gggaagaagg agctgcctct acggctgagg aaanagccaa gaaaaaaga 120
cgaaagaaga agaagagcaa agggccttct gcaggtaaag agagttttat gttttccag 180
tcccctccgg gaacggctga actgtttggc tcaggcccgt tgagggggcc gggaccgggg 240
ccccagagcc ccgactagac tgattcttgg gcctgacagg gtggcaaagc cgggctatag 300
atcanggtgc acctgagctt tctctgatgt atgcccangc agatctccag gtattcagag 360
cacctgcttn cccancctgt tagtcttagt nacccaaccc tcctgtgcan a 411
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<210> 698

<211> 135

<212> DNA

<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>
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<220>
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<223> n equals a,t,g, or c

<220>
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<222> (79)
<223> n equals a,t,g, or c

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ccctncaact ggaagatgna ttctgagccg atttcaagta caaagtttta gaacttgggg 120
tgcggtgat taggg 135

<210> 699
<211> 434
<212> DNA
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<220>
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<220>
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<222> (368)
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<220>
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<222> (369)
<223> n equals a,t,g, or c

<220>
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<222> (391)
<223> n equals a,t,g, or c

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<222> (394)
<223> n equals a,t,g, or c

<220>
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<222> (427)
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<400> 699
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ngcacagttt tctctcttgg agcatgcatg gaaggcctga atattttgct taacagactg 120
ttgggggattt cattatatgc agagcagcct gcaaaaggag aggtgtggag cgaagatgtc 180
cgaaaactgg ctgttgttca tgaatctgaa ggattgttgg ggtacattta ctgtgatttt 240
tttcagcgag cagacaaacc acatcaggat tgccatttca ctatccgtgg aggcagacta 300
aaaggaagat gggagactat ncaactccca gttgtaagtt cttatgctgg aatcttcccc 360
gttcccgnna gggagttctc caactttggc naangcctgg gcatgatggg aaaacctttc 420
ccagganggg ggac 434

<210> 700
<211> 435

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (118)

<223> n equals a,t,g, or c

<400> 700

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cagatgagac cgggtgtccag ggtactggct cctcatctca ctcgggctta tgccaaanat 120
gtaaaatttg gtgcagatgc ccgagcctta atgcttcaag gtgtagacct tttagccgat 180
gctgtggccg ttacaatggg gccaaagggg agaacagtga ttattgagca gagttgggga 240
agtcccaaag taacaaaaga tgggtgtgact gttgcaaagt caattgactt aaaagataaa 300
tacaagaaca ttggagctaa acttgttcaa gatgttgcca ataacacaaa tgaagaagct 360
ggggatggca ctaccactgc tactgtactg gcacgctcta tagccaagga aggccttcgag 420
aagattagca aaggt                                     435
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<210> 701

<211> 406

<212> DNA

<213> Homo sapiens

<400> 701

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aaaatttggt gcagatgccc gagccttaat gcttcaaggt gtagaccttt tagccgatgc 60
tgtggccggtt acaatggggc caaaggggag aacagtgatt attgagcaga gttgggggag 120
tcccaaagta acaaaagatg gtgtgactgt tgcaaagtca attgacttaa aagataaata 180
caagaacatt ggagctaaac ttgttcaaga tgttgccaat aacacaaatg aagaagctgg 240
ggatggcact accactgcta ctgtactggc acgctctata gccaaaggag gcttcgagaa 300
gattagcaaa ggtgctaata cagtggaaat caggagaggt gtgatgttag ctgttgatgc 360
tgtaattgct gaacttaaaa agcagtctaa acctgtgacc acccct                                     406
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<210> 702

<211> 266

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (203)

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<220>

<221> misc feature

<222> (215)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (230)

<223> n equals a,t,g, or c

<220>
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<222> (239)
<223> n equals a,t,g, or c

<220>
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<222> (252)
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<400> 702
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gcaggggtcca agcggccttt cttctggatg caggaaccca agacagacca ggatgaggag 120
cattgccgga aagtcaacga gttatctgga acaaccccc gatgcctggg gcactggggg 180
ccagcgggaac agcgggccacg aantctctgc gctangcggt tgaggtggcn tgcagagcnt 240
gctggggaaa cntgagccac agccag 266

<210> 703
<211> 244
<212> DNA
<213> Homo sapiens

<220>
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<220>
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<222> (207)
<223> n equals a,t,g, or c

<220>
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<222> (208)
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<222> (211)
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<220>
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<400> 703
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ataaaatgac agtttgaaca tacaaaaccc accccattcc tccccacact catcgccctt 120

accacgctac tcctacctat ctccccctttt atactaataa tcttataaaa aaaaaaaaaa 180
aaaaaaaaaa aaangggggg gccgggnncc natttngccc aaaggggggg ggttttaaaa 240
ttca 244

<210> 704

<211> 462

<212> DNA

<213> Homo sapiens

<220>

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<220>

<221> misc feature

<222> (45)

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<222> (102)

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<221> misc feature

<222> (162)

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<222> (168)

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<222> (183)

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<222> (186)

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<222> (189)

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<220>

<221> misc feature

<222> (206)
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<222> (215)
<223> n equals a,t,g, or c

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<220>
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ccaaccttcc cgccagacta cggcttcccc gaacgcaagg ancgcganat ggtggccaca 180

cancangana tgatggacgc gcactnaagc tccanctgcg ggantactgc gcccaccaac 240
tcatccgggt gctcaattnc aaccttaaan cttccccac ttccttggt tgcnaaccag 300
gaacgggaca aatnggaata ntccaaaca cccanaant tttntnccc ttaaanantt 360
tttaaacgga aacgaagggt ntcccccccg gaaaaaaaaac nggggnaaaa aaaggggaaa 420
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<211> 436

<212> DNA

<213> Homo sapiens

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caaataccga tactttgctt gtttgatgag agcccggttt gaagaacata agaataaaa 180
ggatatggcg aagggcaccg agctgctgaa ggaggccgag gaagaattct ggtaccgtca 240
gcattccacg ccatacatct tccctgactc tcctgggggc acctcctatg agagatacga 300
ttgctacaag gtcccagaat ggtgcttaga tgactggcat ccttctgaga aggcaatgta 360
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tnttgntgn aagattgcca cttgatgccg ccaaacgatt ncatgatgag ctgggnaatg 180
aaagaccttn tgcttacatg anggagcaca atcaattaaa tggctggtnt tctgatgaaa 240
atgactggaa tgaaaaactc taccagtggt ggaagcggng agacatgang tngaaaaaac 300
tgctggaagg gagggccgtg tgcaaggcgg tcctgaccag ngactnacca acccttgng 360
ggctcaaata naacattngc cggngaacct gatattccct aaangccaaa aggaagaagc 420
caatggcaac ataggctatg anaagaactg ganaaatgaa gctgggntaa acagctgaac 480
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tatcttttcg gttgtgaact aaaggccgac aaagattatc actttaagggt ggataatnat 180
gaaaatgagc accagttatc tttagaacg gtcngtttng gggctggtgc aaaggatgag 240
ttgcacattg ttgaagcaga ggcaatgaat tacgaaggca gtccaattaa agtaaacactg 300
gcaactttga aaatgtctgt acagccaacg gttttccctt tgggggcttt gaataacacc 360
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gctttctttt taatcccctg catcggatca ccggcggtgcc ccaccatgtc agacgcagcc 180
gtagacacca gtcccgaaat caccaccaag gacttaaagg agaagaagga agttgtggaa 240
gaggcagaaa tggaagagac gccctgctaa cgggatgcta atgaggnaat ggggagcagg 300
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<212> DNA

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ggcccacccat cccggcgngg accttttccg ttagcgtggg tgatattgtt cctgctcgag 180
gcncaaattng gtccttgga tctccttcca tctgcccatt aactctcgca agtgcctccg 240
ngaggaaatt cnc 253

<210> 710
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tgctcttcaa aacatcattc tttatcacct acaccaggag ttttcattgg aaaaggattt 180
gaacctgggtg ttactaacat ttttaaagac cacacaaggn agcaaaatct ttctggaagg 240
aagtgaatat gttacacttc tggatgaatg atttggaat ccaaaagant ctgacatcca 300
tgggccacca anggtggtaa tttcatgttg taggttaaac tncnctttc cagcagncac 360
accttttggg natggntcaa ctggtnggga tacttgatta ttnatncaa tnnctcccn 420
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tgcccagtgat atcttgatg ctgctttcct gcctcatgct gctgtctcag gttcaagggtg 180
aagaacccca gagggaaactg ccctctgcac ggatccgctg ncccaaaggc tccaaggcct 240
atggctccca ctgctatgcc ttgtttttgt caccaaaatc ctggacagat gcagatctgg 300
cctgccagaa gcggccctct ggaaacctgg tgtctgngct cagtggggct gagggatcct 360
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<212> DNA

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caacctggca gccgccgccc tggaagagca gtatagctgt gactatggat ctggcagatt 240
ctttatcctt tgtggacttg gaggaattat tagctgtggc acaacacata cagcattggt 300
tcctctagat ctggttaaat gcagangcag gtttgttttt gcatgctgga cttagagcna 360
ttgaagcntg actgangtta agtattagna ta 392

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gatgaacgtc tccggaaaga gttttctcca ttggtacaa tcactagtgc aaagggtatg 180
atggagggtg gtcgcagcaa agggtttgggt ttgtatggt tctcctccc agaanaagcc 240
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gcaagtgtac ganctgttcc caaccctgta atcaaccct accagccagc acctccttca 420
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aaattgctca actaanacca agtctcgtc ggactgctca gggtgccata actcatccat 540
tccaaaatat gcccggtgct atccgcccag ctgctcctan aacaccattt agtactatga 600
naacagcttc ttctcagcaa catcttaatg cacagccaca anttacaatg cacancctgc 660
tgttcatggt caaggtcagg aacctttgan tgcttccatg ttngcatctg ccccccccca 720
aaacaaaacc aatt 734

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gtttttaaac aaagtgactg aggcacagga agatggccag tcaacttctg aattgattgg 180
ccagtttggt gtcggtttct attccgcctt ccttgttagca gataaggtta ttgtcacttc 240
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tgctgaccca agaggaaaca ctctaggacg gggaacgaca attacccttg tcttaaaaga 360
agaagcatct gattaccttg aattggatac aattaataat ctcgtcaaaa aatattcaca 420

gttcataaac tttcctatatt atgtatggng cagcaagact gaaactgttn aggagcccat 480
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<210> 715

<211> 491

<212> DNA

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<222> (353)

<223> n equals a,t,g, or c

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<222> (360)
<223> n equals a,t,g, or c

<220>
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<222> (398)
<223> n equals a,t,g, or c

<220>
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<220>
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<222> (422)
<223> n equals a,t,g, or c

<220>
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<222> (473)
<223> n equals a,t,g, or c

<220>
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<222> (474)
<223> n equals a,t,g, or c

<400> 715
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anaantacaa caagtgggaa acgatatagg cttggactca acaagtcgcc actganaatc 120
cagccctcat ctctcgcagt gttatcgga ccacatttga gggacgcgct atttacctcc 180
tgaaggttgg caaagctgga caaaataagc ctgccatttt catggactgt gggtttccca 240
tgccaganan ttggatttct ccctgcattc ngccagtngg tttntaaaa aangcgggttc 300
ccttcctatn gacntttana ncccanttga caaacttcnc caacaattta aanttttatn 360
ttccgcgcct gtggcccca tattgaaggg caacttcnac cccgggaacn aaaaccctaat 420
tntggaaaaa aaaaccccc cccccctgg tgggattctt gctttggttg ggnnccaccc 480
caaaaaaatt t 491

<210> 716
<211> 331
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (242)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (303)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (321)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (322)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (326)
<223> n equals a,t,g, or c

<400> 716
gtaaagccgg ggcagcagcc ggcggtccgg gtgtaagcgg cgtgtgcgtg tgcaagagcc 60
gctacccggt gtgcggcagc gacggcacca cctacccgag cggtgccag ctgcgcgccg 120
ccagccagag ggcgagagc cgcggggaga aggccatcac ccaggtcagc aagggcacct 180
gcgagcaagg tccttccata gtgacgccc ccaaggacat ctggaatgtc actggtgcc 240
angtgtactt gagctgtgag gtcacgga tcccgacacc tgcctcatc tggaacaagg 300
tanaaagggg tcactatgga nntcanagga c 331

<210> 717
<211> 486
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<220>
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<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature

655

<222> (38)
<223> n equals a,t,g, or c

<220>
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<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (68)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (78)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (99)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (107)
<223> n equals a,t,g, or c

<400> 717
tatcnttact aagggtacaa agttnngggtc tnccaccnngg tngaggaccg ctcctagcaa 60
ctagtggntc ccccggnct gcaggaattc ggcacgagna tattagnacg cggttattcg 120
gtgagcgggtg gtgggtttatt ctcccggtga gtttaagggtc ccgtggacat ctcaggtctt 180
cagggtcttc catctggaac tatataaagt tcagaaaaca tgtctcgaga tatgactcca 240
ggaccactat attttctcca gaaggtcgct tataccaagt tgaatatgcc atggaagcta 300
ttggacatgc aggcacctgt ttgggaattt tagcaaatga tgggtgtttg cttgcagcag 360
agagacgcaa catccacaag cttcttgatg aagtcctttt ttctgaaaaa atttataaac 420
tcaatgagga catggcttgc agtgtggcag gcataacttt ctgatgctaa tgttctgact 480
aatgac 486

<210> 718
<211> 479
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (436)
<223> n equals a,t,g, or c

<400> 718
tcgacccacg cgtccgcagc ccacccatcc acgttgactc atcctcagag acgaatcgac 60

accctcaact cagatggata caccctgag ccagacaaac cgcgccgat gcccatggac 120
acgagcgtgt atgagagccc ctacagcgac ccagaggagc tcaaggacaa gaagctcttc 180
ctgaagcgcg ataacctcct catagctgac attgaacttg gctgcggcaa ctttggtc 240
gtgcgccagg gcgtgtaccg catgcgcaag aagcagatcg acgtggccat caaggtgctg 300
aagcagggca cggagaaggc agacacggaa gagatgatgc gcgaggcgca gatcatgcac 360
cagctggaca acccctacat cgtgcggctc attggcgtct gccaggccga agccctcatg 420
ctggtcatgg agatgntggg ggcgggcgct gcacaagttc ctggtcggca agaaggaag 479

<210> 719

<211> 572

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (418)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (421)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (501)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (503)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (526)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (546)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (559)

<223> n equals a,t,g, or c

<400> 719

gcgtgccc atgagaatgaga tcaccaaagt gcgaaaagt actttcaatg gactgaacca 60
gatgattgtc atagaactgg gcaccaatcc gctgaagagc tcaggaattg aaaatggggc 120

tttccaggga atgaagaagc tctcctacat ccgcattgct gataccaata tcaccagcat 180
tcctcaaggt cttcctcctt cccttacgga attacatctt gatggcaaca aaatcagcag 240
agttgatgca gctagcctga aaggactgaa taatttggct aagttgggat tgagtttcaa 300
cagcatctct gctgttgaca atggctctct ggccaacacg cctcatctga gggagcttca 360
cttggaacaac aacaagctta ccagagtacc tgggtgggctg cagagcataa agtacatnca 420
nggtggctac cttcataaca accatatctc tgtagttgga tcaaagtac ttctggccac 480
ctggacacaa ccacccaaaa ngnttcttaa ttccgggtgg gaagcntttt aacaaacccg 540
ggccangact ggggagaana cagccatcca cc 572

<210> 720

<211> 487

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (376)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (447)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (459)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (460)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (467)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (468)

<223> n equals a,t,g, or c

<400> 720

ggntaaatca gaactcgaat ggccttggtt tcttgctctg gggctcttat gctcagaaga 60

agggcagtgc cattgatagg aagcggcacc atgtactaca gacggctcat ccctcccctt 120
tgtcagtgtg tagagggttc ttggatgta gacacttttc aaagaccaat gagctgctgc 180
agaagtctgg caagaagccc attgactgga aggagctgtg atcatcagct gaggggtggc 240
ctttgagaag ctgctgttaa cgtatttgcc agttacgaag ttccactgaa aattttccta 300
ttaattctta agtactctgc ataaggggga aaagcttcca gaaagcagcc atgaaccagg 360
ctgtccagga atggancctg tatccaacca caaacaacaa aggctaccct ttgacccaaa 420
tgtctttctc tgcaacatgg cttcgggcta aaatatgcnn aagacannat gagggccaat 480
acttaat 487

<210> 721

<211> 464

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (222)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (312)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (347)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (349)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (364)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (415)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (436)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (443)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (448)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (455)

<223> n equals a,t,g, or c

<400> 721

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tcctgggttg tgaggagtcg ccgctgccgc cactgcctgt gcttcatgag gaagatgctc 120
gccgccgtct cccgcgtgct gtctggcgct tctcagaagc cggcaagcag agtgctggta 180
gcatcccgtg attttgcaaa tgatgctaca ttgaaatta anaaatgtga ccttcaccgg 240
ctggaagaag ccctcctgtc acaacagtgc tcaccaaggg aagatgggct caaatactac 300
aggatgatgc anactgtacc cgaatggaat tgaaacagat cactgtntna acagaaaatt 360
atcntgggtt ctgtccttgt gtgatgtcag aacttgctgt gtggcctgga gccgnatcac 420
cccaaacact ctccanctac ggntccgntt atttnccggg cttc 464
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<210> 722

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (12)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (43)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (113)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (142)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (152)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (153)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (182)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (211)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (263)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (275)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (281)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (299)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (308)

<223> n equals a,t,g, or c

<400> 722

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gttgacacgc anctgcacgc gccgtggetc cggatctctt cgnctttgca gcgtagcccg 60
agtcggtcag cgccggatga cctcagcagc catgtcgaag ccccatagtg aanccgggac 120
tgccttcatt cagaccacgc anctgcacgc anncatggct gacacattcc tggagcacat 180
gngccgcctg gacattgatt caccacccat nacaggccgg aacactggca tcatctgtac 240
cattggccca gcttcccgat cangtggaga cggtnaagga natgattaaa gcctggaang 300
aatgtggntc gtctgaactt                                     320
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<210> 723

<211> 152
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (87)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (111)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (127)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (148)
<223> n equals a,t,g, or c

<400> 723
gcccaccatg gctgcaatcc gaaagaagct ggtgatcggtt ggggatgggtg cctgtgggaa 60
gacctgcctc ctcatcgnt tcagcangga tcagtttccg gaggtctacg nccctactgt 120
cctttgngaa ctatattgcg cacattgngg cg 152

<210> 724
<211> 573
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (463)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (514)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (553)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (559)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (569)

<223> n equals a,t,g, or c

<400> 724

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gctgctatgt tcaatataag aaatattgga aagacgctcg tcaccaggac ccaaggaacc 60
aaaattgcat ctgatggctc caagggtcgt gtgtttgaag tgagtcttgc tgatttgag 120
aatgatgaag ttgcatttag aaaattcaag ctgattactg aagatgttca gggtaaaaac 180
tgcctgacta acttccatgg catggatctt acccgtgaca aaatgtgttc catgggtcaa 240
aaatggcaga caatgattga agctcacgtt gatgtcaaga ctaccgatgg ttacttgctt 300
cgtctgttct gtgttggttt tactaaaaaa cgcaacaatc agatacggaa gacctcttat 360
gctcagcacc aacaggtccg ccaaatccgg aagaagatga tggaaatcat gacccgagag 420
gtgcagacaa atgacttgaa agaagtggtc aataaattga ttncagacgc attggaaaaa 480
acatagaaaa ggcttggcaa tctattatcc tctncatgat ggcttcgtta gaaaagtaaa 540
aatgctgaag aanccaagnt tgaatgggna aac 573
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<210> 725

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (9)

<223> n equals a,t,g, or c

<400> 725

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gcttgaaant aaccctcact aaaggaaca aaagctggag ctccaccgag gtgcggccgc 60
tctagaacta gtggatcccc cgggctgcag gaattcggca cgagtcctgg tccgcgccag 120
agcccagcgc gcctcgtcgc catgcctcgg aaaattgagg aaatcaagga cttcctgctc 180
acagcccagc gaaaggatgc caaatctgtc aagatcaaga aaaataagga caacgtgaag 240
tttaaagtgc gatgcagcag atacctttac accctgggtc tcaactgaca agagaaggca 300
gagaaaactga agcagtcctt gcccccggt ttggcagtga aggaactgaa atgaaccaga 360
cacactgatt ggaactgtat tatattaaaa tactaaaaat cct 403
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<210> 726

<211> 502

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (8)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (256)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (281)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (380)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (391)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (428)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (456)
<223> n equals a,t,g, or c

<400> 726
cgcaagnncg anactaacc tcactaaagg gaacaaaagc tggagctcca ccgcggtgcg 60
gccgctctag aactagtga tccccgggc tgcaggaatt cggcacgaga gccatcaggt 120
aagccaagat ggggtgcatac aagtacatcc aggagctatg gagaaagaag cagtctgatg 180
tcatgcgctt tcttctgagg gtccgctgct ggcagtaccg ccagctctct gctctccaca 240
gggctccccg ccccanccgg cctgataaag cgcgccgact nggctacaag gccaaagcaag 300
gttacgttat atataggatt cgtgttcgac gtggtggccg aaaacgccca gttcctaagg 360
gtgcaattac ggcaagcctn tocatcatgg ngttaaccag ctaaagtttg ctcgaagcct 420

tcagtccttt gcagaggagc gagctggacg ccactntggg gctctgagag tcctgaattc 480
ttactggggtt ggtgaagatt cc 502

<210> 727

<211> 361

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (309)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (318)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (360)

<223> n equals a,t,g, or c

<400> 727

ggcacgagcg aacgcgnaga gcacgccatg aaggcctcgg gcacgctacg agagtacaag 60
gtagtggggtc gctgcctgcc ccccccaaa tgccacacgc cgcccctcta ccgcatgcga 120
atctttgcgc ctaatcatgt cgtcgccaag tcccgtttct ggtactttgt atctcagtta 180
aagaagatga agaagtcttc aggggagatt gtctactgtg ggcagggtgt tgagaagtc 240
cccctgcggg tgaagaactt cgggatctgg ctgcgctatg actcccggag cggcacccac 300
aacatgtanc gggaatancg ggacctgacc aacgcaggcg ctgtcaacca gtgtaacggn 360
g 361

<210> 728

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (6)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (200)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (234)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (251)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (319)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (332)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (360)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (389)
<223> n equals a,t,g, or c

<400> 728
gaagangctc gcctctagtg tcctccgctg tggcaagaag aagtctggtt agacccaat 60
gagaccaatg aaatcgccaa tgccaactcc cgtcagcaga tccggaagct catcaaagat 120
gggctgatca tccgcaagcc tgtgacggtc cattcccggg ctcgatgccg gaaaaacacc 180
ttggcccgcc ggaaaggcan gcacatgggc atagttagcg gaaaggtagc gccnatgccc 240
gaatgccaaa naaggtcaca tggattaaga aaatgaagat tttgcgcccg ctgctcaaaa 300
aatacgtgaa tcttaaaana tcgatcgcca cntntttcac agcctgttcc taaagttaan 360
ggaatttttt caaaaacaac cgattctcnt ggaacacttc c 401

<210> 729
<211> 530
<212> DNA
<213> Homo sapiens

<220>

666

<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (14)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (60)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (527)
<223> n equals a,t,g, or c

<400> 729
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ccgctctaga actagtggat cccccgggct gcaggaattc ggacagagcc gccatcttcc 120
agtaattcgc caaaatgacg aacacaaagg gaaagaggag aggcacccga tatatgttct 180
ctaggccttt tagaaaacat ggagttgttc ctttggccac atatatgcga atctataaga 240
aaggtgatat tgtagacatc aagggaatgg gtactgttca aaaaggaatg cccacacaagt 300
gttaccatgg caaaactgga agagtctaca atgttaccga gcatgctgtt ggcattgttg 360
taaacaaca agttaagggc aagattcttg ccaagagaat taatgtgcgt attgagcaca 420
ttaagcactc taagagccga gatagcttcc tgaaacgtgt gaaggaaaat gatcagaaaa 480
agaaagaagc caaagagaaa ggtacctggg ttcaactaaa gcgccancct 530

<210> 730
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (87)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (97)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (111)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (121)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (124)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (125)
<223> n equals a,t,g, or c

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<222> (142)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (181)
<223> n equals a,t,g, or c

<220>
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<222> (190)
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<222> (354)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (367)

<223> n equals a,t,g, or c

<400> 730

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tggacgctac tccggacgca aagctgntca tcgtaanaga acattgaatg ntggcacctc 120
naanngcccc tacagccatg cncctgggtggc tgggaattga accgctaccc ccgcaaatga 180
ncngctgcn tggggcanga agaagntcgc caggagggtca aagatatant cttttgtgaa 240
ngtgtgtnac tacaatcacc tnatgccnc aaggtactct gtngatatt ccccttgggg 300
caaagctgta cgttcattag gntgtcttcc ganattcctg gctcttaaac gctnggcccg 360
aaggagnccc aggtc 375
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<210> 731

<211> 207

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (143)

<223> n equals a,t,g, or c

<220>

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<222> (177)

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<220>

<221> misc feature

<222> (187)

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<220>

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<222> (201)

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<220>

<221> misc feature

<222> (207)

<223> n equals a,t,g, or c

<400> 731

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actgctccag tttcctgatc aagaggaata agcagaccta cagcactgag cccaataact 120
tgaaggcccg caattccttc cgtacaacg gactgattca ccgcaagact gtgggcntgg 180
agccggnagc cgacggcaaa ngtgctcn 207

<210> 732

<211> 702

<212> DNA

<213> Homo sapiens

<220>

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<222> (620)

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<222> (628)

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<222> (655)

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<222> (686)

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<220>

<221> misc feature

<222> (690)

<223> n equals a,t,g, or c

<400> 732

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gaagtggtaa cccgagaata caccatcaac attcacaagc gcatccatgg agtgggcttc 120
aagaagcgtg cacctcgggc actcaaagag attcggaaat ttgcatgaa ggagatggga 180
actccagatg tgcgcattga caccaggctc aacaaagctg tctgggccaa aggaataagg 240
aatgtgccat accgaatccg tgtgcgctg tccagaaaac gtaatgagga tgaagattca 300
ccaaataagc tatatacttt ggttacctat gtacctgtta ccactttcaa aaatctacag 360
acagtcaatg tggatgagaa ctaatcgctg atcgtcagat caaataaagt tataaaattg 420
caaaaaaaaa aaaaaagggc ggccgctcta gaggatccaa gcttacgtac gcgtgcatgc 480
gacgtcatag ctcttctata gtgtcaccta aattcaattc actgccgtcg gtttacaacg 540

tcgtgactgg gaaaaccctg cgttacccaa cttaatcgcc ttgcagcaca tccccttctg 600
ccagctgcgt aataacgaan aggcccgna cgcgcgcctt tccacagttg cgcancctga 660
atggcgcaatg gacgcgcctt taccgngcan taagcgccgc gg 702

<210> 733

<211> 441

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (22)

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<221> misc feature

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<222> (99)

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<222> (101)

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<222> (126)

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<222> (152)

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<222> (185)
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<220>
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<222> (310)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (356)
<223> n equals a,t,g, or c

<400> 733
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anctagtggg tcccccgggc tgcaggattt cggcacganc ncgtgcagat tcgagcanag 120
gagcgnaagg gaacgtcatc gtttggaaag cntcgcaata agacgcacac gttgtgccgc 180
cgctntggct ctaaggccta ccaccttcag angtcgacct gtggcaaatt tggtaccct 240
gccaaagcga agagaaagtn taactggagt gccaaaggcta aaagacgaaa taccaccgga 300
actggtcgan tgaggcacct aaaatttga taccgcagat tcaggcatgg tttccntgaa 360
ggaacaacac ctaaacccaa gagggcagct gttgcagcat ccagttcatc ttaagattgt 420
caacgattag tcatgcaata a 441

<210> 734
<211> 379
<212> DNA
<213> Homo sapiens

<220>
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<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (323)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (324)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (342)

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<220>

<221> misc feature

<222> (346)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (375)

<223> n equals a,t,g, or c

<400> 734

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cacacgttgt gccgccgtg tggctctaag gcctaccacc ttcagaagtc gacctgtggc 120
aaatgtgggt accctgccaa gcgcaagaga aagtataact ggagtgccaa ggctaaaaga 180
cgaaatacca ccggaactgg tcgaatgagg cacctaaaaa ttgtataccg cagattcagg 240
catggattcc gtgaaggaac aacacctaaa cccaagaggg cagctgtgtc agcattccag 300
ttcatcttta agaatgtcaa cgnntttagt catgcaataa antgtntctg ggttttaaaa 360
aattaaaaga aaagnaaaa 379
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<210> 735

<211> 187

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (172)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (176)

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<220>

<221> misc feature

<222> (177)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (179)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (185)

<223> n equals a,t,g, or c

<400> 735

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gcgggatcgt cggtaaatac gggacccgct atggggcctc cctccggaaa atggtgaaga 60
aaattgaaat cagccagcac gccaaagtaca ctgtctcttt ctgtggcaaa accaagatga 120
agagacgagc tgtggggatc tggcactgtg gttcctgcat gaagacagtg gntggngng 180
cctgnac 187
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<210> 736

<211> 576

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (94)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (334)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (340)

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<220>

<221> misc feature

<222> (361)

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<220>

<221> misc feature

<222> (371)

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<220>

<221> misc feature

<222> (397)

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<221> misc feature

<222> (409)

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<222> (436)
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<222> (444)
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<221> misc feature
<222> (452)
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<220>
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<222> (466)
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<222> (479)
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<220>
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<222> (490)
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<220>
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<222> (519)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (553)
<223> n equals a,t,g, or c

<400> 736

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ggtcacgta ttgaggaagt tcctgaactt cttntggtag ttgaagataa agttgaaggc 120
tacaagaaga ccaaggaagc tgttttgctc ctttaagaac ttaaagcctg ggaatgatat 180
caaaaaggtc tatgcctctc agcgaatgag agctgggcaa aggcaaatg gagaaaccgt 240
cgccgtatcc agcgcagggc ccgtgcatca tctataatga ggataatggt atcatcaagg 300
ccttcagaa acatccctgg aattactctg cttnaatgtn aagcaagctg aaacattttg 360
naagcttgct ncctggtggg gcatgtgggg acgtttncgg cattgggang gaaatggctt 420
ttccgggant ttaganggan tgtnacgggc antgggcgta aagcgnnttc cctccaagng 480
ttaactacan tcttcccagg caccaagatg gattaatana gatcttggca gaatctggaa 540
aagcccagag gtnccaaggg cccttcgggc accagc 576

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<210> 737

<211> 297

<212> DNA

<213> Homo sapiens

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<222> (243)

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<220>

<221> misc feature

<222> (254)

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<222> (261)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (266)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (275)

<223> n equals a,t,g, or c

<400> 737

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ctggcaaaaa tgtcactttg cctgctgtat tcaaggctcc tattcgacca gatattgtga 120
actttgttca caccaacttg cgcaaaaaca acagacagcc ctatgctgtc agtgaattag 180
caggctcatca gactagtgtc gagtcttggg gtactggcag agctgtggct cgaattccca 240

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ganttcgagg tggnggggact naccgntctg gccanggtgc ttttggaac atgtgtc 297

<210> 738

<211> 354

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)

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<220>

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<222> (74)

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<222> (120)

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<222> (148)

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<222> (193)

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<222> (286)

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<222> (303)
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<220>
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<222> (329)
<223> n equals a,t,g, or c

<220>
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<222> (351)
<223> n equals a,t,g, or c

<220>
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<222> (353)
<223> n equals a,t,g, or c

<400> 738
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actctgaagg gacncacagn tatngtgaag ggcccccag gaaccctgcg gagggacttn 120
aatcacatca atgtataact cagccttntt ggaaagaaaa aaaagaggct ccgggttgac 180
aaatggtggg gtnacagaaa ggaactggct accgttcgga ctatttgtag tcatgtacag 240
aacatgatca aggggtgttac actgggcttc cgttacaaga tgaggncgtg gtatgctcac 300
ttncatcatca acgttgttat ccaagagant ggggtctattg ttgaaatcca nant 354

<210> 739
<211> 504
<212> DNA
<213> Homo sapiens

<400> 739
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atcgacgcag cgtccccact tgggtgaagt tgacatctga cgacgtgaag gacgagattt 120
acaaactggc caagaagggc cttactcctt cacagatcgg tgtaatcctg agagattcac 180
atggtgttgc acaagtacgt tttgtgacag gcaataaaat ttaagaatt ctaagtcta 240
agggaattgc tcctgatctt cctgaagatc tctaccattt aattaagaaa gcagttgctg 300
ttcgaaagca tcttgagagg aacagaaagg ataaggatgc taaattccgt ctgattctaa 360
tagagagccg gattcaccgt ttggctcgat attataagac caagcgagtc ctccctccca 420
attggaaata tgaatcatct acagcctctg ccctggctgc ataaatttgt ctgtgtactc 480
aagcaataaa atgattgttt aact 504

<210> 740
<211> 399
<212> DNA
<213> Homo sapiens

<400> 740

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atagaaaagt actacacgcg cctgggcaac gacttccaca cgaacaagcg cgtgtgcgag 120
gagatcgcca ttatccccag caaaaagctc cgcaacaaga tagcaggtta cgtcacgcat 180
ctgatgaagc gaattcagag agggccagta agaggtatct ccatcaagct gcaggaggag 240
gagagagaaa ggagagacaa ttatgttctt gaggtctcag ccttggatca ggagattatt 300
gaagtagatc ctgacactaa ggaaatgctg aagcttttgg acttcggcag tctgtccaac 360
cttcagtcac tcagcctaca gttgggatga tttcaaaac 399

<210> 741

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (335)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (393)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (417)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (425)

<223> n equals a,t,g, or c

<400> 741

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cgcccggtgc gtgcccaagg ataaggccat caagaagttt gtcattcgga acattgtaga 120
agccgctgct gtcagggaca tatctgaagc aagcgtcttc gacgcctacg tgcttcccaa 180
gctctatgtc aagctgcatt attgcgtgac tgtgccatcc atagcaaggt tgtaggaat 240
cgatcccgtc aagcccggaa ggaccgaaca cccccaccac gattcagacc tgctggcgct 300
gcaccttcga cctccaccaa agcccatgta aagangccgt ttttgtaagg acggaaggaa 360
aattaccttg gaaaaataaa atggaagttg tanttttaaa aaaaaaaaaa aaaccnagg 420
ggggncccgt c 431

<210> 742

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (178)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (240)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (273)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (297)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (324)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (352)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (353)

<223> n equals a,t,g, or c

<400> 742

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ttcatggatg tcatcagcat tgacaagacg ggagagaatt tccgtctgat ctatgacacc 120
aagggtcgct ttgctgtaca tcgtattaca cctgaggagg ccaagtacaa gttgtgcnaa 180
gtgagaaaga tctttgtggg cacaaaagga atccctcatc tgggtgactca tgatgcccgn 240
accatccgct accccgatcc cctcatcaag gtnaatgatc cattcatatt gatttanaga 300
ctggcaagat tactgatttc atcnatttcg acactggtaa cctgtgtatg gnnactg 357

<210> 743

<211> 249

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (42)

<223> n equals a,t,g, or c

<220>

681

<221> misc feature
<222> (77)
<223> n equals a,t,g, or c

<220>
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<222> (115)
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<222> (122)
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<220>
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<222> (158)
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<220>
<221> misc feature
<222> (200)
<223> n equals a,t,g, or c

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<220>
<221> misc feature
<222> (221)
<223> n equals a,t,g, or c

<220>
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<222> (248)
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<400> 743
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taactccatg atgatgnacg ggcgcaacaa cggcaagaag ctcatgactg tgcgnatcgt 120
cnagcatgcc ttcgagatca tacgcctgct cacaggcnaa gaaccctctg caggtcctgg 180
tgaacgcat catcaacatn ggtccccggg aagantccac ncgattggg cgcgccggga 240
ctgttgana 249

<210> 744
<211> 383
<212> DNA
<213> Homo sapiens

<400> 744
gaagaattgc atcgtgctca tcgacagcac accgtaccga cagtggtagc agtcccacta 60
tgcgctgccc ctgggcccga agaagggagc caagctgact cctgaggaag aagagatttt 120
aaacaaaaaa cgatctaaaa aaattcagaa gaaatatgat gaaaggaaaa agaatgccaa 180
aatcagcagt ctcttgagg agcagttcca gcagggaag cttcttgctg gcacgccttc 240
aaggccggga cagtgtggcc gagcagatgg ctatgtgcta gagggcaaag agttggagtt 300
ctatcttagg aaaatcaagg cccgcaaagg caaataaatc cttgttttgt cttcacccat 360
gtaataaagg tgttttattgg ttt 383

<210> 745
<211> 452
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (314)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (328)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (352)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (403)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (416)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (429)
<223> n equals a,t,g, or c

<220>
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<222> (435)

<223> n equals a,t,g, or c

<220>

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<222> (451)

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<400> 745

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ggcagccttc ctcaaaaagt ccgggaagct gaaagtcccc gaatgggtgg ataccgtcaa 120
gctggccaag cacaaagagc ttgctcccta cgatgagaac tggttctaca cgcgagctgc 180
ttccacagcg cggcacctgt acctccgggg tggcgctggg gttggctcca tgaccaagat 240
ctatggggga cgtcagagaa acggcgctcat gcccagccac ttcagccgag gctccaagag 300
tgtggcccgc cggntcctcc aagccctngg aggngctgaa aatggtggaa anggaccaag 360
atggcgggcc gcaaactgac acctcagggg caaagagatc tgnacagaat cgccgnacag 420
gtggcagcnt gccancaaag aagcattaga nc 452
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<210> 746

<211> 114

<212> DNA

<213> Homo sapiens

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<400> 746

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ctgtctgcaa accaatgtgc cgtgncagcc aaggacangg tgnactgtgg ctac 114

<210> 747

<211> 165

<212> DNA

<213> Homo sapiens

<400> 747

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gcagtgagcg tgggcccccg ggtgcacatc attgaggagc tgcagatctt ctcatcgga 120
cagcccgtgg cagaatctgc tcctgggaca cccacagggg ggctg 165

<210> 748

<211> 583

<212> DNA

<213> Homo sapiens

<220>

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atgacccttg gattggcaag ttattgtatc ttgaggactt cttcgtgatg agtgattata 180
gaggcttttg cataggatca gaaattctga agaattctaag ccagggtgca atgagggtgc 240
gctgcagcag catgcacttt tttggtagca gaatggaatg aaccattcat naacttctat 300
aaaagaagag gtgcttctga tctgtccagt gaagaagggt ngagacttgt taagaatcga 360
caaggagtct tgctaaaaat ggcaacntag gagtgaggaa tgcttgctgt agatgacaac 420
ctccattcta ttttagaata aaattcccca actttctntt gnttttctat gctgggttgg 480
agtgaatta atttaaatga gcaccattt caaaagcttt aattaccaag tgggcnnttg 540
ntnccntgtt ttgaaaattg aaggtcttgt tttaaaagg 583

<210> 749
<211> 419
<212> DNA
<213> Homo sapiens

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<220>
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<222> (351)
<223> n equals a,t,g, or c

<220>
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<222> (376)
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<222> (419)
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tgaccgggtcc ggaattcccg ggtcgaccca cgcgtccggg cgtgatgtct cacagaaagt 120
tctccgctcc cagacatggg tccctcggtt tctgcctcg gaagcgana gcaggcatcg 180
tggaaggtg aagagcttcc ctaaggatga cccgtccaag ccggtccacc tcacagcctt 240
cctgggatac aaggctggca tgactcacat cgtgcgggaa gtcgacaggc cgggatccaa 300
ggtgaacaag aaggagggtg gtggaggctg tgaccattgt anagacacca nccatggtg 360
tttgtgggca ttgttngcta cgttggaata ccctcgangg ctccggaact tcaagaatn 419

<210> 750

<211> 507

<212> DNA

<213> Homo sapiens

<220>

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<222> (453)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (475)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (497)

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<220>

<221> misc feature

<222> (499)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (503)

<223> n equals a,t,g, or c

<400> 750

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tactgtcttc agaaaactca tgatgatcct ggccatgaat gaaaaggata agaagaaaga 120
gaagaaatga agtgaccatc cagcctttcc caattagact tcctctcctt ccacccctca 180
tttctttttt gcacacatta cagggtggtg gttctgtgat aatgaaaagc atcagaaaag 240
cttttgtact ttgtggtttc ctctattttg aattttttga tcaaaaaact gattagcaga 300
atatagtttg gagtttggtt tcatcttctt ggggttcccc tcaactccctt ttttggaac 360
cccatctgta gcctcttctt ctactcaggc agtcgacccg ccacgatgag aagtgggacc 420
agcagagggc gccaaactta ggagcccgtt tnnccacca gcttcattca cccantggac 480
ctgaactgtt tgggtananc ccnccgg 507

<210> 751

<211> 435
<212> DNA
<213> Homo sapiens

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<222> (34)
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<220>
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<220>
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<222> (420)

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<400> 751

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ggatcccccg ggctgcaggt agcctgagct tagctcagcg ccggggcttn accaagacct 120
acactgttgg ctgngaggaa tgcacagtgg ntccctgntt atccatcccc tgcaaactgc 180
agagtggcac tcattgctng tggacggacc agctnctnca aggctntgaa aagggcttnc 240
agncccgtea ccttgcntgc ctgcctcggg agccagggct gggcacctgg cagtnctgc 300
ggtcccagat agcctgaata ntgnccggag nggaagctga agcctgcaca gtgtncaccc 360
tgntnccact cccatctttc ttctggacaa tgaaataaag agntaccacc cagcaaaaan 420
aaaaaaaaaa acctg 435
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<210> 752

<211> 591

<212> DNA

<213> Homo sapiens

<220>

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (240)

<223> n equals a,t,g, or c

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<220>
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<220>
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<220>
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<222> (586)
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gcttctggca tcctgttggt gctgtggctg atagcccccgcagggcctg cacctgtgtc 120
ccacccacc cacagacggc cttctgcaat tccgacctcg tcatcagggc caagtctctg 180
gggacaccag aagtnaacca gaccacctta taccagcgtt atgagatcaa gatgaccaan 240
atgtataaag ggtccaagc cttaggggat gccgctgaca tccggttcgt ctacaccccc 300
gccatggaga gtgtctgcng atactttcac aggtcccaca accgnagcga ggagtctctc 360
attgntggaa aactgcagga tggacttttg cacatcacta cctgcanttt tgtggctccc 420
tggaacagcc tgagcttagc tcagcgcccg gncctnacca agacctacac tgttggtcgn 480
gaggaaatgc acaagtgcct ccctgtttat ccatccccctg caaactgcag agtgggcact 540
cattgcttgt aggaacngacc agctcctacn angtctctna aaaggncctt c 591

<210> 753
<211> 547
<212> DNA
<213> Homo sapiens

<220>
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<220>
<221> misc feature
<222> (454)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (489)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (503)
<223> n equals a,t,g, or c

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<222> (512)
<223> n equals a,t,g, or c

<400> 753

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cacagaagga ttccgaggct ggaatggaca gtgccttgat gtggacgagt gcctggaacc 120
aaacgtctgc gcaaatggtg attgttccaa ccttgaaggc tcctacatgt gttcatgcc 180
caaaggctat acccggaactc cggaccacaa gcactgtaga gatattgatg aatgtcagca 240
agggaaatcta tgtgtaaacg ggcagtgcaa aaataccgag ggctccttca ggtgcaactgt 300
ggacaggggt taccagctgt cggcagctaa agaccagttt gaagacattg atgaatgcc 360
caccgtcatc tctgttgctc atgggcatgc aagaacactg aagctctttt ccatgtgttt 420
tttgaccang gttacagaac atctgggctt gganacactg tgaaaaattt caatgaatgc 480
ttggaagana aaatttttgc canaaaagaa antgctttat actgcagggt cctatgatgt 540
cttgtcc 547
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<210> 754

<211> 384

<212> DNA

<213> Homo sapiens

<220>

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<222> (307)

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<220>

<221> misc feature

<222> (374)

<223> n equals a,t,g, or c

<400> 754

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gaacgggagg aagcagagtc tgggggagct catcggcact ctgaacggcg ccaaggtgcc 120
ggccgacacc gaggtggttt gtgctcccc tactgcctat atcgacttcg cccggcagaa 180
gctagatccc aagattgctg tggtgctgca gaactgctac aaagtgacta atggggcttt 240
tactggggag atcagccctg gcatgatcaa agactgcgga ccacgtgggt ggtcctgggg 300
cactcanaga gaagcatgtc ttgggggaat cagatgagct gattgggcag aaagtggccc 360
atgctctggc aganggactc ggat 384
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<210> 755

<211> 253

<212> DNA

<213> Homo sapiens

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<220>

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<222> (217)

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<220>
<221> misc feature
<222> (240)
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<222> (252)
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<220>
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<222> (253)
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cagtgcgaagc agccctgcca gccacctcct gtgtgcccca cgccaaagtg cccaagagcc 120
atgtccaccc ccgaagtgcc ctgagcctta cctgcctcct ccttgtccac ctgagcattg 180
cccacctcca ccttgccagt ataaatgccc tcctgtngca accataccac cctggcagcn 240
gaanttcccc cnn 253

<210> 756
<211> 183
<212> DNA
<213> Homo sapiens

<220>
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<222> (5)
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<220>
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<222> (9)
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<222> (108)

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<222> (141)

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<222> (144)

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<220>

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<222> (146)

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<220>

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<222> (148)

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<400> 756

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ctaccttctg ccctgtgtnt ggnacctaca tccttaatga ttgtcctntt acccattctg 120
gaattttttt ttttttaaaa naantncnga aagcattttg aaaaaaaaaa aacaaaaaaaa 180
aag 183

<210> 757

<211> 99

<212> DNA

<213> Homo sapiens

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<222> (33)

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<222> (79)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (82)

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<400> 757

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tcagcgtccg ggattgnanc anctgggatt ggagtttgg 99

<210> 758

<211> 60

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (36)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (38)

<223> n equals a,t,g, or c

697

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<400> 758
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<210> 759
<211> 66
<212> DNA
<213> Homo sapiens

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<222> (6)
<223> n equals a,t,g, or c

<220>
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<222> (59)
<223> n equals a,t,g, or c

<220>
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<222> (63)
<223> n equals a,t,g, or c

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<222> (65)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (66)
<223> n equals a,t,g, or c

<400> 759
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centnn 66

<210> 760
 <211> 487
 <212> DNA
 <213> Homo sapiens

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<220>
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 <222> (433)
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<220>
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 <222> (473)
 <223> n equals a,t,g, or c

<220>
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 <222> (475)
 <223> n equals a,t,g, or c

<220>
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 <222> (477)
 <223> n equals a,t,g, or c

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 ttggaagaa gttttttact ttggtttagt ctttttttcc ttccttttta ttcagctaga 180
 atttctggtg ggttgatggt agggataat gtgtctgtgt tgcttcaaat tggcttgaaa 240
 ggctatcctg ctgaaagtcc tgctttccta tctagcattt atttctctgg caaacttttc 300
 tttcttttct tttttaagt aaacttgtgt attgagctta actgtatttc agtatttcca 360
 gcttatgtgt acattattcc aatgatacc aacagttatt tatattttnt aacaaattca 420
 cagtctgaat gangacttta tttcatggat tataataagg aatgaggtaa ttngngnctc 480
 acattca 487

<210> 761
 <211> 422
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (253)
 <223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (297)
<223> n equals a,t,g, or c

<220>
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<222> (350)
<223> n equals a,t,g, or c

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<220>
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<222> (382)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (403)
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<220>
<221> misc feature
<222> (406)
<223> n equals a,t,g, or c

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gggtggggct gtgagctctt aatttgtttt tgattctgaa aaactctgct tcctggcatc 120
caggagttag agattgagcc ttcatcttc tttctcaaaa ctagtttttg atgctttctt 180
tcatgggaat agtcactttt ttatttagta aatcgattg ctggaaccac caaggatgtg 240
gaatgtcctt gantgtatta tttatgcaag tcacagtcac gtttgccatc atggcantat 300
ttgaaacact aataatgtgt ttttactttt ttatccccgt taaaatgatn ttnaaaagga 360
aaaagggtgt tatagcccct anaatttctg ggtccaaatt atnccnaaaa tttcctaaaa 420
aa 422

<210> 762
<211> 375
<212> DNA
<213> Homo sapiens

<220>
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<222> (279)
<223> n equals a,t,g, or c

700

<220>
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<220>
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<222> (373)
<223> n equals a,t,g, or c

<400> 762
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ctttattggt acttcatcag tgtttccttt tgaaagggtg atgaattcat tacattttta 180
ttctaattgta ttatctgtag attagaagat aaaatcaagc atgtatctgc ctatactttg 240
tgagttcacc tgtctttata ctcaaaagtg tcccttaana gtgtccttcc ctgaaataaa 300
tacctaaggg agtgnaacag tctctggagg accactttga gcctttggaa gttaagggtt 360
cctcagccac ctngt 375

<210> 763
<211> 372
<212> DNA
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<220>
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<220>
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<222> (344)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (354)

<223> n equals a,t,g, or c

<400> 763

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atattttcat caagagaaga ataactttac taaattttat ttctttattt gcaaaagaat 120
ctttattaaa acaaacaatc ttaactatgc acatgatgtg accagatcat cttgaaaata 180
ttcctcttta gtaggaactc tttgttttta actcttggtg tggtcagaat ataatacttc 240
cataattact tataattcct ntccgggtac tgggggctat aaatacaact tttttaaatg 300
naattcatgg ttatcaaccn ggctccaagt accattangg ggtnccctat gggnaattac 360
cttgggaaag tc 372
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<210> 764

<211> 195

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (46)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (52)

<223> n equals a,t,g, or c

<220>

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<222> (60)

<223> n equals a,t,g, or c

<220>

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<220>

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<222> (71)

<223> n equals a,t,g, or c

<220>

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<222> (86)

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<220>

<221> misc feature

<222> (94)

<223> n equals a,t,g, or c

<220>
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<220>
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<220>
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<220>
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<223> n equals a,t,g, or c

<220>
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ctttganatt naggaaggtg aggatnggtc agangatgta acttgatgtg agcagtaata 120
aacctgtntt aaatatcata ctgtgnatat ntnattgaaa atttatttca ggcggaaaa 180
acnttagcta aaatc 195

<210> 765
<211> 103
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>
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<222> (76)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (83)
<223> n equals a,t,g, or c

<220>
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<222> (91)
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<220>
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<400> 765
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aattaagggtt agcggntcat gtncaagctg ngtntgaaag tgg 103

<210> 766
<211> 538
<212> DNA
<213> Homo sapiens

<220>
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<223> n equals a,t,g, or c

<220>
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<222> (316)
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<220>
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<222> (327)
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<220>
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<222> (379)
<223> n equals a,t,g, or c

<220>
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<222> (436)
<223> n equals a,t,g, or c

<220>
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<222> (441)
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<220>

<221> misc feature
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<220>
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<222> (450)
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<220>
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<222> (474)
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<220>
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<222> (504)
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<222> (516)
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<220>
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<220>
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (526)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (534)
<223> n equals a,t,g, or c

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ggcttcatcc tcaccgagcg cctgggcagc ggcacgtacg ccacggtgta caaggcctac 120
gccaagaagg aactcgtga agtggttagc ataaagtgtg tagccaagaa aagtctgaac 180
aaggcatcgg tggagaacct cctcacggag attgagatcc tcaaggcatt cgacatcccc 240
acattgtgca gctgaaagac tttcagtggtg agctgggggc ggggncgctg ccaaaaggag 300
tggagaagga catctntttc aggcgcgctc tctgcctctt aaaacaacag ttgggaacag 360

ttgaaccaat taatcttanc ttcaatccat tgggaagttt ttttgccggc caaggggggg 420
gccggaaacc ttggtncctc nggcntttcn aatcccaatt aaaccccggc caanggaatt 480
ttcttgcccc cttgaaagaa aaanggtttg ggcccncccn tnggtncctt tccnaatg 538

<210> 767

<211> 415

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (350)

<223> n equals a,t,g, or c

<400> 767

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ctgcagtgat acttctggta gatgtcacc agtggttttt gttagggtcaa atgttcctgt 120
atagtttttg caaatagagc tgtatactgt ttaaattgtag caggtgaact gaactggggg 180
ttgctcacct gcacagtaaa ggcaaacctc aacagcaaaa ctgcaaaaag gtgggtttttg 240
cagtaggaga aaggaggatg tttatttgca gggcgccaag caaggagaat tgggcagetc 300
atgcttgaga cccaatctcc atgatgacct acaagctaga gtattttaa gcagtggtaa 360
atttcagga aagccagaag ttaaaggcca aaattgtaaa tcagtcgaga tcggg 415

<210> 768

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (351)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (381)

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<220>

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<222> (389)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (422)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (423)

<223> n equals a,t,g, or c

<400> 768

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gacccctcag gccaggccct gatccagttc tccagggtct ttctcagggg caggtccatg 120
gggagaccat ggggtgcttg tctgacactg acctcgccct gctgagtccc cccatcagac 180
tgtccttcct ctgcagcgag tgtctgcagg gtctggatcc aggaaaggaa ttctgatctg 240
tggaagtttg tctcccccggt gtgtgtcctg cactaaatgt ccaaaccctg atacaggatg 300
taatgcagag agggccacag gcacaaccca ggccgtgaaa tcccgtatgt nggaagtaga 360
actgaccccc aacaccacaga ngtcatgtng aaatactcac ggtatacatg gaaaaaaaaa 420
annaa 425
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<210> 769

<211> 256

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (34)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (60)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (83)

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<222> (151)

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<220>
<221> misc feature
<222> (211)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (235)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (250)
<223> n equals a,t,g, or c

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gcaccagctg gcctcccaaa ggngnggcag ccgtgcttat atttttatgg tnacaatggn 120
cacaaaatta ttatcaacct aactaaaaca ntccctttct ctnttttcct ggaattatca 180
tggagttttc taattctctn ttttggaat ngtagattgt ttttgaaatg ctttnacgat 240
gttaaaatan ttatt 256

<210> 770
<211> 316
<212> DNA
<213> Homo sapiens

<220>
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<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (158)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (173)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (200)

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<222> (228)

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<220>

<221> misc feature

<222> (266)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (267)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (281)

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<220>

<221> misc feature

<222> (284)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (291)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (294)

<223> n equals a,t,g, or c

<400> 770

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ctgtctcttg tggagacaat aaggaggagt tacagatgca gccacagatt gatcatctgc 120
ctttaacgtg aatcggagat gctttgtaat ctactgtgcc agctgaagca ctncatgtta 180

cgaggaagaa actacaagtn atgttcaa atcttttggg tcattttnat gtacctttgg 240
gttcaggcat tatttggggg gttttnttc caaaggaact naantaaagt natnttgctt 300
attaaaaaaaa ggaaaaa 316

<210> 771

<211> 68

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (8)

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<220>

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<222> (14)

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<220>

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<222> (22)

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<220>

<221> misc feature

<222> (32)

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<220>

<221> misc feature

<222> (36)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (55)

<223> n equals a,t,g, or c

<400> 771

caaaagcngg agcncaccg cnggcgaccg cncctanaact agtggatccc ccggncctgca 60
ggaattca 68

<210> 772

<211> 258

<212> DNA

<213> Homo sapiens

<220>

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<220>

<221> misc feature

<222> (19)

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<222> (235)
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<222> (250)
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<220>
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<222> (257)
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nttgggtcat ttccacatgc ttattccag caatcaaaat aattaaaaac atctcaaatt 120
attatacaca tacaaaatng gtacagagtc ttttntttcc tcccaccctt agggggaaaa 180
actgctttnt gctttgggaa gttgtctctg aaaccggggg acagnggacg caggncagac 240
taggagggan ccgggang 258

<210> 773
<211> 587
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (535)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (559)
<223> n equals a,t,g, or c

<220>
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<222> (565)
<223> n equals a,t,g, or c

<220>
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<222> (570)
<223> n equals a,t,g, or c

<220>
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<222> (572)

<223> n equals a,t,g, or c

<400> 773

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cgctagagaa gcaatttctg acccctcttt ctttctctgg tcaactcaatt tcaggacagg 120
agttgctcct tcccaaagag ttttggggta tctttctctc cattctaggt tatteggagc 180
ccccttttta ccgttaagga gatctgagtt aatggcttgc tcaagttccc aggaatcggg 240
tgtggactga ggaactcggc cccgggctct tagtacgccg tcccttggtc aggtatccag 300
ggacggttct caccctctgtc ttttctcctt gcagggtgact cctgcacctg cgccggctcc 360
tgcaaatgca aagagtgcaa atgcacctcc tgcaagaaaa gtaagtggga tcctctcttt 420
cctctacccc ttcctgtcct ccagcctgtc ccctcttcac catcctcagg ggaattaaag 480
caagtctggg gatgccccat tgcgccggga aattggtggc ctcctcagtg atccntatca 540
aggagaagca aggaatccnt aattnccggn gnccgttgta cttaact 587
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<210> 774

<211> 89

<212> DNA

<213> Homo sapiens

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<222> (20)

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<220>

<221> misc feature

<222> (74)

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<220>

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<222> (76)

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<222> (77)

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<222> (79)

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<220>

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<222> (83)

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<220>

<221> misc feature

<222> (86)

<223> n equals a,t,g, or c

<400> 774

ggcagagggg aacatcaggn atgctaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60
aaaaaaaaaa aaanannana aanaantat 89

<210> 775

<211> 113

<212> DNA

<213> Homo sapiens

<220>

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<222> (10)

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<220>

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<222> (30)

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<222> (32)

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<222> (57)

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<220>

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<222> (59)

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<222> (75)

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<222> (77)

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<220>

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<222> (106)

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<400> 775

gggtccggcgn ggtggaggga aacgcctccn tntctatata aggaatttcc cgggtgtntnc 60
gggtcctttt ccctntnttc agagtggggg gcccaaattt gggcgntctg ttt 113

<210> 776

<211> 66

<212> DNA

<213> Homo sapiens

<220>

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<222> (5)

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<220>

<221> misc feature

<222> (13)

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<220>

<221> misc feature

<222> (49)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (65)

<223> n equals a,t,g, or c

<400> 776

ggcanaggat ttnaaccctc accttcgtgt ttcccccaat gtttaaaang ttgggatggt 60
ttgtng 66

<210> 777

<211> 441

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (401)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (436)

<223> n equals a,t,g, or c

<400> 777

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aatttacttt tttgcctaatt taggaggaag cttgggcata aggaaaaaga gctgtgttta 120
ggaaatagtg tgtgcccttt gaattaatgg agtgacaccg tgattcatga caggattcca 180
tttactggct gtatgccagc tgctgacagt ctataagtct taatagagat ggagtagagg 240
agctgaaggt tggcatctgc tcattgatga caactatgtt tacaatatgt tgtggactag 300
ttggggcact gaggcaggag aatcacgtgg agcccacggg ttcaagacca gcctgggaaa 360
catagcaaga ccttgtttct aaaaaaaaaa aaaaaaaaac ncgagggggg gcccggtacc 420
caattcgccc taaagngagt c 441

<210> 778

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (335)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (356)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (471)

<223> n equals a,t,g, or c

<220>

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<222> (472)

<223> n equals a,t,g, or c

<220>

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<222> (478)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (481)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (482)

<223> n equals a,t,g, or c

<400> 778

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cgagaagacc ctatggagct ttaatttatt aatgcaaaca gtaccttaaca aaocccacagg 120

tcctaaacta ccaaacctgc attaaaaatt tcggttgggg cgacctcgga gcagaaccca 180
acctccgagc agtacatgct aagacttcac cagtcaaagc gaactactat actcaattga 240
tccaataact tgaccaacgg aacaagttac cctagggata acagcgcaat cctattctag 300
agtccatata aacaataggg tttagacct cgatnttggg tcaggacatc ccgatngtgc 360
agccgctatt aaaggttcgt ttgttcaacg attaaagtcc tacgtgatct gagttcagac 420
cggagtaatc caggtcgggt tctatctact tcaaattcct ccctggaaaa nnagaagngg 480
nng 483

<210> 779

<211> 389

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (261)

<223> n equals a,t,g, or c

<220>

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<222> (325)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (337)

<223> n equals a,t,g, or c

<220>

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<222> (362)

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<220>

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<222> (367)

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<220>

<221> misc feature

<222> (389)

<223> n equals a,t,g, or c

<400> 779

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ctcccccgga gcggagcgca cctagggtcc ctcttcgctc ccccagccc agctaccgt 120
tcagaccagc agcctcgggg ggcaccccc cgccagcctg cctccctccc gctcagccct 180
gccaggttcc ccagccatg aatctcttcc gattcctggg aaaactctcc caactcctcg 240
ccatcatctt gctactgctc naaatctgga attcccgtc gtgcgccgaa attcaggaaa 300
aaaacagtcc cgtttggtgt ggggntttca atggccnaat ttgaaatcct ttcacaataa 360
tntttantct aaaaattttt ttaaagggn 389

<210> 780
<211> 66
<212> DNA
<213> Homo sapiens

<220>
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<222> (18)
<223> n equals a,t,g, or c

<400> 780
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acaaaa 66

<210> 781
<211> 255
<212> DNA
<213> Homo sapiens

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<220>
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<220>
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<222> (172)
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<222> (182)
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<222> (209)
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<220>
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<222> (224)
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gtaactgcgg acaagttgct ttnacctgaa ttnatgata catttcatta aggttccagt 120
tataaaatat ttngttaaat atttattaan gtggactata gantgcaaac tnccatttnc 180
cngntaaact tgtttttaa ttatggccnt aggtaacca tatngtaggg tattaatttc 240
cttgaacca aacca 255

<210> 782
<211> 348
<212> DNA
<213> Homo sapiens

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<220>
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<222> (28)
<223> n equals a,t,g, or c

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<222> (296)
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<220>
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<220>
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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<220>
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<222> (346)
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tgaatccacc cgagnttggc ctccaagtg gctgggcatt ataggcgtga gcactcacgt 120
ccncgcctca aaatngcata ttcaaagaag caatttcagt tcctttctaa gctttgtgag 180
tnaaggggct cactgactt cctagggcct gtaaatttaa accagtcttt aagggtttgc 240
caggaaagtt cccttctttc caagtgggtt ttccaaatg ggcacaatgg caagcnanac 300
agaggangaa acattaataaa aannaaaaaa aatttggggg ggggnncc 348

<210> 783
<211> 160
<212> DNA
<213> Homo sapiens

<220>
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<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (49)
<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

<220>
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<222> (82)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (131)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (141)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (142)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (144)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (146)
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atctgatgaa aaggtcacac tnaaacgcct tgcacggctt ctgggcttga tcacagctcc 120
ctaggtaggt naccacagag nngncncttc tagtgagcct 160

<210> 784
<211> 81
<212> DNA
<213> Homo sapiens

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<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (77)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (78)
<223> n equals a,t,g, or c

<220>
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<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (81)
<223> n equals a,t,g, or c

<400> 784
ggcaccgagcc gggatcgtgc cattncattc cagtctgggt gacagagcta gactccatct 60
caaaaaaaaa aaaaaannng n 81

<210> 785
<211> 541
<212> DNA
<213> Homo sapiens

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<220>
<221> misc feature
<222> (265)
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<221> misc feature
<222> (354)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (355)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (356)
<223> n equals a,t,g, or c

<220>
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<220>
<221> misc feature

<222> (364)
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<220>
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<222> (369)
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<220>
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<222> (405)
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<222> (411)
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<220>
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<222> (489)
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<220>
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<222> (521)
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<221> misc feature
<222> (530)
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<222> (539)

<223> n equals a,t,g, or c

<400> 785

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tcctcttcc ctctccctgc ccagccctcc ctctcttct ctgccggcaa ggcaggacc 120
cacagtggct gcctgcctcc gggagggag gagagggagg gtgggtgggt ggganggggc 180
cttctccag ggaatgtgac tctcccaggc cccagaatag ctctggacc caagcccaag 240
gcccagcctg ggacaaagct ccganggtcg gctggccgga gctatttta cctccgcct 300
cccctgctgg tgccccacc tggacgtctt gctgcagagt ctgacactgg attnnnaaaa 360
nctnaaaang aaccctggtg cccaattctg ggncccgnc ctaanctcg ncccaacca 420
tcatctgtgg acaatggagt ctggaataaa tgctgtttgt canatcaaca aaaaaaaaaa 480
aaaaggggng gccgctttag aggattcaaa gcttaagtaa nggtgcatgn gaagttcana 540
a 541
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<210> 786

<211> 433

<212> DNA

<213> Homo sapiens

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<220>

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<222> (350)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (400)

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<222> (402)

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<220>

<221> misc feature

<222> (405)

<223> n equals a,t,g, or c

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<222> (422)

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<400> 786

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cccacgcgtc cggctaca cgtgcgcgag tcgggggctc gcacgaaagc cgccgtggcg 60
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caatgaaggt gaaggccggc gcgctcgccg gccgaggtgg gatcccgagg cctctccagt 120
ccgccgaggg cgcaccaccg gcccgctctcg cccgccgcgc cggggaggtg gagcacgagc 180
gcacgtgtta ggacccgaaa gatggtgaac tatgcctggg cagggcgaan cagaaggaaa 240
ctctggtgga ggtccgtagc ggtcctgacg tgcaaatcgg tcgtccgacc tgggtatagg 300
ggcgaaaagac taaatcgaac catcttagta agctggtttc cctccgaaan tttccctcaa 360
gataagcttg gcgctctcgc aagaccccgga aggaaccccn gncanggaat ttttatccgg 420
tnaaagcgaa ttg 433

<210> 787

<211> 527

<212> DNA

<213> Homo sapiens

<220>

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<223> n equals a,t,g, or c

<400> 787

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cttggctctc atcttggtcc cttccaatct gaaacctcgt gcctggctcg tctgccacct 120
acatttctct ttccagctgc tgttttgtaa aaagaaaaag aaaaaagaag cccaaactag 180
tgagagtaat atctaattat ctcatttttt gtaggtctgt gataaagaac ttagtcatcc 240
cttccacctc ctactgtgaa gaacagaccc tgggtcccac actgaaatcc cctctagtca 300
cccattccca cccccaggg agctgcctcc caggcagggg gtgcagaaaa tgattgatgg 360
gctggggaac cctggagagc ctgactccg gaagtctcaa ggtgcctcct cctctcctta 420
gctggcccgt tggttttctg agcagggggc tgaactgtga acaagtcaga caaataaagc 480
aagggtctgc ancatctgca atgtcaaaaa aaaaaaaaaa aaaaaaa 527

<210> 788

<211> 203

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (121)

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<220>

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<222> (160)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (179)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (181)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (192)

<223> n equals a,t,g, or c

<400> 788

gcttcatgtg gtctgacaat ttatttttgc catcattttt ttaattaaag aaaaaatttc 60
cagaagagga aaaaaaaact acaaaaaaca aaacattgaa gggtgatatt ttatgtggaa 120
naacatttga attgaattca gaatttttct gaaggtgtan atactttttt ttttttttna 180
ncaaaaaccc tnatttcaaa agg 203

<210> 789

<211> 124

<212> DNA

<213> Homo sapiens

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<222> (70)

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<222> (87)

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<222> (94)

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<220>

<221> misc feature

<222> (113)

<223> n equals a,t,g, or c

<400> 789

ggcacgagca gcctacagcc gcctgcatct gtatccancg ccaggtcccg ccagtcccag 60
ctgcgcgcgn cccccagtcc cgcaccngtt cgggccaggc taagttagcc ctnaccatgc 120
cggt 124

<210> 790

<211> 293

<212> DNA
<213> Homo sapiens

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<222> (275)

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<222> (281)

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<221> misc feature

<222> (287)

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<400> 790

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ctggcaaaga tggaaccant ggacatccag gtgccattgg accaccaggg cctcgaggta 120
acagnggtga aagnggatct nagggctccc cagggccacn cagggcaacc agggccctnc 180
tggnacctcc tgggtcccct ggtccttgct gtggtggtgt tngagccgct gccattgctg 240
ggattgggag gttgaaaaag cttggnccgt tttgnccccc ngtttantgg ggg          293
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<210> 791

<211> 129

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (93)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (104)

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<220>

<221> misc feature

<222> (113)
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<220>
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<222> (119)
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<400> 791
gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60
aaaaaaaaaa aaaaaaaagg ggcggccgttt tanaggatcc aagnttacgt acncgngcnt 120
gcaacgtca 129

<210> 792
<211> 267
<212> DNA
<213> Homo sapiens

<220>
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<220>
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<222> (250)
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<220>
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<222> (253)
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<220>
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<220>
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<222> (267)
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ggcgccgcgg ggaggagggc ctgcgcgcag tcccgggcgc gttctagggc gccatgctgc 120

gggaagtctc gcgcgattag tggggaggtc tcgcggcttc tggctacttg gtggcgaggt 180
gaagagcttc tgcaggtgct gggggcggcg aacgcggcgg gaaagaaaaa aaaaaaaaaa 240
aaaaaanctn ggnaagtatt tttnan 267

<210> 793
<211> 453
<212> DNA
<213> Homo sapiens

<220>
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<222> (68)
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<220>
<221> misc feature
<222> (347)
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<220>
<221> misc feature
<222> (443)
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gccgtagnag ccggggacag gtcagtccga gacgagagaa gcggtcagtg ttgtacagtg 120
ttttgggcat gcacgtgata ctacacagtg ggcttctgct caccaacaga tgaagacaga 180
tgcaccaacg aggctgatgg gaaccatcct gtagagggtcc atctgcgttc agaccagac 240
gatgccagag ctatgactgg gcctgcaggt gtggcgccga ggggagatca gccatggagc 300
agccacagga ggaagcccct gaggtccggg aagaggagga gaaagangaa gtggcagaag 360
cagaaggagc cccagagctc aattggggac cacagcatgc acttccttcc agcagctaca 420
cagactctcc cggagctcct cgncaacctt atg 453

<210> 794
<211> 141
<212> DNA
<213> Homo sapiens

<220>
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<222> (15)
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<222> (17)
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<220>
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<222> (30)
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<220>
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<222> (54)
<223> n equals a,t,g, or c

<220>
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<222> (63)
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<220>
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<222> (108)
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<220>
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<220>
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<222> (137)
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ggngggggcg cgccggtctc ccggagcggg accgggtcgg aggatggncg agaatcacga 120
gcgacggtgg tngtgngtg t 141

<210> 795
<211> 167
<212> DNA
<213> Homo sapiens

<220>
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<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<220>
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<222> (56)

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<220>

<221> misc feature

<222> (61)

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<222> (149)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (164)

<223> n equals a,t,g, or c

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ngcggcacag cagcagcgac gcagcggcga cantcagagc agggaggccg cnccacctgc 120
gggccggccg gagcgggcag ccccgangcnc cctccccggg cacncgc 167

<210> 796

<211> 331

<212> DNA

<213> Homo sapiens

<220>

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<222> (10)

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<222> (16)
<223> n equals a,t,g, or c

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<220>
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<220>
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<220>
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<220>
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gannnnnggcc nnagttaata tatccngtgt acctcactgt ccaatatgaa aaccgtaaag 180
tgcccttatag gnatttgctg aactaacaca ccctggttca ttganctnta cttgctgaag 240
nngnaaaaga caggataagn tttcaatagt ggcataccan atgggacttt tgatgaaatg 300
aatatcaata ttttctgcaa ttccatgngc t 331

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ccaagcataa tatagcaagg actaaccctt ataccttctg cataatgaat taactagaaa 180
taacttttga aggagagcca aagctaagac ccccgaaacc agacgagcta cctaagaaca 240
gctaaaagag cacaccctgc tatgtagcaa aatagtggga agatttatag gtagaggcga 300
caaacctacc gagcctggtg atagctggtt gtccaagata gaatcttagt tcaactttaa 360
atttgcccac agaaccctct aaatcccctt gtaaatttaa ctgntagtcc aaagaggaaac 420
agctcttttg aactagtaga aaaaccttgt agagagagta aaaaatttaa caccatagat 480
aggcctaaaa gcagccacca attaagaaag cgttcaagct naacaccacac tacctaaaaa 540
aatcccaaac atataactga actnctacac ccaattgggc caatctatna ccctatnnaa 600
gaactaatgg tagtataagt acatgaaaac catnttctct cgnataagcc ttgcgtnaga 660
attaaaacac tgaactgnac attaaacagc caatntcta 699

<210> 798
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<212> DNA
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaanccccc 120
gggggggncc ccncccc 138

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agcttggtatc tgatatacgc actggattgt agaacttggt gctgattttg accttgatt 120
gaagttaact gttccccttg gtatttggtt aataccctgt acatatcttt gagttcaacc 180
tttagtacgt gtggcttggt cacttcgtgg ctaaggtaag aacgtgcttg tggaagacaa 240
gtctgtggct tggtagtct gtgtggccag cagcctctga tctgtgcagg gtattaacgt 300
gtcaaggctg agtggtcttg ggaattctct agaggctggc aagaaccagt tggttttgtc 360
cttgcggggt ctgtcaaggg ttggaaatcc caagccgtag gaccagttc cctnccttaa 420
ccgaagtctt tggccaaaca cnngggccgt aactggcctt gaggttggaac ggttgcataa 480
gccgnaaagn atcaac 496

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<211> 516

<212> DNA

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tntactagc ccaccagccc accagggana aaataancca tganangcng cgnccgccac 180
ccngtgnen cantccccc cttcccgntt cccttagaan cctgccgcgt cctatctcat 240
gacgctcatg gaaccncttt ctttgatctn ctntntctta tctccccctc tttntngttc 300
taaagaaaat cattttgatg caaggctctg cctggnatca natccgaagt gctcctgcag 360
tnacccttn cctggcattt ctctccacg cgacaagtct gctagtgaga tcttgcatga 420
ctcactttgt ttccaaaacc cggggctatt ttgcatctca agtttcctgg ggcctgcttc 480
ctgtgtacca cttaggggcn nctgggcaa gactgt 516

<210> 801

<211> 284

<212> DNA

<213> Homo sapiens

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atatatatag atatatatat agatatatat agatatatat agatatatat agatatatag 180
atatatatag atatatatat atatatagat atatatagat atatatagat atatatatag 240
atatagatat atagatat atatatctgg ctcatgcatg aaaa 284

<210> 802

<211> 153

<212> DNA

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cgaagccacc atccccaccc tgtcttcac anccgcctga aagccacaat gagaatgant 120
cacactgagg cctngatgtn ctntaatcac ttg 153

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attgtgcctt tattttatga gccccagttt tctgggctta gtttaaaaaa aaaatcaagt 120
ctaaacattg catttagaaa gcttttggtc ttggataaaa agtcatacac tttaaaaaaa 180
aaaaaaactt tttccaggaa aatatattga aatcatgctg ctgagcctct attttctttc 240
tttggatggt ttggattcag tattccttta nccataaatt tttagcattt aaaaattcac 300
nggatgttac attaagccaa taaactggct ttaatggatt acccaaaaaa aaaaaaaaaa 360
aaaggggggn cgcnnccagag ggn 383

<210> 804
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agagttttgt caagagccag tagagcagac agatgctgaa agccatagtt tcatggcagg 180
ctttggccag tgaacaaatc ctactctgaa gctagacatg tgctttgaaa tgattatcat 240
cctaatatca tgggggaaaa aataccagat ttaaattata tgttttgtgc tctcatttat 300
ttatcatttt tttctgtaca aatctattat ttctaggttt ttgtattaca tgatagacat 360
aaattgggtt atctcctcca ggcagtttgt cttttcnant nctccccctt caaccgtgtc 420
acaaagacca gacngtgcg ggaaagtgtt ttttctccgt attgttaaag gttccatnca 480
attaggttta ataaaggctt nttntccag 509
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<211> 753

<212> DNA

<213> Homo sapiens

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aattataacc aagcataata tagcaaggac taaccctat accttctgca taatgaatta 180
actagaaata actttgcaag gagagccaaa gctaagaccc ccgaaaccag acgagctacc 240
taagaacagc taaaagagca caccctcta tgtagcaaaa tagtgggaag atttataagg 300
agaggcgaca aacctaccga gcctggtgat agctggtgt ccaagataga atcttagttc 360
aactttaaat ttgcccacag aaccctctaa atcccctgt aaatttaact gtagtccaa 420
agaggaacag ctctttggac actaggaaaa aacctgttag agagagtaaa aaatttaaca 480
cccatagtag gcctaaaagc agccaccaat taagaaagcg ttcaagctca acaccacta 540
cctaaaaaat cccaaacata taactgaact cctcacaccc aattggacca atctatcacc 600
ctatagaaga actaatggtg gtataagtaa catgaaaaca ttctcctncg cataagcctg 660
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<210> 806
<211> 404
<212> DNA
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aaactaaagc tgaagaggta ctttccataa atacctocca ctgattgaat cagtgtcttt 120
aaagaaatth ctcaatcctt cagccgggtg tagcacgttc ttaatgtctc tttttattgc 180
ctgtaatgth attgcagatc cacatctctc gctcaactgt taatgtctca acctccagag 240
gcacccacc cagcacactg tcagtaaagg ggcagaatga aacagtgaga gtttaagggtg 300
caggaagaaa atttgcattg ttgcaagtga ctagaatcag atagtaagtg gnggtgggtt 360
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<210> 807

<211> 428

<212> DNA

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aggcagatgc tcctctggtg ggagggtgnt ggcccggcaa gattgaagga tgtgcagggc 120
ttcctctcag agccgcccga actgccttga tgtgtggagg ggangcaaga tgggtaaggg 180
ctcaggaagt tgctccanga acagtagctg atganctgcc cagagtgcct ggctccagcc 240
tgtacccttg gtatgccttg aacatntggt ttccccaccc aantgcggct aagtctcttt 300
ttccttggat cagccaggcg aaattggggc ttgtacaagg aattttctaa ggaaaccttg 360
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ggnttnag 428

<210> 808

<211> 403

<212> DNA

<213> Homo sapiens

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 cnccgctccg gggacagtgc caggngggga gtttgactgg ggcggtacac ctgtcaaacg 120
 gtaacgcagg tgctctaagg cgagctcagg gaggacagaa acctcccgtg gagcagaagg 180
 gcaaaaagctc gcttgatctt cattttcagt acgaatacag accgtgaaag ccgggcctca 240
 cgatcctcct gacctnnncg ntttncagcn ggaggtgtca gaaaantnac cacagggata 300
 actcgcttgt cgcggccaag cgttcatagc gacgtcgctt tnccangtnc gatgtcggat 360
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<210> 809
<211> 583
<212> DNA
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ccccatagtg attgagtctt caaaaccacc gattctgaga gcaaggaaga ttttggaaga 180
aaatctgact gtggattatg acaaagatta tcttttttct taagtaatct atttagatcg 240
ggctgactgt acaaatagact cctggaaaaa actcttcacc tagtctagaa taagggaggt 300
gggagaatga tgacttaccg tgaagtcctt cccttgactg ccgcactggg ggcctgttct 360
gtgccctggg agcatnntgc ccagctaagt ggggttcagg cagtgggcag ctttcccaat 420
nantcgattt ccattncagn gganttaaaa ccagttggcc aaatttccaa gnccttgnaa 480
ntaaggantc catttaccaa cccgcgggtt tgtggtcagt gccccaaggg ggtaggttga 540
agggggctta acaaacatgg aagtnggggg nanaagggat nan 583

<210> 810
<211> 272
<212> DNA
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<222> (259)
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<220>
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gtatacagat gaggggtgcc gctgctgctt tccttcggaa tccagtgtt ccacagagat 120
tancctgtan cttatatattg acattcttca ctgtctgttg ttnancnacc gtagcttttt 180
accgttcact tccccttcca actatgtcca gatgtgcagg ctcctccnct ctggactttc 240
tccaaaggca ctgaccctng gncctnnactt tg 272

<210> 811
<211> 300
<212> DNA
<213> Homo sapiens

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<220>
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<222> (252)
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<222> (259)
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cagatctttt taaaaagata cttctgtaac ttaagaaacc tgggcattta aatcatattt 120
tgtcttttagg taaaagcttt ggtttgtgtt cgtgttttgt ttgtttcact tgttccctc 180
ccagccccaa accttttgtt ctctccgtga acttaccttt ccctttttct ttctctttt 240
tttttttga anattaatng tttncataa aatttncatn gccattaaaa aaaaaaaaaa 300

<210> 812

<211> 478

<212> DNA

<213> Homo sapiens

<220>

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<222> (294)

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<220>

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<222> (325)

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<222> (427)

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<220>

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<222> (445)

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<222> (460)

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<222> (468)

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<400> 812

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gaaattgaaa cctggcgcaa tagatatagt accgcaaggg aaagatgaaa aattatagcc 120
aagcataata tagcaaggac taacccttat accttctgca taatgaatta actagaaata 180
actttgcaag gagagccaaa gctaagaccc ccgaaaccag acgagctacc tnagaacagc 240
tgaaagagca caccgtcta ttagcaaaaa tagtgggaag atttataggt tgangcgaca 300
aacctaccga gcctggtgat agctngttgt tccaanattg aatccttagt tccactttta 360
atttggcccc aaaaaccccc taattcccct tggttaattt taactgttng tccccaaaaa 420
ggaaccngct ctttgggacc cttanggaaa aaaaccttgn ttaaaaaanaa ttaaaaaa 478
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<210> 813

<211> 63

<212> DNA

<213> Homo sapiens

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<220>

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<222> (50)

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<222> (53)

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<221> misc feature

<222> (57)

<223> n equals a,t,g, or c

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<222> (59)

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<400> 813

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tga                                                                 63
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<210> 814
<211> 73
<212> DNA
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<222> (52)
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gagggtcctg ctg 73

<210> 815
<211> 102
<212> DNA
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<222> (93)

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<220>

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<222> (102)

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<400> 815

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tctcctttgc ctggccggga gggccttggc ngncctcan cn 102

<210> 816

<211> 379

<212> DNA

<213> Homo sapiens

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<220>

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<222> (348)

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<220>

<221> misc feature

<222> (358)

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aggcgggcat aacacagcaa gacgagaaga ccctatggag cttaattta ttaatgcaaa 120
cagtacctaa caaaccaca ggtcctaaac taccaaacct gcattaaaaa ttctggttg 180

ggcgacctcg gagcagaacc caacctccga gcagtacatg ctaagacttc accagtcaaa 240
gcgaactact atactcaatt gatccaataa cttgaccaac ggaacaagtt accctaggga 300
taacagcgca atcctattct agagtccata tcaacaatan ggtttacnac ctcgatgnnn 360
ggatcaggac attccaatg 379

<210> 817

<211> 500

<212> DNA

<213> Homo sapiens

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<222> (148)

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<222> (158)

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<222> (185)

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<222> (215)

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<222> (238)

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<222> (240)

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<222> (484)

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<400> 817

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cgcggttcgct gcctccttca gctccaggat gatcggccag aagacgctct actccttttt 120
ctccccacgc cccgccaaga agcgacangg cccaagncc cgagccggcc gtcaagggga 180
ccggngtggtc tnggggtgct naagaaagcg gaatncgggg ggcattccag ccaagaangn 240
cccggtggg naggagaanc tngggaacgc cggcctcctt ggncgctgaa ttnccgaaca 300
ttttggaacc ggattccaga ggaacaaagg gcccgnggnc cttgnttaan aatncggggg 360
ccngnaaang ttnccccttg gggtttttg gaanaanaac ctgggaaaga aagcanccta 420
aggggggggn attttcgggg gaaancgtta tttttaatca aagctaaatt ggggattttn 480
tttncaaaaa ggaaaggaaa 500
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<210> 818

<211> 329

<212> DNA

<213> Homo sapiens

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<222> (45)

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<222> (52)

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<220>

<221> misc feature

<222> (209)

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<220>

<221> misc feature

<222> (239)

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<220>
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<222> (279)
<223> n equals a,t,g, or c

<220>
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<222> (320)
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ctcactaatg ggaacanaag ctggagctcc accgngtagg cggnccgtct agaactagtg 120
tgatcccccg ggctgcagga attcggcncg agaggaaana gaaaccgtct gaactatgct 180
gnnngccatc atnctnggcc tcatcgcnnt tccatcccta cgcattgctt acatagcana 240
cgaggtgacg atgcncctt taccatcaag atcantgnc caccaatggt acttgaacct 300
acgagtacac ccgaccacn ggtggacta 329

<210> 819
<211> 648
<212> DNA
<213> Homo sapiens

<220>
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<222> (369)
<223> n equals a,t,g, or c

<220>
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<222> (518)
<223> n equals a,t,g, or c

<220>
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<222> (547)

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<400> 819

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attacaaata aacagttggt acttagcaag acctgaaaat atgtctgcag gtttctcctt 180
gaagcaaatg tgtgggatca ttgcatttcc agaaatctgc ctcttcacc ctccgttgac 240
agtatatgtc atgcctcact ttcttctagc tgagctttaa atcattagag cttaaattgt 300
cagatcggtc attgcctttc caggggtatt tagtaaagtt tggtgaaaac aaaaacgcct 360
tttcttggnt cttttttcag ttattttgaa ggccagcatc ctgattaaat gctgacacat 420
taatgaatga ccagcaacag ctttcagctc ttaaaaagac acttatattt gaatttacat 480
gctgggtacc tgggtccaat ggtggcaaaa ggccactntt cattaaaagg ggtcctccat 540
ttcntanccc caaggacttc ctcanttttc aaattgggaa gggnacctaa aaggggggtac 600
aattaaaacc ctgggggtaaa gggggnaaaa aaaaaaaaaa aaaaaaaaaa 648
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<210> 820

<211> 469

<212> DNA

<213> Homo sapiens

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<220>

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<222> (284)

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<221> misc feature

<222> (293)

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<222> (428)
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<220>
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<222> (465)
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taaccaagca taatatagca aggactaacc cctatacctt ctgcataatg aattaactag 180
aaataacttt gcaaggagag ccaaagctaa aacccccaat aaaccttgaa cagtgaanaa 240
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaacctcgag gtcnacggta tcnataacct 300
tgatatcnaa ttcggcacna gcaacctca ttccccaacc cacgccggag gctgcgctg 360
caggacctgn ctgaccgatt ggtggatcct ctgaanatga acacgactca ccactgctca 420
ncgaggcntg cttgagcaaa atccgccaat tataaaaaaa aaacnctcc 469

<210> 821
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<212> DNA
<213> Homo sapiens

<220>

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<220>
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<220>
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<222> (425)
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ggcacgagag aaactgtgtg tgaggggaag aggcctgttt cgctgtcggg tctctagttc 60
ttgcacgctc tttaagagtc tgcactggag gaactctgcc attaccagct cccttggtgc 120
agaaggaagg ggaaacatac atttattcat gccagtctgt tgcattgcagg ctttttggct 180
tcctaccttg caacaaaata attgcaccaa ctcttagtg ccgattccgc ccacagagag 240
tcctggagcc acagtctttt ttgctttgca ttgtaaggag agggactaaa gtgctagaga 300
ctatgtcgtc ttcctgagct aacgagagcg ctcgtgaact ggantcaact gctttcaggg 360
aaaaagaaaa aaaaaaaaaa aaaanccggg ggggggcccg gtaaccatt tccccctana 420
gngngggggt tt 432

<210> 822
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (323)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (367)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (382)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (385)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (425)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (427)
<223> n equals a,t,g, or c

<400> 822
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tcattagtga aagtgtctt ttatgtcctc ccagcagaca gacatcaagg atgagttaac 120
caggagacta ctctgtgga ctgtggagct ctggaaggct tgggtgggagt gaatttgccc 180
acaccttaca attgtggcag gatccagaag agcctgtctt tttatatcca ttccttggat 240
gtcattgggc ctctcccacc gatttcatta cgggtgccacg catccatggg atctggggta 300
gtccggaaaa acaaaaggag ggnagacagc ctggtaatgg ataagatcct taccacagtt 360
ttcccanggg gaatacctta tnaanccttc aacttttttt tttcccttaa gaattaaaac 420
ggggnana 428

<210> 823
<211> 100
<212> DNA
<213> Homo sapiens

<220>
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<222> (32)
<223> n equals a,t,g, or c

<220>
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<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (63)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (71)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (78)

<223> n equals a,t,g, or c

<400> 823

ctcagctcct gggggctcct gctactctgg gntcccgagg gtgccaaaat gtgncatcca 60
agntgaccca ntctcgncc ctccctgtct gcagctggtg 100

<210> 824

<211> 173

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (79)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (111)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (117)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (156)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (165)

<223> n equals a,t,g, or c

<400> 824

cggacgcgtg ggcggacgcg tggcgggacg cgtggggccga gaaccacagg tgtacaccct 60
gccccatcc cgggaggana tgaccaagaa acagtcagct gaactgcctg nttctanagg 120
tttctatccc acgaaatccc cttgaattgg gaaacnattg ggcancgaa aaa 173

<210> 825

<211> 341

<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (283)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (313)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (317)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (335)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (339)
<223> n equals a,t,g, or c

<400> 825
cccaaacccta ctccacctta ctaccagaca accttagcca aaccatttac ccaaataaag 60
tataggcgat agaaattgaa acctggcgca atagatatag taccgcaagg ggaaagatga 120
aaaattataa ccaagcataa tatagcaagg actaaccctt ataccttctg cataatgaat 180
taactagaaa taactttgca aggagagcca aagctaagac ccccgaaacc agaacgagct 240
accttagaac agcttaaaga gcacaccctt ctatTTTTgc canaatagtg ggaaagattt 300
ataggttgaa ggnaacnaac ctaccgagcc tggtnaatnc t 341

<210> 826
<211> 492
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (337)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (416)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (446)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (471)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (475)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (480)

<223> n equals a,t,g, or c

<400> 826

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gcaaaccac tccaccttac taccagacaa ccttagccaa accatttacc caaataaagt 60
ataggcgata gaaattgaaa cctggcgcaa tagatatagt accgcaaggg aaagatgaaa 120
aattataacc aagcataata tagcaaggac taaccctat accttctgca taatgaatta 180
actagaaata actttgcaag gagagccaaa gctaagaccc ccgaaaccag acgagctacc 240
taagaacagc taaaagagca caccctgcta tgtagcaaaa tagtggaag atttataggt 300
agaggcgaca aacctaccga gcctggtgat agctggntgt ccaagataga atcttagttc 360
aactttaaat ttgccacag aaccctctaa atccccttgt aaatttaact gttagnccaa 420
agagggaaca gctctttgga cactangaaa aaaccttgta tagagaggaa naaanatttn 480
acaaccata ct 492
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<210> 827

<211> 290

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (59)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (230)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (250)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (262)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (264)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (290)

<223> n equals a,t,g, or c

<400> 827

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ggtcgtgctc tcccgggccc ggtccgagcc gcgacgggag aggggaggac gttcgtggng 60
aacgggaccg tccttctcgc tccgccccgc ggggggtcccc tcgtctctcc tctccccgcc 120
cgccggcggt gcgtgtggga aggcgtgggg tgcggacccc ggcccagacct cgccgtcccc 180
cccgcgcct tctgcgtcgc ggggtcgggc cggcggggtc ctctgacgcn gcagacagcc 240
ctcgtgtctn cctccagtgg angncgactt gcgggcggta ctcctacgan 290
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<210> 828

<211> 420

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (149)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (334)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (382)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (396)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (403)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (405)

<223> n equals a,t,g, or c

<400> 828

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agcgtgcacc aagggcttgg tctgcggggg ccttggagct cctgctcttc tcccgcacct 120
ccatggatgc actgctgccg agcagagcng cctctgccag gccccgccct gggattccta 180
gagactagct tcagttttgc tttttttttt aagtgggaga aggggtgggca gttatcactg 240
gggaagagag gaccggccac ctgtccagca tgggctccag agccttcctc tctcacaggg 300
cagagtcttg tcggcaaggc agcctcctgg ccantttctc tgetcatgtt tctgggttagc 360
agagttcaga gccaattggt tnacttcttg gttgtncctg tgnangaagc ctttcaaac 420

<210> 829

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (19)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (20)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (30)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (56)

<223> n equals a,t,g, or c

<220>

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<222> (57)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (109)

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<222> (125)

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<222> (129)
<223> n equals a,t,g, or c

<220>
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<222> (171)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (181)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (191)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (267)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (268)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (269)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (281)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (287)
<223> n equals a,t,g, or c

<400> 829
ttcagaaaaa acaatagtnn tgtgcctctn tcttctcaaa caatggatga cacaanncta 60
tggagagtga caaaatggtg acaggtagct ggggacctag gctatctcnc catgaagggt 120
gttcngctna ttgtatatct gtgtatgtag tgtaactata ttgtacaatg ngaagactgt 180
naactactat ntaggggtgt tgcagattga aatttagttg tctcattggc tgtctgagga 240

agtggtggact tctatatata gatctannnt gaaaactgct ncatgantga aaaccaca 298

<210> 830

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (10)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (21)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (35)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (408)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (475)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (477)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (497)

<223> n equals a,t,g, or c

777

<220>

<221> misc feature

<222> (513)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (515)

<223> n equals a,t,g, or c

<400> 830

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ncggnaactn ctcactatag ntgaaagctg gtacncctgc aggtaccggt ccggaattcc 60
cgggggcatc cccttggtccc caagagaccc gacgcttgct tcatggccta cacgttcgag 120
agagagtctt cgggagagga ggaggagtag ggccgcctcg gggctgggca tccggccccct 180
ggggccaccc cttgtcagcc gggtaggttag gaaccgtaga ctcgctcatc tcgcctgggt 240
ttgtccgcat gttgtaatcg tgcaaataaa cgctcactcc gaattagcgg tgtatttctt 300
gaagttaaat attgtgtttg tgatactgaa gtatttgctt taattctaaa taaaaattta 360
tattttactt ttttattgct ggtttaagat gattcagatt atccttgnac tttgaggaga 420
agtttcttat ttggagcttt tggaaacagc ttaagctttt aacttgaaa gatangnatt 480
aatccccctt attggtntcc aaaagccaat aangng 516

```

<210> 831

<211> 636

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (414)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (453)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (530)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (617)

<223> n equals a,t,g, or c

<400> 831

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ggaaaaaaat gagttccatt taaaattttg gcatatggca ttttctaact taggaagcca 60
caatgttctt ggcccatcat gacattgggt agcatctaact gtaagttttg tgcttccaaa 120
tcactttttg gtttttaaga atttcttgat actcttatag cctgccttca attttgatcc 180

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tttattcttt ctatttgtca ggtgcacaag attaccttcc tgtttttagcc ttctgtcttg 240
tcaccaacca ttcttacttg gtggccatgt acttggaata aggccgcatg atctttcttg 300
ctccactcag tgtctaaggc accctgcttc ctttgcttgc atcccacaga ctatttcctt 360
catcttattt actgcagcaa atctctcctt agttgatgag actgtgttta tctnccttta 420
aaaccctacc taccctgaat ggtctgtcat tgnctgcctt taaaatcctt cctctttctt 480
cctctcttat tctctaaata atgatggggc ttaagttata cccaaagctn actttacaaa 540
atatttcctc aagactttgc agaaacacca acaaaatgcc atttaaaaaa ggggattttc 600
tttaaaggaa ctctaanaca ggcaaggttc tgatgt 636

<210> 832

<211> 466

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (421)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (443)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (446)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (453)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (466)

<223> n equals a,t,g, or c

<400> 832

gatcagatta tgagttactg tttaaaagaa aaatgctgtt tattcatgct gaggtgattc 60
agttccctcc ttcttacaga agtatttta ttcacccac actagaaatg cagcatcttt 120
gtggcagctt ttttcacaag cctccaaggc tccttagatt gggtcgttac taaaagtaca 180
ttaaaacact cttgtttatc gaagtatatt gatgtattct aaagctagta aacttcctta 240
acgtttaatt gccctacaga tgcttctctt gctgtgggtt ttcttttggt agtggcttga 300
aataattatt ttctgtttct attaatatcat aagtgtattt tgcacaaaaa aattaacctg 360
gtcaaatagt gattacaaaa atatataatta ataactttgg gcaaattttt gccattttata 420
ngaaaacatt ttttaaccac ggntangttc tanattttatt ctttcn 466

<210> 833

<211> 405

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (237)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (278)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (335)
<223> n equals a,t,g, or c

<400> 833
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gggaggagtc tgtgcagttt ctgacacttg ttggtgaaca tggctaaata caatgggtat 120
cgctgagact aagttgtaaa aaattaacaa atgtgctgct tgggtaaaat ggctacactc 180
atctgactca ttctttattc tattttagtt ggtttgatc ttgcctaagg tgcgtantcc 240
aactcttggt attaccctcc taatagtcac actagtantc atactccctg gtgttatgta 300
ttctctaaaa gctttaaatg tctgcattgc aaccngccat caaatattga atgggctctc 360
ttttggctgg aattacaaac tcaaaaaatg tttctcagga aaaaa 405

<210> 834
<211> 402
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (277)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (332)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (354)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (359)
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (390)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (400)

<223> n equals a,t,g, or c

<400> 834

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gcaaaccac aggtcctaaa ctaccaaacc tgcattaaaa atttcggttg gggcgacctc 60
ggagcagaac ccaacctccg agcagtacat gctaagactt caccagtcaa agcgaactac 120
tatactcaat tgatccaata acttgaccaa cggaacaagt taccctaggg ataacagcgc 180
aatcctattc tagagtccat atcaacaata gggtttacga cctcgatgtt ggatcaggac 240
atcccgatgg tgcagccgct attaaagggt cgtttgntca acgattaaag tcctacgtga 300
tctgagttca gaccggagta atccaggtcg gnttctatct acttcaaatt cctncctgna 360
cgaaaggaca agagaaataa gggctacttn acaaagcgcn tt 402
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<210> 835

<211> 121

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (40)

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<220>

<221> misc feature

<222> (77)

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<220>

<221> misc feature

<222> (100)

<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (110)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (117)
<223> n equals a,t,g, or c

<400> 835
nttnaaaaaa aaaaaaaaaa aaaaaaaaaa aagaaaaaan aaaaaaaaaa aaaaaaaaaa 60
aaaaaggcg gccgttntaa aggatccaag cttacgtacn cgtgcatgcn acgtcanagc 120
t 121

<210> 836
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (340)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (344)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (357)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (386)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (408)
<223> n equals a,t,g, or c

<400> 836
agtaagcctg ccagacacgc tgtggcggtt gcctgaagct agtgagtcgc ggcgccgcgc 60
acttgtggtt gggtcagtgc cgcgcgccgc tcggtcggtta ccgcgaggcg ctggtggcct 120
tcaggctgga cggcgcggtt cagccctggt ttgccggctt ctgggtcttt gaacagccgc 180
gatgtcgatc ttcaccccca ccaaccagat ccgcctaacc aatgtggccg tggtagcgat 240
gaagcgcgcc aggaagcgct tcgaaatcgc ttgctacaga aacaagtcgt cggctggcgg 300
agggccttgg aaaaagactt gatgaatttt gcagacccan caangtttgt aaagttncca 360

aagtcagttt ccaaaaggaa attcancagg ggtttgaaa atgccaanga a 411

<210> 837

<211> 386

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (381)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (383)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (384)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (385)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (386)

<223> n equals a,t,g, or c

<400> 837

gcggcagctc agcaagtggg ggaccaggcc acagaggcgg ggcagaaagc catggaccag 60
ctggccaaga ccaccagga aaccatcgac aagactgcta accaggcctc tgacaccttc 120
tctgggatcg ggaaaaaatt cggcctcctg aaatgacagc agggagactt gggtcggcct 180
cctgaaatga tagcaggag acttggtga ccccccttc aggcgccatc tagcacagcc 240
tgccctgat ctccgggcag ccaccacctc ctcggtctgc cccctcatta aaattcacgt 300
tcccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 360
aaaaaaaaa aaaaaaaaaa ngnnnn 386

<210> 838

<211> 124

<212> DNA

<213> Homo sapiens

<400> 838

gctttcaata gatcgagcg agggagctgc tctgctacgt acgaaacccc gaccagaag 60
caggctcgtc acgaatggtt tagcgccagg ttccccacga acgtgcggtg cgtgacgggc 120
gagg 124

<210> 839
<211> 270
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (26)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (56)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (107)
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<220>
<221> misc feature
<222> (130)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (175)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (178)
<223> n equals a,t,g, or c

<220>
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<222> (250)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (260)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (261)
<223> n equals a,t,g, or c

<400> 839

atctggttgt gggtacaatg aaaatnagaa gcattattga tggattcgca taagcncaat 60
gtgatgtcct gcgcggttct gccccctctc ccttccaggg tgaggggnetg gggtgagggt 120
taatgttcgn accagtgtctg gctgttcccc tcaccctaac cctctcccca aaggncgnag 180
gggcccgggt acccaattcg ccctatagtg agtcgtatta caattcactg gccgtcgttt 240
tacaagacgn agggaggagn ntgatgaaaa 270

<210> 840

<211> 430

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (210)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (262)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (263)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (348)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (369)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (390)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (395)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (409)

<223> n equals a,t,g, or c

<400> 840

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ctctacatca cgcgccccgac cttagctctc accatcgctc ttctactatg aacccccctc 60
cccataccga accccctggt caacctcaac ctaggcctcc tatttattct agccacctct 120
agcctagccg ttactcaat cctctgatca gggtagcat caaactcaaa ctacgccctg 180
atcggcgcac tgcgagcagt agcccaaacn atctcatatg aagtcaccct agccatcatt 240
cctactatca acattactaa tnngttggt cctttaacct ctccaccctt atcacaacac 300
aagaacactc ctgaatatcc tgccatcata acccttggtc catatatnat tatcttcac 360
actagggana acaacgaacc cccttcgaan cttngaaaag ggaatttcna ataattctca 420
ggttcaaatt 430
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<210> 841

<211> 650

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (519)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (555)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (564)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (573)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (589)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (634)

<223> n equals a,t,g, or c

<400> 841

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gccgtcatct actctacat ctttgcaggc aactcatca cagcgctaag ctgcgactga 60
ttttttacct gagtaggctt agaaataaac atgctagctt ttattccagt tctaaccaaa 120
aaaataaacc ctggttcac agaagctgcc atcaagtatt tcctcacgca agcaaccgca 180
tcataaatcc ttctaatagc tatctcttc aacaatatac tctccggaca atgaaccata 240
accaataata ccaatcaata ctcatcatta ataataataa tggctatagc aataaaacta 300
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ggaatagccc cctttcactt ctgagtccca gaggttaccc aaggcacccc tctgacatcc 360
 ggcttgcttc ttctcacatg acaaaaacta gcccctatct caatcatata ccaaattctct 420
 ccctcactag acgtaagcct tctcctcact ctctcaatct tatccatcat agtaggcagt 480
 tgagggtgga ttaaaccaaa acccagctac gcaaaatcnt agcatacttc ctcaattacc 540
 cacataggat gaatnaatag cagnttctac cgnacaaccc ttacataanc atttcttaaa 600
 ttaactaatt atattaatcc taactactac ggantctact actaacttaa 650

<210> 842

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (438)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (455)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (462)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (468)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (482)

<223> n equals a,t,g, or c

<400> 842

gcctgtgtct gctaaaaaag aaaagaaagt ttcctgcatg ttcattcctg atgggcgggt 60
 gtctgtctct gctcgaattg acagaaaagg attctgtgaa ggtgatgaga tttccatcca 120
 tgctgacttt gagaatacat gttcccgaat tgtggtcccc aaagctgcca ttgtggcccc 180
 ccacacttac cttgccaatg gccagaccaa ggtgctgact cagaagtgtg catcagtcag 240
 aggcaatcat attatctcag ggacatgcgc atcatggcgt ggcaagagcc ttcgggttca 300
 gaagatcagg cttcttatcc tgggctgcaa catccttcga gttgaatatt ccttactgat 360
 ctatgttagc gttcctggat ccaagaaggc catccttgac ctgcccctgg taattggcag 420
 cagatcaggc ctaagcanca gaacatccag ctggncagcc cnaaccanct ctgaagatga 480
 gntgggtaga tctgaacatc ctgataccc 509

<210> 843

<211> 158

<212> PRT

787

<213> Homo sapiens

<400> 843

Lys Arg Asp Trp Val Ile Pro Pro Ile Ser Cys Pro Glu Asn Glu Lys
1 5 10 15

Gly Pro Phe Pro Lys Asn Leu Val Gln Ile Lys Ser Asn Lys Asp Lys
20 25 30

Glu Gly Lys Val Phe Tyr Ser Ile Thr Gly Gln Gly Ala Asp Thr Pro
35 40 45

Pro Val Gly Val Phe Ile Ile Glu Arg Glu Thr Gly Trp Leu Lys Val
50 55 60

Thr Glu Pro Leu Asp Arg Glu Arg Ile Ala Thr Tyr Thr Leu Phe Ser
65 70 75 80

His Ala Val Ser Ser Asn Gly Asn Ala Val Glu Asp Pro Met Glu Ile
85 90 95

Leu Ile Thr Val Thr Asp Gln Asn Asp Asn Lys Pro Glu Phe Thr Gln
100 105 110

Glu Val Phe Lys Gly Ser Val Met Glu Gly Ala Leu Pro Gly Thr Ser
115 120 125

Val Met Glu Val Thr Ala Thr Asp Ala Asp Asp Gly Cys Gly Thr Pro
130 135 140

Thr Met Pro Pro Ser Leu Thr Pro Ser Ser Ala Gln Asp Pro
145 150 155

<210> 844

<211> 601

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (36)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (64)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (106)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (152)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (358)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (383)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 844
Thr Glu Leu Leu Lys Ser Ala Ala Arg His Gly Thr Ala Glu Ser Ala
1 5 10 15
Pro Trp Pro Arg Gly Gln Gly Trp Gln Gln Trp Gln Gln Gln Trp Arg
20 25 30
Arg Arg Trp Xaa Ser Trp Arg Lys Asp Arg Ala Arg Thr Arg Arg Gln
35 40 45
Glu Glu Leu Ala Leu Ser Gln Glu Pro Lys Ser Ser Ser Arg Gly Xaa
50 55 60
Ser Pro Gly Ala Ser Pro Ala Ser Pro Thr Ser Gln Gln Phe Cys Cys
65 70 75 80
Phe Arg Leu Asp Gln Val Ile His Ser Asn Pro Ala Gly Ile Gln Gln
85 90 95
Ala Leu Ala Gln Leu Ser Xaa Arg Gln Xaa Ser Val Thr Ala Pro Gly
100 105 110
Gly His Pro Arg His Lys Pro Gly Pro Pro Gln Ala Pro Gln Gly Pro
115 120 125
Ser Pro Arg Pro Pro Thr Arg Tyr Glu Pro Gln Arg Val Asn Ser Gly
130 135 140

Leu Ser Ser Asp Pro His Phe Xaa Glu Pro Gly Pro Met Val Arg Gly
 145 150 155 160
 Val Gly Gly Thr Pro Arg Asp Ser Ala Gly Val Ser Pro Phe Pro Pro
 165 170 175
 Lys Arg Arg Glu Arg Pro Pro Arg Lys Pro Glu Leu Leu Gln Glu Glu
 180 185 190
 Ser Leu Pro Pro Pro His Ser Ser Gly Phe Leu Gly Ser Lys Pro Glu
 195 200 205
 Gly Pro Gly Pro Gln Ala Glu Ser Arg Asp Thr Gly Thr Glu Ala Leu
 210 215 220
 Thr Pro His Ile Trp Asn Arg Leu His Thr Ala Thr Ser Arg Lys Ser
 225 230 235 240
 Tyr Arg Pro Ser Ser Met Glu Pro Trp Met Glu Pro Leu Ser Pro Phe
 245 250 255
 Glu Asp Val Ala Gly Thr Glu Met Ser Gln Ser Asp Ser Gly Val Asp
 260 265 270
 Leu Ser Gly Asp Ser Gln Val Ser Ser Gly Pro Cys Ser Gln Arg Ser
 275 280 285
 Ser Pro Asp Gly Gly Leu Lys Gly Ala Ala Glu Gly Pro Pro Lys Arg
 290 295 300
 Pro Gly Gly Ser Ser Pro Leu Asn Ala Val Pro Cys Glu Gly Pro Pro
 305 310 315 320
 Gly Ser Glu Pro Pro Arg Arg Pro Pro Pro Ala Pro His Asp Gly Asp
 325 330 335
 Arg Lys Glu Leu Pro Arg Glu Gln Pro Leu Pro Pro Gly Pro Ile Gly
 340 345 350
 Thr Glu Arg Ser Gln Xaa Thr Asp Arg Gly Thr Glu Pro Gly Pro Ile
 355 360 365
 Arg Pro Ser His Arg Pro Gly Pro Pro Val Gln Phe Gly Thr Xaa Asp
 370 375 380
 Lys Asp Ser Asp Leu Arg Leu Val Val Gly Asp Ser Leu Lys Ala Glu
 385 390 395 400
 Lys Glu Leu Thr Ala Ser Val Thr Glu Ala Ile Pro Val Ser Arg Asp
 405 410 415

790

Trp Glu Leu Leu Pro Ser Ala Ala Ala Ser Ala Glu Pro Gln Ser Lys
 420 425 430

Asn Leu Asp Ser Gly His Cys Val Pro Glu Pro Ser Ser Ser Gly Gln
 435 440 445

Arg Leu Tyr Pro Glu Val Phe Tyr Gly Ser Ala Gly Pro Ser Ser Ser
 450 455 460

Gln Ile Ser Gly Gly Ala Met Asp Ser Gln Leu His Pro Asn Ser Gly
 465 470 475 480

Gly Phe Arg Pro Gly Thr Pro Ser Leu His Pro Tyr Arg Ser Gln Pro
 485 490 495

Leu Tyr Leu Pro Pro Gly Pro Ala Pro Pro Ser Ala Leu Leu Ser Gly
 500 505 510

Val Ala Leu Lys Gly Gln Phe Leu Asp Phe Ser Thr Met Gln Ala Thr
 515 520 525

Glu Leu Gly Lys Leu Pro Ala Gly Gly Val Leu Tyr Pro Pro Pro Ser
 530 535 540

Phe Leu Tyr Ser Pro Ala Phe Cys Pro Ser Pro Leu Pro Asp Thr Ser
 545 550 555 560

Leu Leu Gln Val Arg Gln Asp Leu Pro Ser Pro Ser Asp Phe Tyr Ser
 565 570 575

Thr Pro Leu Gln Pro Gly Gly Gln Ser Gly Phe Leu Pro Ser Gly Ala
 580 585 590

Pro Ala Ser Arg Cys Phe Tyr Pro Trp
 595 600

<210> 845

<211> 67

<212> PRT

<213> Homo sapiens

<400> 845

Thr Gln Lys Thr Ser Ser Leu Leu Pro Ala Leu Ser Leu Gln Leu Pro
 1 5 10 15

Leu Leu Thr Arg Phe Ser Ile Met Cys Ser Val Lys Glu Glu Phe Trp
 20 25 30

791

Arg Val Gln Ser Ile Ile Thr Glu Leu Val Leu Lys Gly Glu Phe Gly
 35 40 45

Val Glu Glu Ala Met Lys Leu Ile Thr Gly Thr Glu Ala Lys Tyr Lys
 50 55 60

Ser Ile Asp
 65

<210> 846
 <211> 146
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (16)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 846
 Ser Gln Gly Pro Asp His Pro Ser Ser Gln Leu Gln Pro Leu Asn Xaa
 1 5 10 15

Ser Leu Ser His Leu Leu Val Pro Cys Leu Ser Ile Met Ser Leu Leu
 20 25 30

Asn Lys Pro Lys Ser Glu Met Thr Pro Glu Glu Leu Gln Lys Arg Glu
 35 40 45

Glu Glu Glu Phe Asn Thr Gly Pro Leu Ser Val Leu Thr Gln Ser Val
 50 55 60

Lys Asn Asn Thr Gln Val Leu Ile Asn Cys Arg Asn Asn Lys Lys Leu
 65 70 75 80

Leu Gly Arg Val Lys Ala Phe Asp Arg His Cys Asn Met Val Leu Glu
 85 90 95

Asn Val Lys Glu Met Trp Thr Glu Val Pro Lys Ser Gly Lys Gly Lys
 100 105 110

Lys Lys Ser Lys Pro Val Asn Lys Asp Arg Tyr Ile Ser Lys Met Phe
 115 120 125

Leu Arg Gly Asp Ser Val Ile Val Val Leu Arg Asn Pro Leu Ile Ala
 130 135 140

Gly Lys
 145

<210> 847
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (8)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (179)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 847
 Ala Arg Met Ala Ala Asp Lys Xaa Pro Ala Ala Gly Pro Arg Ser Arg
 1 5 10 15
 Ala Ala Met Ala Gln Trp Arg Lys Lys Lys Gly Leu Arg Lys Arg Arg
 20 25 30
 Gly Ala Ala Ser Gln Ala Arg Gly Ser Asn Ser Glu Asp Gly Glu Phe
 35 40 45
 Glu Ile Gln Ala Glu Asp Asp Ala Arg Ala Arg Lys Leu Gly Pro Gly
 50 55 60
 Arg Pro Leu Pro Thr Phe Pro Thr Ser Glu Cys Thr Ser Asp Val Glu
 65 70 75 80
 Pro Asp Thr Arg Glu Met Val Arg Ala Gln Asn Lys Lys Lys Lys Lys
 85 90 95
 Ser Gly Gly Phe Gln Ser Met Gly Leu Ser Tyr Pro Val Phe Lys Gly
 100 105 110
 Ile Met Lys Lys Gly Tyr Lys Val Pro Thr Pro Ile Gln Arg Lys Thr
 115 120 125
 Ile Pro Val Ile Leu Asp Gly Lys Asp Val Val Ala Met Ala Arg Thr
 130 135 140
 Gly Ser Gly Lys Thr Ala Cys Phe Leu Leu Pro Met Phe Glu Arg Leu
 145 150 155 160
 Lys Thr His Ser Ala Gln Thr Gly Ala Arg Ala Ser Ser Ser Arg Arg
 165 170 175

Pro Glu Xaa Trp Pro Cys Arg Pro
180

<210> 848

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (35)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 848

Ala Arg Ala Ser Ser Glu Cys Ala Arg Cys Ala Ala Ala Val Arg Thr
1 5 10 15

Cys Arg Arg Arg His Arg His His Ala Gln Leu Arg Arg His Leu Glu
20 25 30

Asp Ala Xaa Ser Glu Asn Phe Asp Glu Leu Leu Lys Ala Leu Gly Val
35 40 45

Asn Ala Met Leu Arg Lys Val Ala Val Ala Ala Ala Ser Lys Pro His
50 55 60

Val Glu Ile Arg Gln Asp Gly Asp Gln Phe Tyr Ile Lys Thr Ser Thr
65 70 75 80

Thr Val Arg Thr Thr Glu Ile Asn Phe Lys Val Gly Glu Gly Phe Glu
85 90 95

Glu Glu Thr Val Asp Gly Arg Lys Cys Arg Ser Leu Ala Thr Trp Glu
100 105 110

Asn Glu Asn Lys Ile His Cys Thr Gln Thr Leu Leu Glu Gly Asp Gly
115 120 125

Pro Lys Thr Tyr Trp Thr Arg Glu Leu Ala Asn Asp Glu Leu Ile Leu
130 135 140

Thr Phe Gly Ala Asp Asp Val Val Cys Thr Arg Ile Tyr Val Arg Glu
145 150 155 160

794

<210> 849
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (50)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 849
Val Gln Asn Val Gly Tyr Gln Ser Lys His Cys Gly Ala Val Xaa Tyr
1 5 10 15
Ala Arg Leu Pro Cys Glu Met Ile Gln Asp Gln Asn Lys Ala Leu Asp
20 25 30
Cys Ser Lys Thr Gln Asn Ser Ser Arg Ala Glu Gly Gly Arg Leu Ile
35 40 45
Trp Xaa Glu Gly Pro Lys Tyr Lys Thr Asp Gly Leu Arg Leu Glu Thr
50 55 60
Arg Gly Leu Arg Trp Lys Ala His Val Pro Arg
65 70 75

<210> 850
<211> 383
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (299)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 850
Ser Thr His Ala Ser Ala His Ala Ser Val Ala Asn Glu Val Ile Lys
1 5 10 15
Cys Lys Ala Ala Val Ala Trp Glu Ala Gly Lys Pro Leu Ser Ile Glu
20 25 30

795

Glu Ile Glu Val Ala Pro Pro Lys Ala His Glu Val Arg Ile Lys Ile
 35 40 45
 Ile Ala Thr Ala Val Cys His Thr Asp Ala Tyr Thr Leu Ser Gly Ala
 50 55 60
 Asp Pro Glu Gly Cys Phe Pro Val Ile Leu Gly His Glu Gly Ala Gly
 65 70 75 80
 Ile Val Glu Ser Val Gly Glu Gly Val Thr Lys Leu Lys Ala Gly Asp
 85 90 95
 Thr Val Ile Pro Leu Tyr Ile Pro Gln Cys Gly Glu Cys Lys Phe Cys
 100 105 110
 Leu Asn Pro Lys Thr Asn Leu Cys Gln Lys Ile Arg Val Thr Gln Gly
 115 120 125
 Lys Gly Leu Met Pro Asp Gly Thr Ser Arg Phe Thr Cys Lys Gly Lys
 130 135 140
 Thr Ile Leu His Tyr Met Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val
 145 150 155 160
 Val Ala Asp Ile Ser Val Ala Lys Ile Asp Pro Leu Ala Pro Leu Asp
 165 170 175
 Lys Val Cys Leu Leu Gly Cys Gly Ile Ser Thr Gly Tyr Gly Ala Ala
 180 185 190
 Val Asn Thr Ala Lys Leu Glu Pro Gly Ser Val Cys Ala Val Phe Gly
 195 200 205
 Leu Gly Gly Val Gly Leu Ala Val Ile Met Gly Cys Lys Val Ala Gly
 210 215 220
 Ala Ser Arg Ile Ile Gly Val Asp Ile Asn Lys Asp Lys Phe Ala Arg
 225 230 235 240
 Ala Lys Glu Phe Gly Ala Thr Glu Cys Ile Asn Pro Gln Asp Phe Ser
 245 250 255
 Lys Pro Ile Gln Glu Val Leu Ile Glu Met Thr Asp Gly Gly Val Asp
 260 265 270
 Tyr Ser Phe Glu Cys Ile Gly Asn Val Lys Val Met Arg Ala Ala Leu
 275 280 285
 Glu Ala Cys His Lys Gly Trp Gly Val Thr Xaa Val Val Gly Val Ala
 290 295 300

796

Ala Ser Gly Glu Glu Ile Ala Thr Arg Pro Phe Gln Leu Val Thr Gly
305 310 315 320

Arg Thr Trp Lys Gly Thr Ala Phe Gly Gly Trp Lys Ser Val Glu Ser
325 330 335

Val Pro Lys Leu Val Ser Glu Tyr Met Ser Lys Lys Ile Lys Val Asp
340 345 350

Glu Phe Val Thr His Asn Leu Ser Phe Asp Glu Ile Asn Lys Ala Phe
355 360 365

Glu Leu Met His Ser Gly Lys Ser Ile Arg Thr Val Val Lys Ile
370 375 380

<210> 851

<211> 154

<212> PRT

<213> Homo sapiens

<400> 851

Ala Arg Ala Pro Arg Ala Thr Leu Asn Gly Pro Gly Ala Arg Gly Arg
1 5 10 15

Val Gly Val Val Val Leu Arg Pro Arg Pro Arg Gly Leu Arg Phe Pro
20 25 30

Trp Cys Pro Gly Arg Pro Ala Ser Gly Ala Val Ser Tyr Glu Ser Ala
35 40 45

His Ala Ala Ser Val Arg Leu Thr Leu Arg Thr Met Glu Gly Gly Phe
50 55 60

Gly Ser Asp Phe Gly Gly Ser Gly Ser Gly Lys Leu Asp Pro Gly Leu
65 70 75 80

Ile Met Glu Gln Val Lys Val Gln Ile Ala Val Ala Asn Ala Gln Glu
85 90 95

Leu Leu Gln Arg Met Thr Asp Lys Cys Phe Arg Lys Cys Ile Gly Lys
100 105 110

Pro Gly Gly Ser Leu Asp Asn Ser Glu Gln Lys Cys Ile Ala Met Cys
115 120 125

Met Asp Arg Tyr Met Asp Ala Trp Asn Thr Val Ser Arg Ala Tyr Asn
130 135 140

Ser Arg Leu Gln Arg Glu Arg Ala Asn Met

797

145

150

<210> 852

<211> 396

<212> PRT

<213> Homo sapiens

<400> 852

Asp Ser Arg Val Asp Pro Arg Val Arg Ala Ile Ile Ala Lys Thr Phe
1 5 10 15

Lys Gly Arg Gly Ile Thr Gly Val Glu Asp Lys Glu Ser Trp His Gly
20 25 30

Lys Pro Leu Pro Lys Asn Met Ala Glu Gln Ile Ile Gln Glu Ile Tyr
35 40 45

Ser Gln Ile Gln Ser Lys Lys Lys Ile Leu Ala Thr Pro Pro Gln Glu
50 55 60

Asp Ala Pro Ser Val Asp Ile Ala Asn Ile Arg Met Pro Ser Leu Pro
65 70 75 80

Ser Tyr Lys Val Gly Asp Lys Ile Ala Thr Arg Lys Ala Tyr Gly Gln
85 90 95

Ala Leu Ala Lys Leu Gly His Ala Ser Asp Arg Ile Ile Ala Leu Asp
100 105 110

Gly Asp Thr Lys Asn Ser Thr Phe Ser Glu Ile Phe Lys Lys Glu His
115 120 125

Pro Asp Arg Phe Ile Glu Cys Tyr Ile Ala Glu Gln Asn Met Val Ser
130 135 140

Ile Ala Val Gly Cys Ala Thr Arg Asn Arg Thr Val Pro Phe Cys Ser
145 150 155 160

Thr Phe Ala Ala Phe Phe Thr Arg Ala Phe Asp Gln Ile Arg Met Ala
165 170 175

Ala Ile Ser Glu Ser Asn Ile Asn Leu Cys Gly Ser His Cys Gly Val
180 185 190

Ser Ile Gly Glu Asp Gly Pro Ser Gln Met Ala Leu Glu Asp Leu Ala
195 200 205

Met Phe Arg Ser Val Pro Thr Ser Thr Val Phe Tyr Pro Ser Asp Gly
210 215 220

798

Val Ala Thr Glu Lys Ala Val Glu Leu Ala Ala Asn Thr Lys Gly Ile
225 230 235 240

Cys Phe Ile Arg Thr Ser Arg Pro Glu Asn Ala Ile Ile Tyr Asn Asn
245 250 255

Asn Glu Asp Phe Gln Val Gly Gln Ala Lys Val Val Leu Lys Ser Lys
260 265 270

Asp Asp Gln Val Thr Val Ile Gly Ala Gly Val Thr Leu His Glu Ala
275 280 285

Leu Ala Ala Ala Glu Leu Leu Lys Lys Glu Lys Ile Asn Ile Arg Val
290 295 300

Leu Asp Pro Phe Thr Ile Lys Pro Leu Asp Arg Lys Leu Ile Leu Asp
305 310 315 320

Ser Ala Arg Ala Thr Lys Gly Arg Ile Leu Thr Val Glu Asp His Tyr
325 330 335

Tyr Glu Gly Gly Ile Gly Glu Ala Val Ser Ser Ala Val Val Gly Glu
340 345 350

Pro Gly Ile Thr Val Thr His Leu Ala Val Asn Arg Val Pro Arg Ser
355 360 365

Gly Lys Pro Ala Glu Leu Leu Lys Met Phe Gly Ile Asp Arg Asp Ala
370 375 380

Ile Ala Gln Ala Val Arg Gly Leu Ile Thr Lys Ala
385 390 395

<210> 853

<211> 302

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (228)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 853

Ser Arg Leu Gly Leu Gln Ser Cys Gly Leu Ser Thr Gln Ala Ile Thr
1 5 10 15

Leu Ser Glu Thr Ala Ala Ala Leu Asp Cys Ser Leu Pro Arg Leu His

799

20	25	30
Ala Arg Gln Ser Met Arg Val Thr Leu Ala Thr Ile Ala Trp Met Val		
35	40	45
Ser Phe Val Ser Asn Tyr Ser His Thr Ala Asn Ile Leu Pro Asp Ile		
50	55	60
Glu Asn Glu Asp Phe Ile Lys Asp Cys Val Arg Ile His Asn Lys Phe		
65	70	75
Arg Ser Glu Val Lys Pro Thr Ala Ser Asp Met Leu Tyr Met Thr Trp		
85	90	95
Asp Pro Ala Leu Ala Gln Ile Ala Lys Ala Trp Ala Ser Asn Cys Gln		
100	105	110
Phe Ser His Asn Thr Arg Leu Lys Pro Pro His Lys Leu His Pro Asn		
115	120	125
Phe Thr Ser Leu Gly Glu Asn Ile Trp Thr Gly Ser Val Pro Ile Phe		
130	135	140
Ser Val Ser Ser Ala Ile Thr Asn Trp Tyr Asp Glu Ile Gln Asp Tyr		
145	150	155
Asp Phe Lys Thr Arg Ile Cys Lys Lys Val Cys Gly His Tyr Thr Gln		
165	170	175
Val Val Trp Ala Asp Ser Tyr Lys Val Gly Cys Ala Val Gln Phe Cys		
180	185	190
Pro Lys Val Ser Gly Phe Asp Ala Leu Ser Asn Gly Ala His Phe Ile		
195	200	205
Cys Asn Tyr Gly Pro Gly Gly Asn Tyr Pro Thr Trp Pro Tyr Lys Arg		
210	215	220
Gly Ala Thr Xaa Ser Ala Cys Pro Asn Asn Asp Lys Cys Leu Asp Asn		
225	230	235
Leu Cys Val Asn Arg Gln Arg Asp Gln Val Lys Arg Tyr Tyr Ser Val		
245	250	255
Val Tyr Pro Gly Trp Pro Ile Tyr Pro Arg Asn Arg Tyr Thr Ser Leu		
260	265	270
Phe Leu Ile Val Asn Ser Val Ile Leu Ile Leu Ser Val Ile Ile Thr		
275	280	285
Ile Leu Val Gln His Lys Tyr Pro Asn Leu Val Leu Leu Asp		

800

290

295

300

<210> 854

<211> 237

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (235)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 854

Val Pro Ala Ser Phe Ala Ala Ala Ser Ala Val Leu Ser Ala Val Phe
 1 5 10 15

Pro Gln Glu Pro Ala Tyr Phe Leu Asn Met Glu Ser Val Val Arg Arg
 20 25 30

Cys Pro Phe Leu Ser Arg Val Pro Gln Ala Phe Leu Gln Lys Ala Gly
 35 40 45

Lys Ser Leu Leu Phe Tyr Ala Gln Asn Cys Pro Lys Met Met Glu Val
 50 55 60

Gly Ala Lys Pro Ala Pro Arg Ala Leu Ser Thr Ala Ala Val His Tyr
 65 70 75 80

Gln Gln Ile Lys Glu Thr Pro Pro Ala Ser Glu Lys Asp Lys Thr Ala
 85 90 95

Lys Ala Lys Val Gln Gln Thr Pro Asp Gly Ser Gln Gln Ser Pro Asp
 100 105 110

Gly Thr Gln Leu Pro Ser Gly His Pro Leu Pro Ala Thr Ser Gln Gly
 115 120 125

Thr Ala Ser Lys Cys Pro Phe Leu Ala Ala Gln Met Asn Gln Arg Gly
 130 135 140

Ser Ser Val Phe Cys Lys Ala Ser Leu Glu Leu Gln Glu Asp Val Gln
 145 150 155 160

Glu Met Asn Ala Val Arg Lys Glu Val Ala Glu Thr Ser Ala Gly Pro
 165 170 175

Ser Val Val Ser Val Lys Thr Asp Gly Gly Asp Pro Ser Gly Leu Leu
 180 185 190

801

Lys Asn Phe Gln Asp Ile Met Gln Lys Gln Arg Pro Glu Arg Val Ser
195 200 205

His Leu Leu Gln Asp Asn Leu Pro Lys Ser Val Ser Thr Phe Gln Tyr
210 215 220

Asp Arg Phe Phe Glu Lys Lys Ile Asp Glu Xaa Lys Glu
225 230 235

<210> 855

<211> 272

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (202)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 855

Thr Pro Gly Ile Phe Thr Glu Gln Ser Met Ile Thr Phe Leu Pro Leu
1 5 10 15

Leu Leu Gly Leu Ser Leu Gly Cys Thr Gly Ala Gly Gly Phe Val Ala
20 25 30

His Val Glu Ser Thr Cys Leu Leu Asp Asp Ala Gly Thr Pro Lys Asp
35 40 45

Phe Thr Tyr Cys Ile Ser Phe Asn Lys Asp Leu Leu Thr Cys Trp Asp
50 55 60

Pro Glu Glu Asn Lys Met Ala Pro Cys Glu Phe Gly Val Leu Asn Ser
65 70 75 80

Leu Ala Asn Val Leu Ser Gln His Leu Asn Gln Lys Asp Thr Leu Met
85 90 95

Gln Arg Leu Arg Asn Gly Leu Gln Asn Cys Ala Thr His Thr Gln Pro
100 105 110

Phe Trp Gly Ser Leu Thr Asn Arg Thr Arg Pro Pro Ser Val Gln Val
115 120 125

Ala Lys Thr Thr Pro Phe Asn Thr Arg Glu Pro Val Met Leu Ala Cys
130 135 140

Tyr Val Trp Gly Phe Tyr Pro Ala Glu Val Thr Ile Thr Trp Arg Lys
145 150 155 160

802

Asn Gly Lys Leu Val Met Pro His Ser Ser Ala His Lys Thr Ala Gln
165 170 175

Pro Asn Gly Asp Trp Thr Tyr Gln Thr Leu Ser His Leu Ala Leu Thr
180 185 190

Pro Ser Tyr Gly Asp Thr Tyr Thr Cys Xaa Val Glu His Ile Gly Ala
195 200 205

Pro Glu Pro Ile Leu Arg Asp Trp Thr Pro Gly Leu Ser Pro Met Gln
210 215 220

Thr Leu Lys Val Ser Val Ser Ala Val Thr Leu Gly Leu Gly Leu Ile
225 230 235 240

Ile Phe Ser Leu Gly Val Ile Ser Trp Arg Arg Ala Gly His Ser Ser
245 250 255

Tyr Thr Pro Leu Pro Gly Ser Asn Tyr Ser Glu Gly Trp His Ile Ser
260 265 270

<210> 856

<211> 153

<212> PRT

<213> Homo sapiens

<400> 856

Val Val Ala Arg Phe Ile Arg Ile Tyr Pro Leu Thr Trp Asn Gly Ser
1 5 10 15

Leu Cys Met Arg Leu Glu Val Leu Gly Cys Ser Val Ala Pro Val Tyr
20 25 30

Ser Tyr Tyr Ala Gln Asn Glu Val Val Ala Thr Asp Asp Leu Asp Phe
35 40 45

Arg His His Ser Tyr Lys Asp Met Arg Gln Leu Met Lys Val Val Asn
50 55 60

Glu Glu Cys Pro Thr Ile Thr Arg Thr Tyr Ser Leu Gly Lys Ser Ser
65 70 75 80

Arg Gly Leu Lys Ile Tyr Ala Met Glu Ile Ser Asp Asn Pro Gly Glu
85 90 95

803

His Glu Leu Gly Glu Pro Glu Phe Arg Tyr Thr Ala Gly Ile His Gly
100 105 110

Asn Glu Val Leu Gly Arg Glu Leu Leu Leu Leu Met Gln Tyr Leu
115 120 125

Cys Arg Glu Tyr Arg Asp Gly Asn Pro Arg Val Arg Ser Trp Cys Arg
130 135 140

Thr His Ala Ser Thr Trp Cys Pro His
145 150

<210> 857

<211> 258

<212> PRT

<213> Homo sapiens

<400> 857

Cys Leu Ser Gln Lys Ala Val Arg Ala Pro Arg Phe Leu Arg Gly Leu
1 5 10 15

Pro Ser Gly Arg Val Asn Cys Phe Leu Gln Ala Gly His Gly Ala Ser
20 25 30

Arg Ser Gln Gly Ser Gly Leu Cys Gln Met Leu Lys Glu Gly Ala Lys
35 40 45

His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn Ile Gln Ala Cys
50 55 60

Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly Pro Asn Gly Met
65 70 75 80

Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe Val Thr Asn Asp
85 90 95

Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His Pro Ala Ala Lys
100 105 110

Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu Val Gly Asp Gly
115 120 125

Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu Glu Leu Ala Glu
130 135 140

Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val Ile Glu Gly Tyr
145 150 155 160

Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro Asn Leu Val Cys

804

165 170 175
 Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val Ser Ser Leu Leu
 180 185 190
 Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu Val Phe Leu Ala
 195 200 205
 Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro Asp Ser Gly His
 210 215 220
 Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu Gly Ser Gly Ile
 225 230 235 240
 Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys Lys Glu Thr Glu
 245 250 255
 Val Met

<210> 858

<211> 143

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (14)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (135)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 858

Pro Asp Ser Leu Pro Pro Pro Ser Pro Arg Leu Pro Ala Xaa Gly Pro
 1 5 10 15

Glu Phe Pro Gly Arg Pro Thr Arg Pro Glu Arg Ser Pro Ser Leu Gly
 20 25 30

Ile Pro Lys Cys Phe His Ser Val Ile Arg Thr Glu His Arg Gly Leu
 35 40 45

Thr Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys
 50 55 60

Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val

805

65		70		75		80									
Lys	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr
				85					90					95	
Phe	Ser	Asn	Ala	Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly
			100					105					110		
Leu	Glu	Trp	Val	Gly	Arg	Ile	Lys	Ser	Lys	Thr	Asp	Gly	Gly	Thr	Thr
			115				120					125			
Asp	Tyr	Ala	Ala	Pro	Val	Xaa	Arg	Gln	Ile	His	His	Leu	Lys	Arg	
	130						135					140			

<210> 859

<211> 135

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (132)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (133)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 859

Val	Thr	Met	Ala	Gln	Gln	Ala	Ala	Asp	Lys	Tyr	Leu	Tyr	Val	Asp	Lys
1				5					10					15	
Asn	Phe	Ile	Asn	Asn	Pro	Leu	Ala	Gln	Ala	Asp	Trp	Ala	Ala	Lys	Lys
			20					25						30	
Leu	Val	Trp	Val	Pro	Ser	Asp	Lys	Ser	Gly	Phe	Glu	Pro	Ala	Ser	Leu
		35					40					45			
Lys	Glu	Glu	Val	Gly	Glu	Glu	Ala	Ile	Val	Glu	Leu	Val	Glu	Asn	Gly
	50					55					60				
Lys	Lys	Val	Lys	Val	Asn	Lys	Asp	Asp	Ile	Gln	Lys	Met	Asn	Pro	Pro
65					70					75				80	
Lys	Phe	Ser	Lys	Val	Glu	Asp	Met	Ala	Glu	Leu	Thr	Cys	Leu	Asn	Glu
				85					90					95	
Ala	Ser	Val	Leu	His	Asn	Leu	Lys	Glu	Arg	Tyr	Tyr	Ser	Gly	Leu	Ile

806

100 105 110
Tyr Val Ser Gly Cys Arg Gly Thr Pro Gln Ala Gly Ser Glu Gly Ser
115 120 125

Glu Val Gly Xaa Xaa Ala Gly
130 135

<210> 860

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 860

Ala Xaa Leu Ile Lys Thr Arg Val Leu Ile Tyr Asn Lys Ser Asn Phe
1 5 10 15

Ser Leu Ser Leu Gly Thr Ser Asn Cys Thr Pro Gln Ile Thr Asp Thr
20 25 30

Ser Glu Phe Phe Met Val Lys Lys Ala Pro Thr Leu Thr Tyr Lys Cys
35 40 45

Gly Pro Arg Asn
50

<210> 861

<211> 321

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (18)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 861

Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser
1 5 10 15

Thr Xaa Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser
20 25 30

807

Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr
 35 40 45
 Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser His His
 50 55 60
 Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala
 65 70 75 80
 Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His
 85 90 95
 Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser
 100 105 110
 Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser
 115 120 125
 Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu
 130 135 140
 Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
 145 150 155 160
 Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
 165 170 175
 Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
 180 185 190
 Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
 195 200 205
 Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly
 210 215 220
 Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala Leu Ala
 225 230 235 240
 Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn
 245 250 255
 Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met
 260 265 270
 Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser
 275 280 285
 Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly
 290 295 300

Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn
 305 310 315 320

Leu

<210> 862

<211> 327

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (307)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 862

Phe Gly Thr Ser Leu Thr Gln Val Leu Leu Gly Ala Gly Glu Asn Thr
 1 5 10 15

Lys Thr Asn Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys
 20 25 30

Val His Gln Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val
 35 40 45

Ser Gln Ile Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val
 50 55 60

Asn Ala Ser Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn
 65 70 75 80

Asn Ser Asp Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn
 85 90 95

Thr Asn Asn Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr
 100 105 110

Arg Leu Val Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr
 115 120 125

Thr Phe Asp Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn
 130 135 140

Ser Val Ile Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala
 145 150 155 160

His Phe Ile Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu

809

165 170 175
 Ser His Asn Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His
 180 185 190
 Arg Leu Glu Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala
 195 200 205
 Ile Met Glu Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr
 210 215 220
 Leu Pro Arg Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met
 225 230 235 240
 Glu Lys Leu Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly
 245 250 255
 Leu Thr Glu Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr
 260 265 270
 Val Leu Glu Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala
 275 280 285
 Ile Ser Val Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe
 290 295 300
 Leu Phe Xaa Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly
 305 310 315 320
 Arg Val Tyr Asp Pro Arg Ala
 325

<210> 863

<211> 86

<212> PRT

<213> Homo sapiens

<400> 863

Tyr Tyr Ile Val His Leu Lys Leu Thr Glu Arg Val Asn Leu Lys Cys
 1 5 10 15
 Ser His His Thr Asn Pro Lys Val Thr Met Phe Ser Pro His Lys Pro
 20 25 30
 Lys Gly Asn Tyr Val Leu Ile Ser Leu Ile Val Val Thr Ile Ser Gln
 35 40 45
 Cys Ile His Leu Pro Lys His Tyr Val Val Tyr Leu Glu Tyr Ile Ile
 50 55 60

810

Leu Phe Ile Asn Tyr Thr Ser Ile Lys Leu Lys Glu Gly Ile Thr Asn
65 70 75 80

Ser His Lys Ile Gln Ile
85

<210> 864

<211> 130

<212> PRT

<213> Homo sapiens

<400> 864

Leu Thr Gln Gln Gln Gln Pro Ala Thr Gly Pro Gln Pro Ser Leu Gly
1 5 10 15

Val Ser Phe Gly Thr Pro Phe Gly Ser Gly Ile Gly Thr Gly Leu Gln
20 25 30

Ser Ser Gly Leu Gly Ser Ser Asn Leu Gly Gly Phe Gly Thr Ser Ser
35 40 45

Gly Phe Gly Cys Ser Thr Thr Gly Ala Ser Thr Phe Gly Phe Gly Thr
50 55 60

Thr Asn Lys Pro Ser Gly Ser Leu Ser Ala Gly Phe Gly Ser Ser Ser
65 70 75 80

Thr Ser Gly Phe Asn Phe Ser Asn Pro Gly Ile Thr Ala Ser Ala Gly
85 90 95

Leu Thr Phe Gly Val Ser Asn Pro Ala Ser Ala Gly Phe Gly Thr Gly
100 105 110

Gly Gln Leu Leu Gln Leu Lys Lys Pro Pro Ala Gly Asn Lys Arg Gly
115 120 125

Lys Arg
130

<210> 865

<211> 78

<212> PRT

<213> Homo sapiens

<400> 865

Ser Glu Trp Lys Ile Lys Gly Pro Ser Ser Pro Leu Ala Ser Leu Pro

811

1 5 10 15
 Gly Arg Arg His Gly Gly Ser Ser Ala Thr Gly Ala Cys Gly Glu Ala
 20 25 30
 Met Ala Ala Ala Glu Gly Ser Ser Gly Pro Ala Gly Leu Thr Leu Gly
 35 40 45
 Arg Ser Phe Ser Asn Tyr Arg Pro Phe Glu Pro Gln Ala Leu Gly Leu
 50 55 60
 Ser Pro Ser Trp Arg Leu Thr Gly Phe Ser Gly Met Lys Gly
 65 70 75

<210> 866

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (517)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 866

Pro Pro Pro Glu Pro Arg Ala Xaa Met Ala Glu Asn Pro Ser Leu Glu
 1 5 10 15
 Asn His Arg Ile Lys Ser Phe Lys Asn Lys Gly Arg Asp Val Glu Thr
 20 25 30
 Met Arg Arg His Arg Asn Glu Val Thr Val Glu Leu Arg Lys Asn Lys
 35 40 45
 Arg Asp Glu His Leu Leu Lys Lys Arg Asn Val Pro Gln Glu Glu Ser
 50 55 60
 Leu Glu Asp Ser Asp Val Asp Ala Asp Phe Lys Ala Gln Asn Val Thr
 65 70 75 80
 Leu Glu Ala Ile Leu Gln Asn Ala Thr Ser Asp Asn Pro Val Val Gln
 85 90 95
 Leu Ser Ala Val Gln Ala Ala Arg Lys Leu Leu Ser Ser Asp Arg Asn

812

100	105	110
Pro Pro Ile Asp Asp Leu Ile Lys Ser Gly Ile Leu Pro Ile Leu Val 115 120 125		
Lys Cys Leu Glu Arg Asp Asp Asn Pro Ser Leu Gln Phe Glu Ala Ala 130 135 140		
Trp Ala Leu Thr Asn Ile Ala Ser Gly Thr Ser Ala Gln Thr Gln Ala 145 150 155 160		
Val Val Gln Ser Asn Ala Val Pro Leu Phe Leu Arg Leu Leu Arg Ser 165 170 175		
Pro His Gln Asn Val Cys Glu Gln Ala Val Trp Ala Leu Gly Asn Ile 180 185 190		
Ile Gly Asp Gly Pro Gln Cys Arg Asp Tyr Val Ile Ser Leu Gly Val 195 200 205		
Val Lys Pro Leu Leu Ser Phe Ile Ser Pro Ser Ile Pro Ile Thr Phe 210 215 220		
Leu Arg Asn Val Thr Trp Val Ile Val Asn Leu Cys Arg Asn Lys Asp 225 230 235 240		
Pro Pro Pro Pro Met Glu Thr Val Gln Glu Ile Leu Pro Ala Leu Cys 245 250 255		
Val Leu Ile Tyr His Thr Asp Ile Asn Ile Leu Val Asp Thr Val Trp 260 265 270		
Ala Leu Ser Tyr Leu Thr Asp Gly Gly Asn Glu Gln Ile Gln Met Val 275 280 285		
Ile Asp Ser Gly Val Val Pro Phe Leu Val Pro Leu Leu Ser His Gln 290 295 300		
Glu Val Lys Val Gln Thr Ala Ala Leu Arg Ala Val Gly Asn Ile Val 305 310 315 320		
Thr Gly Thr Asp Glu Gln Thr Gln Val Val Leu Asn Cys Asp Val Leu 325 330 335		
Ser His Phe Pro Asn Leu Leu Ser His Pro Lys Glu Lys Ile Asn Lys 340 345 350		
Glu Ala Val Trp Phe Leu Ser Asn Ile Thr Ala Gly Asn Gln Gln Gln 355 360 365		
Val Gln Ala Val Ile Asp Ala Gly Leu Ile Pro Met Ile Ile His Gln		

813

370 375 380
 Leu Ala Lys Gly Asp Phe Gly Thr Gln Lys Glu Ala Ala Trp Ala Ile
 385 390 395 400
 Ser Asn Leu Thr Ile Ser Gly Arg Lys Asp Gln Val Glu Tyr Leu Val
 405 410 415
 Gln Gln Asn Val Ile Pro Pro Phe Cys Asn Leu Leu Ser Val Lys Asp
 420 425 430
 Ser Gln Val Val Gln Val Val Leu Asp Gly Leu Lys Asn Ile Leu Ile
 435 440 445
 Met Ala Gly Asp Glu Ala Ser Thr Ile Ala Glu Ile Ile Glu Glu Cys
 450 455 460
 Gly Gly Leu Glu Lys Ile Glu Val Leu Gln Gln His Glu Asn Glu Asp
 465 470 475 480
 Ile Tyr Lys Leu Ala Phe Glu Ile Ile Asp Gln Tyr Phe Ser Gly Asp
 485 490 495
 Asp Ile Asp Glu Asp Pro Cys Leu Ile Pro Glu Ala Thr Gln Gly Gly
 500 505 510
 Thr Tyr Asn Phe Xaa Pro Thr Ala Asn Leu Gln Thr Lys Glu Phe Asn
 515 520 525

Phe

<210> 867

<211> 237

<212> PRT

<213> Homo sapiens

<400> 867

Arg Pro Gly Pro Val Arg Arg Arg Gly Lys Val Glu Leu Ile Lys Phe
 1 5 10 15
 Val Arg Val Gln Trp Arg Arg Pro Gln Val Glu Trp Arg Arg Arg
 20 25 30
 Trp Gly Pro Gly Pro Gly Ala Ser Met Ala Gly Ser Glu Glu Leu Gly
 35 40 45
 Leu Arg Glu Asp Thr Leu Arg Val Leu Ala Ala Phe Leu Arg Arg Gly
 50 55 60

Glu Ala Ala Gly Ser Pro Val Pro Thr Pro Pro Arg Ser Pro Ala Gln
65 70 75 80

Glu Glu Pro Thr Asp Phe Leu Ser Arg Leu Arg Arg Cys Leu Pro Cys
85 90 95

Ser Leu Gly Arg Gly Ala Ala Pro Ser Glu Ser Pro Arg Pro Cys Ser
100 105 110

Leu Pro Ile Arg Pro Cys Tyr Gly Leu Glu Pro Gly Pro Ala Thr Pro
115 120 125

Asp Phe Tyr Ala Leu Val Ala Gln Arg Leu Glu Gln Leu Val Gln Glu
130 135 140

Gln Leu Lys Ser Pro Pro Ser Pro Glu Leu Gln Gly Pro Pro Ser Thr
145 150 155 160

Glu Lys Glu Ala Ile Leu Arg Arg Leu Val Ala Leu Leu Glu Glu Glu
165 170 175

Ala Glu Val Ile Asn Gln Lys Leu Ala Ser Asp Pro Ala Leu Arg Thr
180 185 190

Ser Trp Ser Ala Cys Pro Pro Thr Leu Ser Pro Ala Trp Trp Ser Cys
195 200 205

Ser Val Ala Gly Met Thr Ala Leu Ala Gln Ala Glu His Ala Pro Gly
210 215 220

Pro Arg Leu Leu Pro Arg Ser Pro Trp Pro Ala Trp Pro
225 230 235

<210> 868

<211> 196

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (9)

<223> Xaa equals any of the naturally occurring L-amino acids

815

<400> 868

Leu Ser Val Ser Ala Xaa Ala Ala Xaa Val Ala Ala Ala Ala Ile His
1 5 10 15

Ser Asp Ser Ala Ala Ala Pro Gly Gly Gly Ala Ala Arg Asp Phe
20 25 30

Phe Phe Phe Gln Thr Asp Arg Gly Ala Ala Ala Asp Met Ser Thr Pro
35 40 45

Ala Arg Arg Arg Leu Met Arg Asp Phe Lys Arg Leu Gln Glu Asp Pro
50 55 60

Pro Val Gly Val Ser Gly Ala Pro Ser Glu Asn Asn Ile Met Gln Trp
65 70 75 80

Asn Ala Val Ile Phe Gly Pro Glu Gly Thr Pro Phe Glu Asp Gly Thr
85 90 95

Phe Lys Leu Val Ile Glu Phe Ser Glu Glu Tyr Pro Asn Lys Pro Pro
100 105 110

Thr Val Arg Phe Leu Ser Lys Met Phe His Pro Asn Val Tyr Ala Asp
115 120 125

Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Arg Trp Ser Pro Thr Tyr
130 135 140

Asp Val Ser Ser Ile Leu Thr Ser Ile Gln Ser Leu Leu Asp Glu Pro
145 150 155 160

Asn Pro Asn Ser Pro Ala Asn Ser Gln Ala Ala Gln Leu Tyr Gln Glu
165 170 175

Asn Lys Arg Glu Tyr Glu Lys Arg Val Ser Ala Ile Val Glu Gln Ser
180 185 190

Trp Asn Asp Ser
195

<210> 869

<211> 544

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (9)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 869

Ala Asp Ala Trp Val Ala Xaa Ala Xaa Ala Ser Ser Gly Leu Val Val
 1 5 10 15

Ala Arg Pro Thr Ser Ala Val Pro Ala Glu Pro Arg Pro Phe Arg Pro
 20 25 30

Ser Pro Pro His Leu Ala Ala Met Arg Leu Arg Arg Leu Ala Leu Phe
 35 40 45

Pro Gly Val Ala Leu Leu Leu Ala Ala Ala Arg Leu Ala Ala Ala Ser
 50 55 60

Asp Val Leu Glu Leu Thr Asp Asp Asn Phe Glu Ser Arg Ile Ser Asp
 65 70 75 80

Thr Gly Ser Ala Gly Leu Met Leu Val Glu Phe Phe Ala Pro Trp Cys
 85 90 95

Gly His Cys Lys Arg Leu Ala Pro Glu Tyr Glu Ala Ala Ala Thr Arg
 100 105 110

Leu Lys Gly Ile Val Pro Leu Ala Lys Val Asp Cys Thr Ala Asn Thr
 115 120 125

Asn Thr Cys Asn Lys Tyr Gly Val Ser Gly Tyr Pro Thr Leu Lys Ile
 130 135 140

Phe Arg Asp Gly Glu Glu Ala Gly Ala Tyr Asp Gly Pro Arg Thr Ala
 145 150 155 160

Asp Gly Ile Val Ser His Leu Lys Lys Gln Ala Gly Pro Ala Ser Val
 165 170 175

Pro Leu Arg Thr Glu Glu Glu Phe Lys Lys Phe Ile Ser Asp Lys Asp
 180 185 190

Ala Ser Ile Val Gly Phe Phe Asp Asp Ser Phe Ser Glu Ala His Ser
 195 200 205

Glu Phe Leu Lys Ala Ala Ser Asn Leu Arg Asp Asn Tyr Arg Phe Ala
 210 215 220

His Thr Asn Val Glu Ser Leu Val Asn Glu Tyr Asp Asp Asn Gly Glu
 225 230 235 240

Gly Ile Ile Leu Phe Arg Pro Ser His Leu Thr Asn Lys Phe Glu Asp
 245 250 255
 Lys Thr Val Ala Tyr Thr Glu Gln Lys Met Thr Ser Gly Lys Ile Lys
 260 265 270
 Lys Phe Ile Gln Glu Asn Ile Phe Gly Ile Cys Pro His Met Thr Glu
 275 280 285
 Asp Asn Lys Asp Leu Ile Gln Gly Lys Asp Leu Leu Ile Ala Tyr Tyr
 290 295 300
 Asp Val Asp Tyr Glu Lys Asn Ala Lys Gly Ser Asn Tyr Trp Arg Asn
 305 310 315 320
 Arg Val Met Met Val Ala Lys Lys Phe Leu Asp Ala Gly His Lys Leu
 325 330 335
 Asn Phe Ala Val Ala Ser Arg Lys Thr Phe Ser His Glu Leu Ser Asp
 340 345 350
 Phe Gly Leu Glu Ser Thr Ala Gly Glu Ile Pro Val Val Ala Ile Arg
 355 360 365
 Thr Ala Lys Gly Glu Lys Phe Val Met Gln Glu Glu Phe Ser Arg Asp
 370 375 380
 Gly Lys Ala Leu Glu Arg Phe Leu Gln Asp Tyr Phe Asp Gly Asn Leu
 385 390 395 400
 Lys Arg Tyr Leu Lys Ser Glu Pro Ile Pro Glu Ser Asn Asp Gly Pro
 405 410 415
 Val Lys Val Val Val Ala Glu Asn Phe Asp Glu Ile Val Asn Asn Glu
 420 425 430
 Asn Lys Asp Val Leu Ile Glu Phe Tyr Ala Pro Trp Cys Gly His Cys
 435 440 445
 Lys Asn Leu Glu Pro Lys Tyr Lys Glu Leu Gly Glu Lys Leu Ser Lys
 450 455 460
 Asp Pro Asn Ile Val Ile Ala Lys Met Asp Ala Thr Ala Asn Asp Val
 465 470 475 480
 Pro Ser Pro Tyr Glu Val Arg Gly Phe Pro Thr Ile Tyr Phe Ser Pro
 485 490 495
 Ala Asn Lys Lys Leu Asn Pro Lys Lys Tyr Glu Gly Gly Arg Glu Leu
 500 505 510

Ser Asp Phe Ile Ser Tyr Leu Gln Arg Glu Ala Thr Asn Pro Pro Val
 515 520 525

Ile Gln Glu Glu Lys Pro Lys Lys Lys Lys Lys Ala Gln Glu Asp Leu
 530 535 540

<210> 870

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 870

Arg Arg Xaa Ala Ile Phe Thr Cys Glu Val Pro Gly Val Tyr Tyr Phe
 1 5 10 15

Xaa Tyr His Val His Cys Lys Gly Gly Asn Val Trp Val Ala Leu Phe
 20 25 30

Lys Asn Asn Glu Pro Val Met Tyr Thr Tyr Asp Glu Tyr Lys Lys Gly
 35 40 45

Phe Leu Asp Gln Ala Ser Gly Ser Ala Val Leu Leu Leu Arg Pro Gly
 50 55 60

Asp Arg Cys Ser Ser Arg Cys Pro Gln Asn Arg Leu Gln Asp Cys Met
 65 70 75 80

Pro Gly Ser Met Ser Thr Pro Pro Phe Gln Asp Ile Tyr Cys Ile Pro
 85 90 95

Cys Lys Asn Lys Lys Thr Lys Asn Lys Glu Lys Lys Glu Ile Leu
 100 105 110

819

<210> 871

<211> 124

<212> PRT

<213> Homo sapiens

<400> 871

Gly Lys Thr Glu Val Asn Tyr Thr Gln Leu Val Asp Leu His Ala Arg
1 5 10 15

Tyr Ala Glu Cys Gly Leu Arg Ile Leu Ala Phe Pro Cys Asn Gln Phe
20 25 30

Gly Lys Gln Glu Pro Gly Ser Asn Glu Glu Ile Lys Glu Phe Ala Ala
35 40 45

Gly Tyr Asn Val Lys Phe Asp Met Phe Ser Lys Ile Cys Val Asn Gly
50 55 60

Asp Asp Ala His Pro Leu Trp Lys Trp Met Lys Ile Gln Pro Lys Gly
65 70 75 80

Lys Gly Ile Leu Gly Asn Ala Ile Lys Trp Asn Phe Thr Lys Phe Leu
85 90 95

Ile Asp Lys Asn Gly Cys Val Val Lys Arg Tyr Gly Pro Met Glu Glu
100 105 110

Pro Leu Val Ile Glu Lys Asp Leu Pro His Tyr Phe
115 120

<210> 872

<211> 35

<212> PRT

<213> Homo sapiens

<400> 872

Ser Gln His Phe Gly Arg Pro Arg Gln Ala Glu His Leu Lys Glu Phe
1 5 10 15

Lys Thr Ser Val Ala Asn Val Val Asn Pro Val Ser Thr Lys Asn Thr
20 25 30

Lys Ile Val
35

<210> 873

<211> 420

820

<212> PRT

<213> Homo sapiens

<400> 873

Val Cys Leu Gln Leu Cys Gln Ser Thr Val Ser Cys Pro Leu Gly Tyr
 1 5 10 15
 Leu Ala Ser Thr Ala Thr Asn Asp Cys Gly Cys Thr Thr Thr Thr Cys
 20 25 30
 Leu Pro Asp Lys Val Cys Val His Arg Ser Thr Ile Tyr Pro Val Gly
 35 40 45
 Gln Phe Trp Glu Glu Gly Cys Asp Val Cys Thr Cys Thr Asp Met Glu
 50 55 60
 Asp Ala Val Met Gly Leu Arg Val Ala Gln Cys Ser Gln Lys Pro Cys
 65 70 75 80
 Glu Asp Ser Cys Arg Ser Gly Phe Thr Tyr Val Leu His Glu Gly Glu
 85 90 95
 Cys Cys Gly Arg Cys Leu Pro Ser Ala Cys Glu Val Val Thr Gly Ser
 100 105 110
 Pro Arg Gly Asp Ser Gln Ser Ser Trp Lys Ser Val Gly Ser Gln Trp
 115 120 125
 Ala Ser Pro Glu Asn Pro Cys Leu Ile Asn Glu Cys Val Arg Val Lys
 130 135 140
 Glu Glu Val Phe Ile Gln Gln Arg Asn Val Ser Cys Pro Gln Leu Glu
 145 150 155 160
 Val Pro Val Cys Pro Ser Gly Phe Gln Leu Ser Cys Lys Thr Ser Ala
 165 170 175
 Cys Cys Pro Ser Cys Arg Cys Glu Arg Met Glu Ala Cys Met Leu Asn
 180 185 190
 Gly Thr Val Ile Gly Pro Gly Lys Thr Val Met Ile Asp Val Cys Thr
 195 200 205
 Thr Cys Arg Cys Met Val Gln Val Gly Val Ile Ser Gly Phe Lys Leu
 210 215 220
 Glu Cys Arg Lys Thr Thr Cys Asn Pro Cys Pro Leu Gly Tyr Lys Glu
 225 230 235 240
 Glu Asn Asn Thr Gly Glu Cys Cys Gly Arg Cys Leu Pro Thr Ala Cys
 245 250 255

821

Thr Ile Gln Leu Arg Gly Gly Gln Ile Met Thr Leu Lys Arg Asp Glu
260 265 270

Thr Leu Gln Asp Gly Cys Asp Thr His Phe Cys Lys Val Asn Glu Arg
275 280 285

Gly Glu Tyr Phe Trp Glu Lys Arg Val Thr Gly Cys Pro Pro Phe Asp
290 295 300

Glu His Lys Cys Leu Ala Glu Gly Gly Lys Ile Met Lys Ile Pro Gly
305 310 315 320

Thr Cys Cys Asp Thr Cys Glu Glu Pro Glu Cys Asn Asp Ile Thr Ala
325 330 335

Arg Leu Gln Tyr Val Lys Val Gly Ser Cys Lys Ser Glu Val Glu Val
340 345 350

Asp Ile His Tyr Cys Gln Gly Lys Cys Ala Ser Lys Ala Met Tyr Ser
355 360 365

Ile Asp Ile Asn Asp Val Gln Asp Gln Cys Ser Cys Cys Ser Pro Thr
370 375 380

Arg Thr Glu Pro Met Gln Val Ala Leu His Cys Thr Asn Gly Ser Val
385 390 395 400

Val Tyr His Glu Val Leu Asn Ala Met Glu Cys Lys Cys Ser Pro Arg
405 410 415

Lys Cys Ser Lys
420

<210> 874

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (90)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (103)

<223> Xaa equals any of the naturally occurring L-amino acids

822

<220>

<221> SITE

<222> (143)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 874

Arg Gln Val Pro His Glu Arg Ala Val Arg Asp Gly Arg Gly Gly Gly
 1 5 10 15

Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met Arg Arg His Ser
 20 25 30

Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala Val Val Leu Gln
 35 40 45

Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala
 50 55 60

Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr
 65 70 75 80

Asp Ser Pro Phe Pro Asn Ser Cys Ala Xaa Gly Met Ala Asn Gly Asp
 85 90 95

Ala Pro Cys Met Gly Ala Xaa Lys Arg Gly Gly Cys Gly Gly Tyr Ala
 100 105 110

Gln Trp Thr Arg Tyr Thr Cys Gln Arg Pro Ser Ala Arg Ser Phe Arg
 115 120 125

Phe Leu Pro Phe Leu Ser Arg His Val Arg Arg Leu Ser Pro Xaa Ser
 130 135 140

Ser Lys Ser Val Gly Ser Leu
 145 150

<210> 875

<211> 95

<212> PRT

<213> Homo sapiens

<400> 875

Ala Leu Asn Leu Asn Ser Gln Leu Asn Ile Pro Lys Asp Thr Ser Gln
 1 5 10 15

Leu Lys Lys His Ile Thr Leu Leu Cys Asp Arg Leu Ser Lys Gly Gly
 20 25 30

Arg Leu Cys Leu Ser Thr Asp Ala Ala Ala Pro Gln Thr Met Val Met

823

35 40 45
 Pro Gly Gly Cys Thr Thr Ile Pro Glu Ser Asp Leu Glu Glu Arg Ser
 50 55 60
 Val Glu Gln Asp Ser Thr Glu Leu Phe Thr Asn His Arg His Leu Thr
 65 70 75 80
 Ala Glu Thr Pro Arg Pro Val Ser Pro Leu Gln Gly Val Ser Glu
 85 90 95

<210> 876
 <211> 238
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (7)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (10)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (15)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (20)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 876
 Thr Lys Lys Ala Leu Glu Xaa Ser Asn Xaa Arg Phe Ala Ala Xaa Phe
 1 5 10 15
 Phe Arg Thr Xaa Trp Asn Pro Pro Gly Ala Phe Lys Glu Phe Gly Thr
 20 25 30
 Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Ala Asn Met Pro Val Ala
 35 40 45
 Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro Arg Arg Pro Phe
 50 55 60

824

Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile Gly Glu Tyr Gly
65 70 75 80

Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe Thr Leu Ala Lys
85 90 95

Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp Glu Lys Asp Pro
100 105 110

Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg Leu Val Arg Ile
115 120 125

Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr Ile Leu Gly Leu
130 135 140

Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr Gln Val Phe Lys
145 150 155 160

Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val Leu Ile Arg Gln
165 170 175

Arg His Ile Arg Val Arg Lys Gln Val Val Asn Ile Pro Ser Phe Ile
180 185 190

Val Arg Leu Asp Ser Gln Lys His Ile Asp Phe Ser Leu Arg Ser Pro
195 200 205

Tyr Gly Gly Gly Arg Pro Gly Arg Val Lys Arg Lys Asn Ala Lys Lys
210 215 220

Gly Gln Gly Gly Ala Gly Ala Gly Asp Asp Glu Glu Glu Asp
225 230 235

<210> 877

<211> 79

<212> PRT

<213> Homo sapiens

<400> 877

Ala Gly Ile Arg His Glu Pro Ser Ala Ala Ala Met Ser Ser Gly Ala
1 5 10 15

Ser Ala Ser Ala Leu Gln Arg Leu Val Glu Gln Leu Lys Leu Glu Ala
20 25 30

Gly Val Glu Arg Ile Lys Val Ser Gln Ala Ala Ala Glu Leu Gln Gln
35 40 45

Tyr Cys Met Gln Asn Ala Cys Lys Asp Ala Leu Leu Val Gly Val Pro

825

50 55 60
 Ala Gly Ser Asn Pro Phe Arg Glu Pro Arg Ser Cys Ala Leu Leu
 65 70 75

 <210> 878
 <211> 136
 <212> PRT
 <213> Homo sapiens

 <400> 878
 Ile Ala Ile Met Asn Asp Thr Val Thr Ile Arg Thr Arg Lys Phe Met
 1 5 10 15

 Thr Asn Arg Leu Leu Gln Arg Lys Gln Met Val Ile Asp Val Leu His
 20 25 30

 Pro Gly Lys Ala Thr Val Pro Lys Thr Glu Ile Arg Glu Lys Leu Ala
 35 40 45

 Lys Met Tyr Lys Thr Thr Pro Asp Val Ile Phe Val Phe Gly Phe Arg
 50 55 60

 Thr His Phe Gly Gly Gly Lys Thr Thr Gly Phe Gly Met Ile Tyr Asp
 65 70 75 80

 Ser Leu Asp Tyr Ala Lys Lys Asn Glu Pro Lys His Arg Leu Ala Arg
 85 90 95

 His Gly Leu Tyr Glu Lys Lys Lys Thr Ser Arg Lys Gln Arg Lys Glu
 100 105 110

 Arg Lys Asn Arg Met Lys Lys Val Arg Gly Thr Ala Lys Ala Asn Val
 115 120 125

 Gly Ala Gly Lys Lys Pro Lys Glu
 130 135

<210> 879
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 879
 Gly Cys Val Gly Val Arg Pro Ser Leu His Pro Ala Thr Ser Thr Ala
 1 5 10 15

826

Ser Gly Ser Ala Ser Pro Thr Leu Ala Arg Ala Met Ala Ser Val Ser
20 25 30
Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu His Asp Asp Glu Val
35 40 45
Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile Lys Ala Ala Gly Val
50 55 60
Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala Lys Ala Leu Ala Asn
65 70 75 80
Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly Ala Gly Gly Pro Ala
85 90 95
Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro Ala Pro Ser Thr Ala
100 105 110
Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala Lys Lys Glu Glu Ser
115 120 125
Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu Phe Asp
130 135 140

<210> 880

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (14)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (128)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (130)

<223> Xaa equals any of the naturally occurring L-amino acids

827

<220>

<221> SITE

<222> (131)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 880

Ser Ala Gly Ala His Ala His Gly Ala Arg Glu Leu Ala Xaa Phe Leu
1 5 10 15

Thr Pro Xaa Pro Gly Ala Glu Ala Lys Glu Val Glu Glu Thr Ile Glu
20 25 30

Gly Met Leu Leu Arg Leu Glu Glu Phe Cys Ser Leu Ala Asp Leu Ile
35 40 45

Arg Ser Asp Thr Ser Gln Ile Leu Glu Glu Asn Ile Pro Val Leu Lys
50 55 60

Ala Lys Leu Thr Glu Met Arg Gly Ile Tyr Ala Lys Val Asp Arg Leu
65 70 75 80

Glu Ala Phe Val Lys Met Val Gly His His Val Ala Phe Leu Glu Ala
85 90 95

Asp Val Leu Gln Ala Glu Arg Asp His Gly Ala Phe Pro Gln Ala Leu
100 105 110

Arg Arg Trp Leu Gly Ser Ala Gly Ser Pro Pro Ser Gly Thr Ser Xaa
115 120 125

Leu Xaa Xaa Cys Pro
130

<210> 881

<211> 260

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (14)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (124)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (136)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (171)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 881

Ile	Glu	Glu	Pro	Arg	Asp	Thr	Arg	Leu	Gln	Val	Cys	Ser	Xaa	Val	His
1				5					10					15	

Ile	Trp	Cys	Leu	Asp	Lys	Phe	Lys	Met	Arg	Lys	His	Arg	His	Leu	Pro
			20					25						30	

Leu	Val	Ala	Val	Phe	Cys	Leu	Phe	Leu	Ser	Gly	Phe	Pro	Thr	Thr	His
		35					40						45		

Ala	Gln	Gln	Gln	Gln	Ala	Val	Ile	Glu	Val	Asn	Lys	Arg	Asp	Ile	Val
		50				55						60			

Phe	Leu	Val	Asp	Gly	Ser	Ser	Ala	Leu	Gly	Leu	Ala	Asn	Phe	Asn	Ala
65					70					75					80

Ile	Arg	Asp	Phe	Ile	Ala	Lys	Val	Ile	Gln	Arg	Leu	Glu	Ile	Gly	Gln
				85					90					95	

Asp	Leu	Ile	Gln	Val	Ala	Val	Ala	Gln	Tyr	Ala	Asp	Thr	Val	Arg	Pro
			100					105						110	

Glu	Phe	Tyr	Phe	Asn	Thr	His	Pro	Thr	Lys	Arg	Xaa	Val	Ile	Thr	Ala
		115						120					125		

Val	Arg	Lys	Met	Lys	Pro	Leu	Xaa	Gly	Ser	Ala	Leu	Tyr	Thr	Gly	Ser
		130				135						140			

Ala	Leu	Asp	Phe	Val	Arg	Asn	Asn	Leu	Phe	Thr	Ser	Ser	Ala	Gly	Tyr
145					150					155				160	

Arg	Ala	Ala	Glu	Gly	Ile	Pro	Lys	Leu	Leu	Xaa	Leu	Ile	Thr	Gly	Gly
			165						170					175	

Lys	Ser	Leu	Asp	Glu	Ile	Ser	Gln	Pro	Ala	Gln	Glu	Leu	Lys	Arg	Ser
			180					185					190		

Ser	Ile	Met	Ala	Phe	Ala	Ile	Gly	Asn	Lys	Gly	Ala	Asp	Gln	Ala	Glu
		195					200					205			

Leu	Glu	Glu	Ile	Ala	Phe	Asp	Ser	Ser	Leu	Val	Phe	Ile	Pro	Ala	Glu
		210					215					220			

829

Phe Arg Ala Ala Pro Leu Gln Gly Met Leu Pro Gly Leu Leu Ala Pro
225 230 235 240

Leu Arg Thr Leu Ser Gly Thr Pro Glu Val His Ser Asn Lys Arg Asp
 245 250 255

Ile Ile Phe Leu
 260

<210> 882
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

830

<400> 882

Xaa Xaa Glu Ser Glu Xaa Ser Phe Xaa Cys Arg Lys Xaa Ile Ile Xaa
1 5 10 15

Phe Leu Xaa Tyr Lys Arg Val Val Phe Leu Lys Gln Leu Ala Ser Gly
20 25 30

Leu Leu Leu Val Thr Gly Pro Leu Val Leu Asn Arg Val Pro Leu Arg
35 40 45

Arg Thr His Gln Lys Phe Val Ile Ala Thr Ser Thr Lys Ile Asp Ile
50 55 60

Ser Asn Val Lys Ile Pro Lys His Leu Thr Asp Ala Tyr Phe Lys Lys
65 70 75 80

Lys Lys Leu Arg Lys Pro Arg His Gln Glu Gly Glu Ile Phe Asp Thr
85 90 95

Glu Lys Glu Lys Tyr Glu Ile Thr Glu Gln Arg Lys Ile Asp Gln Lys
100 105 110

Ala Val Asp Ser Gln Ile Leu Pro Lys Ile Lys Ala Ile Pro Gln Leu
115 120 125

Gln Gly Tyr Leu Arg Ser Val Phe Ala Leu Thr Asn Gly Ile Tyr Pro
130 135 140

His Lys Leu Val Phe
145

<210> 883

<211> 256

<212> PRT

<213> Homo sapiens

<400> 883

Trp Lys Ser Val Val Val Leu Ala Val Ser Ala Gly Ala Gly Ser Ala
1 5 10 15

His Pro Arg Gln Asn Lys Tyr Ser Val Leu Leu Pro Thr Tyr Asn Glu
20 25 30

Arg Glu Asn Leu Pro Leu Ile Val Trp Leu Leu Val Lys Ser Phe Ser
35 40 45

Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp Asp Gly Ser Pro
50 55 60

831

Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys Ile Tyr Gly Ser
 65 70 75 80
 Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu Gly Leu Gly Thr
 85 90 95
 Ala Tyr Ile His Gly Met Lys His Ala Thr Gly Asn Tyr Ile Ile Ile
 100 105 110
 Met Asp Ala Asp Leu Ser His His Pro Lys Phe Ile Pro Glu Phe Ile
 115 120 125
 Arg Lys Gln Lys Glu Gly Asn Phe Asp Ile Val Ser Gly Thr Arg Tyr
 130 135 140
 Lys Gly Asn Gly Gly Val Tyr Gly Trp Asp Leu Lys Arg Lys Ile Ile
 145 150 155 160
 Ser Arg Gly Ala Asn Phe Leu Thr Gln Ile Leu Leu Arg Pro Gly Ala
 165 170 175
 Ser Asp Leu Thr Gly Ser Phe Arg Leu Tyr Arg Lys Glu Val Leu Glu
 180 185 190
 Lys Leu Ile Glu Lys Cys Val Ser Lys Gly Tyr Val Phe Gln Met Glu
 195 200 205
 Met Ile Val Arg Ala Arg Gln Leu Asn Tyr Thr Ile Gly Glu Val Pro
 210 215 220
 Ile Ser Phe Val Asp Arg Val Tyr Gly Glu Ser Lys Leu Gly Gly Asn
 225 230 235 240
 Glu Ile Val Ser Phe Leu Lys Gly Leu Leu Thr Leu Phe Ala Thr Thr
 245 250 255

<210> 884

<211> 449

<212> PRT

<213> Homo sapiens

<400> 884

Gly Gly Ser Trp Cys Arg Ser Ser Pro Gly Arg Asp Gly Ser Pro Gly
 1 5 10 15

Ala Lys Gly Asp Arg Gly Glu Thr Gly Pro Ala Gly Pro Pro Gly Ala
 20 25 30

Pro Gly Ala Pro Gly Ala Pro Gly Pro Val Gly Pro Ala Gly Lys Ser
 35 40 45

Gly Asp Arg Gly Glu Thr Gly Pro Ala Gly Pro Ala Gly Pro Val Gly
 50 55 60

Pro Val Gly Ala Arg Gly Pro Ala Gly Pro Gln Gly Pro Arg Gly Asp
 65 70 75 80

Lys Gly Glu Thr Gly Glu Gln Gly Asp Arg Gly Ile Lys Gly His Arg
 85 90 95

Gly Phe Ser Gly Leu Gln Gly Pro Pro Gly Pro Pro Gly Ser Pro Gly
 100 105 110

Glu Gln Gly Pro Ser Gly Ala Ser Gly Pro Ala Gly Pro Arg Gly Pro
 115 120 125

Pro Gly Ser Ala Gly Ala Pro Gly Lys Asp Gly Leu Asn Gly Leu Pro
 130 135 140

Gly Pro Ile Gly Pro Pro Gly Pro Arg Gly Arg Thr Gly Asp Ala Gly
 145 150 155 160

Pro Val Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro
 165 170 175

Pro Ser Ala Gly Phe Asp Phe Ser Phe Leu Pro Gln Pro Pro Gln Glu
 180 185 190

Lys Ala His Asp Gly Gly Arg Tyr Tyr Arg Ala Asp Asp Ala Asn Val
 195 200 205

Val Arg Asp Arg Asp Leu Glu Val Asp Thr Thr Leu Lys Ser Leu Ser
 210 215 220

Gln Gln Ile Glu Asn Ile Arg Ser Pro Glu Gly Ser Arg Lys Asn Pro
 225 230 235 240

Ala Arg Thr Cys Arg Asp Leu Lys Met Cys His Ser Asp Trp Lys Ser
 245 250 255

Gly Glu Tyr Trp Ile Asp Pro Asn Gln Gly Cys Asn Leu Asp Ala Ile
 260 265 270

Lys Val Phe Cys Asn Met Glu Thr Gly Glu Thr Cys Val Tyr Pro Thr
 275 280 285

833

Gln Pro Ser Val Ala Gln Lys Asn Trp Tyr Ile Ser Lys Asn Pro Lys
 290 295 300
 Asp Lys Arg His Val Trp Phe Gly Glu Ser Met Thr Asp Gly Phe Gln
 305 310 315 320
 Phe Glu Tyr Gly Gly Gln Gly Ser Asp Pro Ala Asp Val Ala Ile Gln
 325 330 335
 Leu Thr Phe Leu Arg Leu Met Ser Thr Glu Ala Ser Gln Asn Ile Thr
 340 345 350
 Tyr His Cys Lys Asn Ser Val Ala Tyr Met Asp Gln Gln Thr Gly Asn
 355 360 365
 Leu Lys Lys Ala Leu Leu Leu Gln Gly Ser Asn Glu Ile Glu Ile Arg
 370 375 380
 Ala Glu Gly Asn Ser Arg Phe Thr Tyr Ser Val Thr Val Asp Gly Cys
 385 390 395 400
 Thr Ser His Thr Gly Ala Trp Gly Lys Thr Val Ile Glu Tyr Lys Thr
 405 410 415
 Thr Lys Thr Ser Arg Leu Pro Ile Ile Asp Val Ala Pro Leu Asp Val
 420 425 430
 Gly Ala Pro Asp Gln Glu Phe Gly Phe Asp Val Gly Pro Val Cys Phe
 435 440 445
 Leu

<210> 885

<211> 64

<212> PRT

<213> Homo sapiens

<400> 885

Gly Lys Leu Val Thr Leu Gln Val Pro Val Arg Asn Ser Arg Val Asp
 1 5 10 15
 Pro Arg Val Arg Trp Gly Phe Thr Lys Phe Asn Ala Asp Glu Phe Glu
 20 25 30
 Asp Met Val Ala Glu Lys Arg Leu Ile Pro Asp Gly Cys Gly Val Lys
 35 40 45
 Tyr Ile Pro Ser Arg Gly Pro Leu Asp Lys Trp Arg Ala Leu His Ser

834

50

55

60

<210> 886

<211> 132

<212> PRT

<213> Homo sapiens

<400> 886

Thr Thr Leu Arg Ala Leu Ala Leu Asn Leu Trp Pro Pro Lys Ser Arg
 1 5 10 15

Ser Leu Ile Ser Ser Trp Gln Ser Cys Gly Gln Glu Val Leu Lys Gly
 20 25 30

Lys Thr His Ser Asp Asn Cys Ser Pro Ile Tyr Gln Pro Ser Ala Gly
 35 40 45

Val Ser Asp Arg Gly Pro Leu Pro Pro Leu Glu Cys Ala Thr Tyr Glu
 50 55 60

Glu Cys Pro Met Gly Lys Arg Arg Leu Ser Cys Pro Leu Ala Ala Cys
 65 70 75 80

Ala Ser Ile Pro Gly Gln Lys Phe Pro Gln Glu Pro Leu Ala Leu Ala
 85 90 95

Gln Ser His Cys Glu Arg Arg Trp Glu Pro Thr Pro Leu Gly Glu Gly
 100 105 110

Ala Val Leu Leu Gly Thr Ser Gln His Gln Val Arg Ser Leu Lys Leu
 115 120 125

Lys Asn Val Asn
 130

<210> 887

<211> 70

<212> PRT

<213> Homo sapiens

<400> 887

Gly Leu Ser Ser Glu Ala Arg Glu Lys Ser Ser Glu Pro Gln Glu Arg
 1 5 10 15

835

Ser Ser Glu Pro Trp Glu Arg Ser Ser Glu Pro Trp Glu Gly Leu Val
 20 25 30

Thr Phe Glu Asp Val Ala Val Glu Phe Thr Gln Glu Glu Trp Ala Leu
 35 40 45

Leu Asp Pro Ala Gln Arg Thr Leu Tyr Arg Asp Val Met Leu Glu Asn
 50 55 60

Cys Arg Thr Trp Pro His
 65 70

<210> 888

<211> 373

<212> PRT

<213> Homo sapiens

<400> 888

Val Asp Pro Arg Val Arg Phe Arg Glu Glu Phe Leu Phe Ser Ser Leu
 1 5 10 15

Gln Glu Gly Arg Asp Lys Asp Thr Phe Ser Lys Met Ala Met Val Ser
 20 25 30

Glu Phe Leu Lys Gln Ala Trp Phe Ile Glu Asn Glu Glu Gln Glu Tyr
 35 40 45

Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro Gly Ser Ala Val Ser
 50 55 60

Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val Ala Ala Leu His Lys
 65 70 75 80

Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr Ile Ile Asp Ile Leu
 85 90 95

Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile Lys Ala Ala Tyr Leu
 100 105 110

Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu Lys Lys Ala Leu Thr
 115 120 125

Gly His Leu Glu Glu Val Val Leu Ala Leu Leu Lys Thr Pro Ala Gln
 130 135 140

Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys Gly Leu Gly Thr Asp
 145 150 155 160

Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg Thr Asn Lys Glu Ile

836

165	170	175
Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu Lys Arg Asp Leu Ala		
180	185	190
Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe Arg Asn Ala Leu Leu		
195	200	205
Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe Gly Val Asn Glu Asp		
210	215	220
Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu Ala Gly Glu Arg Arg		
225	230	235 240
Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile Leu Thr Thr Arg Ser		
245	250	255
Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr Thr Lys Tyr Ser Lys		
260	265	270
His Asp Met Asn Lys Val Leu Asp Leu Glu Leu Lys Gly Asp Ile Glu		
275	280	285
Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr Ser Lys Pro Ala Phe		
290	295	300
Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly Val Gly Thr Arg His		
305	310	315 320
Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser Glu Ile Asp Met Asn		
325	330	335
Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly Ile Ser Leu Cys Gln		
340	345	350
Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu Lys Ile Leu Val Ala		
355	360	365
Leu Cys Gly Gly Asn		
370		

<210> 889

<211> 336

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (51)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (60)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (67)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (100)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (183)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 889

Gly	Arg	Lys	Lys	His	Leu	Xaa	Ala	Arg	Leu	Val	Thr	Glu	Met	Asp	Ser
1				5					10					15	

Lys	Tyr	Gln	Cys	Val	Lys	Leu	Asn	Asp	Gly	His	Phe	Met	Pro	Val	Leu
			20					25					30		

Gly	Phe	Gly	Thr	Tyr	Ala	Pro	Ala	Glu	Val	Pro	Lys	Ser	Lys	Ala	Leu
	35						40					45			

Glu	Ala	Xaa	Lys	Leu	Ala	Ile	Glu	Ala	Gly	Phe	Xaa	His	Ile	Asp	Ser
	50					55						60			

Ala	His	Xaa	Tyr	Asn	Asn	Glu	Glu	Gln	Val	Gly	Leu	Ala	Ile	Arg	Ser
65					70					75				80	

Lys	Ile	Ala	Asp	Gly	Ser	Val	Lys	Arg	Glu	Asp	Ile	Phe	Tyr	Thr	Ser
				85					90					95	

Lys	Leu	Trp	Xaa	Asn	Ser	His	Arg	Pro	Glu	Leu	Val	Arg	Pro	Ala	Leu
			100					105					110		

Glu	Arg	Ser	Leu	Lys	Asn	Leu	Gln	Leu	Asp	Tyr	Val	Asp	Leu	Tyr	Leu
			115				120						125		

838

Ile His Phe Pro Val Ser Val Lys Pro Gly Glu Glu Val Ile Pro Lys
130 135 140

Asp Glu Asn Gly Lys Ile Leu Phe Asp Thr Val Asp Leu Cys Ala Thr
145 150 155 160

Trp Glu Ala Val Glu Lys Cys Lys Asp Ala Gly Leu Ala Lys Ser Ile
165 170 175

Gly Val Ser Asn Phe Asn Xaa Arg Gln Leu Glu Met Ile Leu Asn Lys
180 185 190

Pro Gly Leu Lys Tyr Lys Pro Val Cys Asn Gln Val Glu Cys His Pro
195 200 205

Tyr Phe Asn Gln Arg Lys Leu Leu Asp Phe Cys Lys Ser Lys Asp Ile
210 215 220

Val Leu Val Ala Tyr Ser Ala Leu Gly Ser His Arg Glu Glu Pro Trp
225 230 235 240

Val Asp Pro Asn Ser Pro Val Leu Leu Glu Asp Pro Val Leu Cys Ala
245 250 255

Leu Ala Lys Lys His Lys Arg Thr Pro Ala Leu Ile Ala Leu Arg Tyr
260 265 270

Gln Leu Gln Arg Gly Val Val Val Leu Ala Lys Ser Tyr Asn Glu Gln
275 280 285

Arg Ile Arg Gln Asn Val Gln Val Phe Glu Phe Gln Leu Thr Ser Glu
290 295 300

Glu Met Lys Ala Ile Asp Gly Leu Asn Arg Asn Val Arg Tyr Leu Thr
305 310 315 320

Leu Asp Ile Phe Ala Gly Pro Pro Asn Tyr Pro Phe Ser Asp Glu Tyr
325 330 335

<210> 890

<211> 195

<212> PRT

<213> Homo sapiens

<400> 890

839

Arg Ser Ser Glu Val Tyr Ala Gln Leu Cys Asn Val Ala Arg Ile Glu
 1 5 10 15
 Ala Glu Arg Glu Ala Gly Val His Phe Arg Pro Gly Tyr Glu Tyr Gly
 20 25 30
 Pro Gly Pro Asp Asp Leu His Tyr Ser Ile Tyr Gly Pro Asp Gly Ala
 35 40 45
 Pro Phe Tyr Asn Tyr Leu Gly Pro Glu Asp Thr Val Pro Glu Pro Ala
 50 55 60
 Phe Pro Asn Thr Ala Gly His Ser Ala Asp Arg Thr Pro Ile Leu Glu
 65 70 75 80
 Ser Pro Leu Gln Pro Ser Glu Leu Gln Pro His Tyr Val Ala Ser His
 85 90 95
 Pro Glu Pro Pro Ala Gly Phe Glu Gly Leu Gln Ala Glu Glu Cys Gly
 100 105 110
 Ile Leu Asn Gly Cys Glu Asn Gly Arg Cys Val Arg Val Arg Glu Gly
 115 120 125
 Tyr Thr Cys Asp Cys Phe Glu Gly Phe Gln Leu Asp Ala Ala His Met
 130 135 140
 Ala Cys Val Asp Val Asn Glu Cys Asp Asp Leu Asn Gly Pro Ala Val
 145 150 155 160
 Leu Cys Val His Gly Tyr Cys Glu Asn Thr Glu Gly Ser Tyr Arg Cys
 165 170 175
 His Cys Ser Pro Gly Tyr Val Ala Glu Ala Gly Pro Pro His Cys Thr
 180 185 190
 Ala Lys Glu
 195

<210> 891

<211> 198

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (108)

<223> Xaa equals any of the naturally occurring L-amino acids

840

<220>

<221> SITE

<222> (109)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 891

Ser Ala Gly Leu Thr Gly Arg Ile Ala Phe Ala Ala Ala Arg Pro Gln
 1 5 10 15

Thr Phe Val Pro Gly Pro Ser Ser Pro Pro Pro Pro Pro Pro Arg
 20 25 30

Pro Ala Glu Leu Ala Pro Ser Pro Pro Ala Asp Met Ser Glu Ser Lys
 35 40 45

Ser Gly Pro Glu Tyr Ala Ser Phe Phe Ala Val Met Gly Ala Ser Ala
 50 55 60

Ala Met Val Phe Ser Ala Leu Gly Ala Ala Tyr Gly Thr Ala Lys Ser
 65 70 75 80

Gly Thr Gly Ile Ala Ala Met Ser Val Met Arg Pro Glu Gln Ile Met
 85 90 95

Lys Ser Ile Ile Pro Val Val Met Ala Gly Ile Xaa Xaa Ile Tyr Gly
 100 105 110

Leu Val Val Ala Val Leu Ile Ala Asn Ser Leu Asn Asp Asp Ile Ser
 115 120 125

Leu Tyr Lys Ser Phe Leu Gln Leu Gly Ala Gly Leu Ser Val Gly Leu
 130 135 140

Ser Gly Leu Ala Ala Gly Phe Ala Ile Gly Ile Val Gly Asp Ala Gly
 145 150 155 160

Val Arg Gly Asn Ala Gln Gln Pro Arg Leu Phe Val Gly Met Ile Leu
 165 170 175

Ile Leu Ile Phe Ala Glu Val Leu Gly Leu Tyr Gly Leu Ile Val Ala
 180 185 190

Leu Ile Leu Ser Thr Lys
 195

<210> 892

<211> 95

<212> PRT

<213> Homo sapiens

841

<400> 892

Asp Ala Trp Ala Pro Ser Glu Ser Arg Glu Ala Leu Leu Thr Pro Pro
 1 5 10 15

Pro His Arg Arg His Thr Ala Ala Ala Ser Val Met Pro Lys His Glu
 20 25 30

Phe Ser Val Asp Met Thr Cys Gly Gly Cys Ala Glu Ala Val Ser Arg
 35 40 45

Val Leu Asn Lys Leu Gly Gly Val Lys Tyr Asp Ile Asp Leu Pro Asn
 50 55 60

Lys Lys Val Cys Ile Glu Ser Glu His Ser Met Asp Thr Leu Leu Ala
 65 70 75 80

Thr Leu Lys Lys Thr Gly Lys Thr Val Ser Tyr Leu Gly Leu Glu
 85 90 95

<210> 893

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (111)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (117)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 893

Gly Glu His Pro Arg Gln Pro Ala Gly Asn Asn Ile Leu Ala Val Leu
 1 5 10 15

Thr Cys Cys Gln Gln Ile His Arg Thr Trp Met Lys Phe Pro Phe Pro
 20 25 30

Leu Val Ser Ser Cys Ser Thr Pro Leu Leu Asp Pro Lys Ser Leu Thr
 35 40 45

Lys Ala Leu Asn Thr Val Lys Met Phe Tyr Ile Pro Phe His Leu Cys
 50 55 60

Cys Phe Phe Asn Cys Ile Leu Pro Asp Val Leu Met Leu Ser Leu Met

842

65 70 75 80
Leu Ile Val Ile Pro Val Arg Val His Phe Ile Phe Met Leu Phe Gln
 85 90 95
Pro Cys Ile Asn Ile His Leu Thr Lys Ile Thr Gln Leu Ile Xaa Lys
 100 105 110
Lys Lys Lys Asn Xaa Gly Gly Gly Pro Gly Thr
 115 120

<210> 894
<211> 172
<212> PRT
<213> Homo sapiens

<400> 894
Gln Phe Val Tyr Cys Gly Lys Lys Ala Gln Leu Asn Ile Gly Asn Val
1 5 10 15
Leu Pro Val Gly Thr Met Pro Glu Gly Thr Ile Val Cys Cys Leu Glu
 20 25 30
Glu Lys Pro Gly Asp Arg Gly Lys Leu Ala Arg Ala Ser Gly Asn Tyr
 35 40 45
Ala Thr Val Ile Ser His Asn Pro Glu Thr Lys Lys Thr Arg Val Lys
50 55 60
Leu Pro Ser Gly Ser Lys Lys Val Ile Ser Ser Ala Asn Arg Ala Val
65 70 75 80
Val Gly Val Val Ala Gly Gly Gly Arg Ile Asp Lys Pro Ile Leu Lys
 85 90 95
Ala Gly Arg Ala Tyr His Lys Tyr Lys Ala Lys Arg Asn Cys Trp Pro
 100 105 110
Arg Val Arg Gly Val Ala Met Asn Pro Val Glu His Pro Phe Gly Gly
 115 120 125
Gly Asn His Gln His Ile Gly Lys Pro Ser Thr Ile Arg Arg Asp Ala
130 135 140
Pro Ala Gly Arg Lys Val Gly Leu Ile Ala Ala Arg Arg Thr Gly Arg
145 150 155 160
Leu Arg Gly Thr Lys Thr Val Gln Glu Lys Glu Asn
 165 170

843

<210> 895
<211> 171
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (37)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 895
Asn Arg Glu Gly Ser Lys Gly Val Glu Thr Arg Arg Val Leu Val Gly
1 5 10 15
Glu Gln Gln Gln Cys Xaa Asp Ala Lys Ser Gln Gln Lys Glu Gln Met
20 25 30
Leu Leu Leu Glu Xaa Lys Ser Ala Ala Tyr Ser Gln Val Leu Leu Arg
35 40 45
Cys Leu Thr Leu Leu Gln Arg Leu Leu Gln Glu His Arg Leu Lys Thr
50 55 60
Gln Ser Glu Leu Asp Arg Ile Asn Ala Gln Tyr Leu Glu Val Lys Cys
65 70 75 80
Gly Ala Met Ile Leu Lys Leu Arg Met Glu Glu Leu Lys Ile Leu Ser
85 90 95
Asp Thr Tyr Thr Val Glu Lys Val Glu Val His Arg Leu Ile Arg Asp
100 105 110
Arg Leu Glu Gly Ala Ile His Leu Gln Glu Gln Asp Met Glu Asn Ser
115 120 125
Arg Gln Val Leu Asn Ser Tyr Glu Val Leu Gly Glu Glu Phe Asp Arg
130 135 140
Leu Val Lys Glu Tyr Thr Val Leu Lys Gln Ala Thr Glu Asn Lys Arg
145 150 155 160
Trp Ala Leu Gln Glu Phe Ser Lys Val Tyr Arg
165 170

844

<210> 896

<211> 99

<212> PRT

<213> Homo sapiens

<400> 896

Arg Glu Val Met Lys Leu Tyr Leu Phe Gln Trp Ala Leu Phe His Phe
 1 5 10 15

Thr Thr Val Pro Leu Phe Gly Ser Trp Ser Tyr Thr Leu Ile Phe Ser
 20 25 30

Ile Leu Leu Leu Asn Tyr Gln His Lys Ala Ile Tyr Leu Lys Asp Ser
 35 40 45

Val Tyr Pro Ala Ile Ala Leu Lys Ser Ser Arg Lys Arg Asn Pro Leu
 50 55 60

Thr Cys Ile Ser Phe Cys Arg Ala Ser Leu Phe Ser Phe Val Leu Cys
 65 70 75 80

Phe Leu Pro Phe Glu Ser Asp Ser Val Leu Val Arg Lys Thr Ser Trp
 85 90 95

Asp His Ser

<210> 897

<211> 289

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (255)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 897

Ala Pro Glu Phe Pro Gly Arg Pro Thr Arg Pro Pro Thr Arg Arg Pro
 1 5 10 15

Arg Val Arg Gly Arg Ser Gln Leu Ser Ala His Gly Pro Ala Ser Phe
 20 25 30

Lys Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly
 35 40 45

845

Asp His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr
 50 55 60

Asn Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys
 65 70 75 80

Thr Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg
 85 90 95

Ser Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr
 100 105 110

Lys Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu
 115 120 125

Glu Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala
 130 135 140

Ser Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser
 145 150 155 160

Leu Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile
 165 170 175

Asn Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile
 180 185 190

Ile Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala
 195 200 205

Lys Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile
 210 215 220

Asp Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly
 225 230 235 240

Thr Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Xaa Pro
 245 250 255

Thr Ser Arg Lys Tyr Leu Ile Gly Thr Arg Val Thr Ala Leu Met Thr
 260 265 270

Cys Trp Lys Ala Ser Gly Lys Arg Leu Lys Glu Thr Trp Lys Met Leu
 275 280 285

Ser

846

<210> 898
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (205)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 898

Asn Pro Arg Gly Lys Val Ala Gly Phe Asp Leu Asp Gly Thr Leu Ile
 1 5 10 15

Thr Thr Arg Ser Gly Lys Val Phe Pro Thr Gly Pro Ser Asp Trp Arg
 20 25 30

Ile Leu Tyr Pro Glu Ile Pro Arg Lys Leu Arg Glu Leu Glu Ala Glu
 35 40 45

Gly Tyr Lys Leu Val Ile Phe Thr Asn Gln Met Ser Ile Gly Arg Gly
 50 55 60

Lys Leu Pro Ala Glu Glu Phe Lys Ala Lys Val Glu Ala Val Val Glu
 65 70 75 80

Lys Leu Gly Val Pro Phe Gln Val Leu Val Ala Thr His Ala Gly Leu
 85 90 95

Tyr Arg Lys Pro Val Thr Gly Met Trp Asp His Leu Gln Glu Gln Ala
 100 105 110

Asn Asp Gly Thr Pro Ile Ser Ile Gly Asp Ser Ile Phe Val Gly Asp
 115 120 125

Ala Ala Gly Arg Pro Ala Asn Trp Ala Pro Gly Arg Lys Lys Lys Asp
 130 135 140

Phe Ser Cys Ala Asp Arg Leu Phe Ala Leu Asn Leu Gly Leu Pro Phe
 145 150 155 160

Ala Thr Pro Glu Glu Phe Phe Leu Lys Trp Pro Ala Ala Gly Phe Glu
 165 170 175

Leu Pro Ala Phe Asp Pro Arg Thr Val Ser Arg Ser Gly Pro Leu Cys
 180 185 190

Leu Pro Glu Ser Arg Ala Leu Leu Ser Ala Thr Arg Xaa Trp Leu Ser
 195 200 205

Gln Trp Asp Ser Leu Gly Pro Gly Ser Pro Pro Phe Ser Arg Ser Thr

847

210 215 220
 Ser Cys Arg Pro Asp Met Ser Thr
 225 230

 <210> 899
 <211> 218
 <212> PRT
 <213> Homo sapiens

 <400> 899
 Leu Arg Val Ala Arg Pro Asp Ala Ala Arg Ala Ala Pro Leu Ala Pro
 1 5 10 15

 Ala Ala Ala Met Lys Ala Val Val Gln Arg Val Thr Arg Ala Ser Val
 20 25 30

 Thr Val Gly Gly Glu Gln Ile Ser Ala Ile Gly Arg Gly Ile Cys Val
 35 40 45

 Leu Leu Gly Ile Ser Leu Glu Asp Thr Gln Lys Glu Leu Glu His Met
 50 55 60

 Val Arg Lys Ile Leu Asn Leu Arg Val Phe Glu Asp Glu Ser Gly Lys
 65 70 75 80

 His Trp Ser Lys Ser Val Met Asp Lys Gln Tyr Glu Ile Leu Cys Val
 85 90 95

 Ser Gln Phe Thr Leu Gln Cys Val Leu Lys Gly Asn Lys Pro Asp Phe
 100 105 110

 His Leu Ala Met Pro Thr Glu Gln Ala Glu Gly Phe Tyr Asn Ser Phe
 115 120 125

 Leu Glu Gln Leu Arg Lys Thr Tyr Arg Pro Glu Leu Ile Lys Asp Gly
 130 135 140

 Lys Phe Gly Ala Tyr Met Gln Val His Ile Gln Asn Asp Gly Pro Val
 145 150 155 160

 Thr Ile Glu Leu Glu Ser Pro Ala Pro Gly Thr Ala Thr Ser Asp Pro
 165 170 175

 Lys Gln Leu Ser Lys Leu Glu Lys Gln Gln Gln Arg Lys Glu Lys Thr
 180 185 190

 Arg Ala Lys Gly Pro Ser Glu Phe Lys Gln Gly Lys Lys His Ser Pro
 195 200 205

Lys Arg Arg Pro Gln Cys Gln Gln Arg Gly
210 215

<210> 900
<211> 152
<212> PRT
<213> Homo sapiens

<400> 900
Ser Lys Arg Gly His Val Pro Trp Gly Leu Glu Glu Ile Leu Asp Val
1 5 10 15
Ile Glu Pro Ser Gln Phe Val Lys Ile Gln Glu Pro Leu Phe Lys Gln
20 25 30
Ile Ala Lys Cys Val Ser Ser Pro His Phe Gln Val Ala Glu Arg Ala
35 40 45
Leu Tyr Tyr Trp Asn Asn Glu Tyr Ile Met Ser Leu Ile Glu Glu Asn
50 55 60
Ser Asn Val Ile Leu Pro Ile Met Phe Ser Ser Leu Tyr Arg Ile Ser
65 70 75 80
Lys Glu His Trp Asn Pro Ala Ile Val Ala Leu Val Tyr Asn Val Leu
85 90 95
Lys Ala Phe Met Glu Met Asn Ser Thr Met Phe Asp Glu Leu Thr Ala
100 105 110
Thr Tyr Lys Ser Asp Arg Gln Arg Glu Lys Lys Lys Glu Lys Glu Arg
115 120 125
Glu Glu Leu Trp Lys Lys Leu Glu Asp Leu Glu Leu Lys Arg Gly Leu
130 135 140
Arg Arg Asp Gly Ile Ile Pro Thr
145 150

<210> 901
<211> 261
<212> PRT
<213> Homo sapiens

<400> 901
Gly Leu Arg Glu Ile Ser Gly Arg Leu Ala Glu Met Pro Ala Asp Ser

849

1	5	10	15
Gly Tyr Pro Ala Tyr Leu Gly Ala Arg Leu Ala Ser Phe Tyr Glu Arg	20	25	30
Ala Gly Arg Val Lys Cys Leu Gly Asn Pro Glu Arg Glu Gly Ser Val	35	40	45
Ser Ile Val Gly Ala Val Ser Pro Pro Gly Gly Asp Phe Ser Asp Pro	50	55	60
Val Thr Ser Ala Thr Leu Gly Ile Val Gln Val Phe Trp Gly Leu Asp	65	70	75
Lys Lys Leu Ala Gln Arg Lys His Phe Pro Ser Val Asn Trp Leu Ile	85	90	95
Ser Tyr Ser Lys Tyr Met Arg Ala Leu Asp Glu Tyr Tyr Asp Lys His	100	105	110
Phe Thr Glu Phe Val Pro Leu Arg Thr Lys Ala Lys Glu Ile Leu Gln	115	120	125
Glu Glu Glu Asp Leu Ala Glu Ile Val Gln Leu Val Gly Lys Ala Ser	130	135	140
Leu Ala Glu Thr Asp Lys Ile Thr Leu Glu Val Ala Lys Leu Ile Lys	145	150	155
Asp Asp Phe Leu Gln Gln Asn Gly Tyr Thr Pro Tyr Asp Arg Phe Cys	165	170	175
Pro Phe Tyr Lys Thr Val Gly Met Leu Ser Asn Met Ile Ala Phe Tyr	180	185	190
Asp Met Ala Arg Arg Val Phe Glu Thr Thr Ala Gln Ser Asp Asn Lys	195	200	205
Ile Thr Trp Ser Ile Ile Arg Glu His Met Gly Asp Ile Leu Tyr Lys	210	215	220
Leu Ser Ser Met Lys Phe Lys Asp Pro Leu Lys Asp Gly Glu Ala Lys	225	230	235
Ile Lys Ser Asp Tyr Ala Gln Leu Leu Glu Asp Met Gln Asn Ala Phe	245	250	255
Arg Ser Leu Glu Asp	260		

850

<210> 902
<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (33)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 902
Phe Pro Gly Arg Pro Thr Arg Pro Arg Gly Ile Ser Val Ser Gly Gly
1 5 10 15
Glu Ala Val Cys Pro Val Gln Trp Arg Leu Arg Lys Leu Ala Ala Ala
20 25 30
Xaa Gly Lys Gly Gln Glu Val Glu Thr Ser Val Thr Tyr Tyr Arg Leu
35 40 45
Glu Glu Val Ala Lys Arg Asn Ser Leu Lys Glu Leu Trp Leu Val Ile
50 55 60
His Gly Arg Val Tyr Asp Val Thr Arg Phe Leu Asn Glu His Pro Gly
65 70 75 80
Gly Glu Glu Val Leu Leu Glu Gln Ala Gly Val Asp Ala Ser Glu Ser
85 90 95
Phe Glu Asp Val Gly His Ser Ser Asp Ala Arg Glu Met Leu Lys Gln
100 105 110
Tyr Tyr Ile Gly Asp Ile His Pro Ser Asp Leu Lys Pro Glu Ser Gly
115 120 125
Ser Lys Asp Pro Ser Lys Asn Asp Thr Cys Lys Ser Cys Trp Ala Tyr
130 135 140
Trp Ile Leu Pro Ile Ile Gly Ala Val Leu Leu Gly Phe Leu Tyr Arg
145 150 155 160
Tyr Tyr Thr Ser Glu Ser Lys Ser Ser
165

<210> 903
<211> 53
<212> PRT
<213> Homo sapiens

851

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 903
Pro Leu Cys Leu Ala Lys Asn Lys Asn Phe Leu Ile Leu Arg Xaa Asn
1 5 10 15
Ile Gln Xaa Ile His Ile Lys Ser Leu Glu Asn Ile Ile Pro Phe Asp
20 25 30
Ser Leu Ile Thr Leu Leu Glu Tyr Lys Glu Met Ile Leu Asn Ile Tyr
35 40 45
Val Val Leu Trp Ser
50

<210> 904
<211> 329
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 904
Arg Arg Xaa Ala Xaa Pro Arg Val Arg Trp Lys Ile Cys Gly Leu Ser
1 5 10 15
Pro Thr Thr Thr Leu Ala Ile Tyr Phe Glu Val Val Asn Gln His Asn

852

20	25	30
Ala Pro Ile Xaa Gln Gly Gly Arg Gly Ala Ile Gln Phe Val Thr Gln		
35	40	45
Tyr Gln His Ser Ser Gly Gln Arg Arg Ile Arg Val Thr Thr Ile Ala		
50	55	60
Arg Asn Trp Ala Asp Ala Gln Thr Gln Ile Gln Asn Ile Ala Ala Ser		
65	70	75 80
Phe Asp Gln Glu Ala Ala Ala Ile Leu Met Ala Arg Leu Ala Ile Tyr		
85	90	95
Arg Ala Glu Thr Glu Glu Gly Pro Asp Val Leu Arg Trp Leu Asp Arg		
100	105	110
Gln Leu Ile Arg Leu Cys Gln Lys Phe Gly Glu Tyr His Lys Asp Asp		
115	120	125
Pro Ser Ser Phe Arg Phe Ser Glu Thr Phe Ser Leu Tyr Pro Gln Phe		
130	135	140
Met Phe His Leu Arg Arg Ser Ser Phe Leu Gln Val Phe Asn Asn Ser		
145	150	155 160
Pro Asp Glu Ser Ser Tyr Tyr Arg His His Phe Met Arg Gln Asp Leu		
165	170	175
Thr Gln Ser Leu Ile Met Ile Gln Pro Ile Leu Tyr Ala Tyr Ser Phe		
180	185	190
Ser Gly Pro Pro Glu Pro Val Leu Leu Asp Ser Ser Ser Ile Leu Ala		
195	200	205
Asp Arg Ile Leu Leu Met Asp Thr Phe Phe Gln Ile Leu Ile Tyr His		
210	215	220
Gly Glu Thr Ile Ala Gln Trp Arg Lys Ser Gly Tyr Gln Asp Met Pro		
225	230	235 240
Glu Tyr Glu Asn Phe Arg His Leu Leu Gln Ala Pro Val Asp Asp Ala		
245	250	255
Gln Glu Ile Leu His Ser Arg Phe Pro Met Pro Arg Tyr Ile Asp Thr		
260	265	270
Glu His Gly Gly Ser Gln Ala Arg Phe Leu Leu Ser Lys Val Asn Pro		
275	280	285
Ser Gln Thr His Asn Asn Met Tyr Ala Trp Gly Gln Glu Ser Gly Ala		

853

290 295 300
 Pro Ile Leu Thr Asp Asp Val Ser Leu Gln Val Phe Met Asp His Leu
 305 310 315 320

Lys Lys Leu Ala Val Ser Ser Ala Ala
 325

<210> 905

<211> 264

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (48)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 905

Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys Tyr Phe
 1 5 10 15

Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu Ala Val Leu
 20 25 30

Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu Asn Met Xaa
 35 40 45

Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg
 50 55 60

Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln Pro Tyr Val
 65 70 75 80

Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly Met Met Glu
 85 90 95

Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp
 100 105 110

Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile Phe Ile
 115 120 125

Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser Glu Val Ala
 130 135 140

Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe Pro Glu Gly
 145 150 155 160

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<210> 906
<211> 189
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

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<400> 906
Xaa Xaa Pro Xaa Pro Glu Phe Pro Gly Arg Thr His Ala Ser Gly Leu
 1             5             10             15
Leu Arg Ser Arg Leu Ala Leu Arg Trp Leu Ser His Val Arg Arg Pro
      20             25             30
Ser Arg Arg Val Pro Arg Met Pro Arg Gly Ser Arg Ser Arg Thr Ser

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855

35 40 45

Arg Met Ala Pro Pro Ala Ser Arg Ala Pro Gln Met Arg Ala Ala Pro
50 55 60

Arg Pro Ala Pro Val Ala Gln Pro Pro Ala Ala Ala Pro Pro Ser Ala
65 70 75 80

Val Gly Ser Ser Ala Ala Ala Pro Arg Gln Pro Gly Leu Met Ala Gln
85 90 95

Met Ala Thr Thr Ala Ala Gly Val Ala Val Gly Ser Ala Val Gly His
100 105 110

Thr Leu Gly His Ala Ile Thr Gly Gly Phe Ser Gly Gly Ser Asn Ala
115 120 125

Glu Pro Ala Arg Pro Asp Ile Thr Tyr Gln Glu Pro Gln Gly Thr Gln
130 135 140

Pro Ala Gln Gln Gln Gln Pro Cys Leu Tyr Glu Ile Lys Gln Phe Leu
145 150 155 160

Glu Cys Ala Gln Asn Gln Gly Asp Ile Lys Leu Cys Glu Gly Phe Asn
165 170 175

Glu Val Leu Lys Gln Cys Arg Leu Ala Asn Gly Leu Ala
180 185

<210> 907

<211> 638

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (43)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (52)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (56)

<223> Xaa equals any of the naturally occurring L-amino acids

856

<220>

<221> SITE

<222> (73)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (427)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 907

Tyr Val Gln Gly Tyr Ser Leu Ser Gln Ala Asp Val Asp Ala Phe Arg
 1 5 10 15

Gln Leu Ser Ala Pro Pro Ala Asp Pro Gln Leu Phe His Val Ala Arg
 20 25 30

Trp Phe Arg His Ile Glu Ala Leu Leu Gly Xaa Pro Cys Gly Lys Gly
 35 40 45

Gln Pro Cys Xaa Leu Pro Ser Xaa Gln Arg Pro Ala Cys Ala Ala Pro
 50 55 60

Val Val Pro Ser Cys Trp Asp Pro Xaa Cys Arg Leu His Leu Tyr Asn
 65 70 75 80

Ser Leu Thr Arg Asn Lys Glu Val Phe Ile Pro Gln Asp Gly Lys Lys
 85 90 95

Val Thr Trp Tyr Cys Cys Gly Pro Thr Val Tyr Asp Ala Ser His Met
 100 105 110

Gly His Ala Arg Ser Tyr Ile Ser Phe Asp Ile Leu Arg Arg Val Leu
 115 120 125

Lys Asp Tyr Phe Lys Phe Asp Val Phe Tyr Cys Met Asn Ile Thr Asp
 130 135 140

Ile Asp Asp Lys Ile Ile Lys Arg Ala Arg Gln Asn His Leu Phe Glu
 145 150 155 160

Gln Tyr Arg Glu Lys Arg Pro Glu Ala Ala Gln Leu Leu Glu Asp Val
 165 170 175

Gln Ala Ala Leu Lys Pro Phe Ser Val Lys Leu Asn Glu Thr Thr Asp
 180 185 190

Pro Asp Lys Lys Gln Met Leu Glu Arg Ile Gln His Ala Val Gln Leu
 195 200 205

Ala Thr Glu Pro Leu Glu Lys Ala Val Gln Ser Arg Leu Thr Gly Glu

210	215	220
Glu Val Asn Ser Cys Val	Glu Val Leu Leu Glu	Glu Ala Lys Asp Leu
225	230	235 240
Leu Ser Asp Trp Leu Asp	Ser Thr Leu Gly Cys Asp	Val Thr Asp Asn
245	250	255
Ser Ile Phe Ser Lys Leu	Pro Lys Phe Trp Glu	Gly Asp Phe His Arg
260	265	270
Asp Met Glu Ala Leu Asn	Val Leu Pro Pro Asp	Val Leu Thr Arg Val
275	280	285
Ser Glu Tyr Val Pro Glu	Ile Val Asn Phe Val	Gln Lys Ile Val Asp
290	295	300
Asn Gly Tyr Gly Tyr Val	Ser Asn Gly Ser Val	Tyr Phe Asp Thr Ala
305	310	315 320
Lys Phe Ala Ser Ser Glu	Lys His Ser Tyr Gly	Lys Leu Val Pro Glu
325	330	335
Ala Val Gly Asp Gln Lys	Ala Leu Gln Glu Gly	Glu Gly Asp Leu Ser
340	345	350
Ile Ser Ala Asp Arg Leu	Ser Glu Lys Arg Ser	Pro Asn Asp Phe Ala
355	360	365
Leu Trp Lys Ala Ser Lys	Pro Gly Glu Pro Ser	Trp Pro Cys Pro Trp
370	375	380
Gly Lys Gly Arg Pro Gly	Trp His Ile Glu Cys	Ser Ala Met Ala Gly
385	390	395 400
Thr Leu Leu Gly Ala Ser	Met Asp Ile His Gly	Gly Gly Phe Asp Leu
405	410	415
Arg Phe Pro His His Asp	Asn Glu Leu Ala Xaa	Ser Glu Ala Tyr Phe
420	425	430
Glu Asn Asp Cys Trp Val	Arg Tyr Phe Leu His	Thr Gly His Leu Thr
435	440	445
Ile Ala Gly Cys Lys Met	Ser Lys Ser Leu Lys	Asn Phe Ile Thr Ile
450	455	460
Lys Asp Ala Leu Lys Lys	His Ser Ala Arg Gln	Leu Arg Leu Ala Phe
465	470	475 480
Leu Met His Ser Trp Lys	Asp Thr Leu Asp Tyr	Ser Ser Asn Thr Met

858

485	490	495
Glu Ser Ala Leu Gln Tyr Glu Lys Phe Leu Asn Glu Phe Phe Leu Asn		
500	505	510
Val Lys Asp Ile Leu Arg Ala Pro Val Asp Ile Thr Gly Gln Phe Glu		
515	520	525
Lys Trp Gly Glu Glu Glu Ala Glu Leu Asn Lys Asn Phe Tyr Asp Lys		
530	535	540
Lys Thr Ala Ile His Lys Ala Leu Cys Asp Asn Val Asp Thr Arg Thr		
545	550	555
Val Met Glu Glu Met Arg Ala Leu Val Ser Gln Cys Asn Leu Tyr Met		
565	570	575
Ala Ala Arg Lys Ala Val Arg Lys Arg Pro Asn Gln Ala Leu Leu Glu		
580	585	590
Asn Ile Ala Leu Tyr Leu Thr His Met Leu Lys Ile Phe Gly Ala Val		
595	600	605
Glu Glu Asp Ser Ser Leu Gly Phe Pro Val Gly Gly Pro Gly Thr Ser		
610	615	620
Leu Ser Leu Glu Ala Thr Val Met Pro Tyr Leu Gln Val Leu		
625	630	635

<210> 908
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 908
 Ser His Pro Leu Arg Ser Arg Leu Pro Ser Ala Thr Gly Val Gly His
 1 5 10 15
 Ala Leu Ala Arg Ser Phe Cys Arg His Leu Gly Ser Ala Phe Pro Ala
 20 25 30
 Gln Asn Ala Arg Arg Ser Thr Glu Thr Val Pro Ala Thr Glu Gln Glu
 35 40 45
 Leu Pro Gln Pro Gln Ala Glu Thr Gly Ser Gly Thr Glu Ser Asp Ser
 50 55 60
 Asp Glu Ser Val Pro Glu Leu Glu Glu Gln Asp Ser Thr Gln Ala Thr
 65 70 75 80

859

Thr Gln Gln Ala Gln Leu Ala Ala Ala Glu Ile Asp Glu Glu Pro
85 90 95

Val Ser Lys Ala Lys Gln Ser Arg Ser Glu Lys Lys Ala Arg Lys Ala
100 105 110

Met Ser Lys Leu Gly Leu Arg Gln Val Thr Gly Val Thr Arg Val Thr
115 120 125

Ile Arg Lys Ser Lys Asn Ile Leu Phe Val Ile Thr Lys Pro Asp Val
130 135 140

Tyr Lys Ser Pro Ala Ser Asp Thr Tyr Ile Val Phe Gly Glu Ala Lys
145 150 155 160

Ile Glu Asp Leu Ser Gln Gln Ala Gln Leu Ala Ala Ala Glu Lys Phe
165 170 175

Lys Val Gln Gly Glu Ala Val Ser Asn Ile Gln Glu Asn Thr Gln Thr
180 185 190

Pro Thr Val Gln Glu Glu Ser Glu Glu Glu Glu Val Asp Glu Thr Gly
195 200 205

Val Glu Val Lys Asp Ile Glu Leu Val Met Ser Gln Ala Asn Val Ser
210 215 220

Arg Ala Lys Ala Val Arg Ala Leu Lys Asn Asn Ser Asn Asp Ile Val
225 230 235 240

Asn Ala Ile Met Glu Leu Thr Met
245

<210> 909

<211> 161

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (46)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (158)

<223> Xaa equals any of the naturally occurring L-amino acids

860

<400> 909

Gln Gly Cys Cys Tyr Gly Ala Gly Arg Arg Val Ala Arg Leu Leu Ala
 1 5 10 15

Pro Leu Met Trp Arg Arg Ala Val Ser Ser Val Ala Gly Ser Ala Val
 20 25 30

Gly Ala Glu Pro Gly Leu Arg Leu Leu Ala Val Gln Arg Xaa Pro Val
 35 40 45

Glu Gln Arg Ser Ala Gly Leu Ala Arg Pro Gln Thr Leu Ser Ala Ala
 50 55 60

Cys Thr Ala Lys Pro Gly Leu Glu Glu Arg Ala Glu Gly Thr Val Asn
 65 70 75 80

Glu Gly Arg Pro Glu Ser Asp Ala Ala Asp His Thr Gly Pro Lys Phe
 85 90 95

Asp Ile Asp Met Met Val Ser Leu Leu Arg Gln Glu Asn Ala Arg Asp
 100 105 110

Ile Cys Val Ile Gln Val Pro Pro Glu Met Arg Tyr Thr Asp Tyr Phe
 115 120 125

Val Ile Val Ser Gly Thr Ser Thr Arg His Leu His Ala Met Ala Phe
 130 135 140

Tyr Val Val Lys Met Tyr Lys His Leu Lys Cys Lys Arg Xaa Pro Ser
 145 150 155 160

Cys

<210> 910

<211> 487

<212> PRT

<213> Homo sapiens

<400> 910

Lys Ala Ala Ser Gly Pro Ala Thr Ser Ile Thr Gly Val Thr Met Gly
 1 5 10 15

Ala Val Leu Gly Val Phe Ser Leu Ala Ser Trp Val Pro Cys Leu Cys
 20 25 30

Ser Gly Ala Ser Cys Leu Leu Cys Ser Cys Cys Pro Asn Ser Lys Asn
 35 40 45

Ser Thr Val Thr Arg Leu Ile Tyr Ala Phe Ile Leu Leu Leu Ser Thr
 50 55 60
 Val Val Ser Tyr Ile Met Gln Arg Lys Glu Met Glu Thr Tyr Leu Lys
 65 70 75 80
 Lys Ile Pro Gly Phe Cys Glu Gly Gly Phe Lys Ile His Glu Ala Asp
 85 90 95
 Ile Asn Ala Asp Lys Asp Cys Asp Val Leu Val Gly Tyr Lys Ala Val
 100 105 110
 Tyr Arg Ile Ser Phe Ala Met Ala Ile Phe Phe Phe Val Phe Ser Leu
 115 120 125
 Leu Met Phe Lys Val Lys Thr Ser Lys Asp Leu Arg Ala Ala Val His
 130 135 140
 Asn Gly Phe Trp Phe Phe Lys Ile Ala Ala Leu Ile Gly Ile Met Val
 145 150 155 160
 Gly Ser Phe Tyr Ile Pro Gly Gly Tyr Phe Ser Ser Val Trp Phe Val
 165 170 175
 Val Gly Met Ile Gly Ala Ala Leu Phe Ile Leu Ile Gln Leu Val Leu
 180 185 190
 Leu Val Asp Phe Ala His Ser Trp Asn Glu Ser Trp Val Asn Arg Met
 195 200 205
 Glu Glu Gly Asn Pro Arg Leu Trp Tyr Ala Ala Leu Leu Ser Phe Thr
 210 215 220
 Ser Ala Phe Tyr Ile Leu Ser Ile Ile Cys Val Gly Leu Leu Tyr Thr
 225 230 235 240
 Tyr Tyr Thr Lys Pro Asp Gly Cys Thr Glu Asn Lys Phe Phe Ile Ser
 245 250 255
 Ile Asn Leu Ile Leu Cys Val Val Ala Ser Ile Ile Ser Ile His Pro
 260 265 270
 Lys Ile Gln Glu His Gln Pro Arg Ser Gly Leu Leu Gln Ser Ser Leu
 275 280 285
 Ile Thr Leu Tyr Thr Met Tyr Leu Thr Trp Ser Ala Met Ser Asn Glu
 290 295 300
 Pro Asp Arg Ser Cys Asn Pro Asn Leu Met Ser Phe Ile Thr Arg Ile
 305 310 315 320

862

Thr Ala Pro Thr Leu Ala Pro Gly Asn Ser Thr Ala Val Val Pro Thr
 325 330 335
 Pro Thr Pro Pro Ser Lys Ser Gly Ser Leu Leu Asp Ser Asp Asn Phe
 340 345 350
 Ile Gly Leu Phe Val Phe Val Leu Cys Leu Leu Tyr Ser Ser Ile Arg
 355 360 365
 Thr Ser Thr Asn Ser Gln Val Asp Lys Leu Thr Leu Ser Gly Ser Asp
 370 375 380
 Ser Val Ile Leu Gly Asp Thr Thr Thr Ser Gly Ala Ser Asp Glu Glu
 385 390 395 400
 Asp Gly Gln Pro Arg Arg Ala Val Asp Asn Glu Lys Glu Gly Val Gln
 405 410 415
 Tyr Ser Tyr Ser Leu Phe His Leu Met Leu Cys Leu Ala Ser Leu Tyr
 420 425 430
 Ile Met Met Thr Leu Thr Ser Trp Tyr Ser Pro Asp Ala Lys Phe Gln
 435 440 445
 Ser Met Thr Ser Lys Trp Pro Ala Val Trp Val Lys Ile Ser Ser Ser
 450 455 460
 Trp Val Cys Leu Leu Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val
 465 470 475 480
 Leu Thr Ser Arg Asp Phe Ser
 485

<210> 911

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (69)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 911

Asp Pro Arg Val Arg His Arg Gly Asn Lys Val Val Lys Lys Val
 1 5 10 15

Leu Val Arg Cys Arg His Phe Ile Cys Pro His Ser Leu Arg Leu Ser
 20 25 30

863

Gln Ser Phe Gln Gln Arg Tyr Val Gly Pro Glu His Pro Glu Phe Thr
 35 40 45
 Thr Ser Val Val Arg Arg Ala Thr Met Arg Arg Ala Leu Gly Arg Ile
 50 55 60
 Cys His Phe Gln Xaa Val Arg Gly Thr Ala Ser Leu Gly Glu Gly Ala
 65 70 75 80
 Leu Gly Cys Asp Ser Arg Thr Cys Lys Ala Ala Ser Gly Leu Trp Arg
 85 90 95
 Gly Arg

<210> 912

<211> 206

<212> PRT

<213> Homo sapiens

<400> 912

Phe Ser Leu Phe Pro Leu Ala Lys Ser Phe Asp Asp Gly Asp Tyr Phe
 1 5 10 15
 Pro Val Trp Gly Thr Cys Leu Gly Phe Glu Glu Leu Ser Leu Leu Ile
 20 25 30
 Ser Gly Glu Cys Leu Leu Thr Ala Thr Asp Thr Val Asp Val Ala Met
 35 40 45
 Pro Leu Asn Phe Thr Gly Gly Gln Leu His Ser Arg Met Phe Gln Asn
 50 55 60
 Phe Pro Thr Glu Leu Leu Leu Ser Leu Ala Val Glu Pro Leu Thr Ala
 65 70 75 80
 Asn Phe His Lys Trp Ser Leu Ser Val Lys Asn Phe Thr Met Asn Glu
 85 90 95
 Lys Leu Lys Lys Phe Phe Asn Val Leu Thr Thr Asn Thr Asp Gly Lys
 100 105 110
 Ile Glu Phe Ile Ser Thr Met Glu Gly Tyr Lys Tyr Pro Val Tyr Gly
 115 120 125
 Val Gln Trp His Pro Glu Lys Ala Pro Tyr Glu Trp Lys Asn Leu Asp
 130 135 140

864

Gly Ile Ser His Ala Pro Asn Ala Val Lys Thr Ala Phe Tyr Leu Ala
145 150 155 160

Glu Phe Phe Val Asn Glu Ala Arg Lys Asn Asn His His Phe Lys Ser
165 170 175

Glu Ser Glu Glu Glu Lys Ala Leu Ile Tyr Gln Phe Ser Pro Ile Tyr
180 185 190

Thr Gly Asn Ile Ser Ser Phe Gln Gln Cys Tyr Ile Phe Asp
195 200 205

<210> 913

<211> 91

<212> PRT

<213> Homo sapiens

<400> 913

Phe Ser Gly Pro Cys Pro Val Asn Thr Leu Gly Trp Glu Val Ser Ser
1 5 10 15

Phe Ser Pro Leu Leu Ser Ser Cys Leu Asn Met Val Arg Thr Lys Ala
20 25 30

Asp Ser Val Pro Gly Thr Tyr Arg Lys Val Val Ala Ala Arg Ala Pro
35 40 45

Arg Lys Val Leu Gly Ser Ser Thr Ser Ala Thr Asn Ser Thr Ser Val
50 55 60

Ser Ser Arg Lys Glu His Val Leu Cys Asn Leu Ile Thr Gln Met Met
65 70 75 80

Lys Lys Asn Arg Thr Phe Ser Phe Ile Phe Glu
85 90

<210> 914

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (132)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

865

<221> SITE

<222> (147)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (154)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 914

Arg Glu Leu Ser Thr Arg Gln Arg Ser Gln Ala Lys Pro Pro Ala Ser
 1 5 10 15

Met Ala Ser Glu Phe Lys Lys Lys Leu Phe Trp Arg Ala Val Val Ala
 20 25 30

Glu Phe Leu Ala Thr Thr Leu Phe Val Phe Ile Ser Ile Gly Ser Ala
 35 40 45

Leu Gly Phe Lys Tyr Pro Val Gly Asn Asn Gln Thr Ala Val Gln Asp
 50 55 60

Asn Val Lys Val Ser Leu Ala Phe Gly Leu Ser Ile Ala Thr Leu Ala
 65 70 75 80

Gln Ser Val Gly His Ile Ser Gly Ala His Leu Asn Pro Ala Val Thr
 85 90 95

Leu Gly Leu Leu Leu Ser Cys Gln Ile Ser Ile Phe Arg Ala Leu Met
 100 105 110

Tyr Ile Ile Ala Gln Cys Val Gly Ala Ile Val Ala Thr Ala Ile Leu
 115 120 125

Ser Gly Ile Xaa Ser Ser Leu Thr Gly Asn Ser Leu Gly Arg Asn Asp
 130 135 140

Leu Ala Xaa Gly Val Asn Phe Gly Pro Xaa Pro Gly His Arg Asp His
 145 150 155 160

Arg Asp Pro Pro Ala Gly Ala Met Arg Ala Gly Tyr Tyr Arg Pro Glu
 165 170 175

Ala Pro

<210> 915

<211> 377

<212> PRT

866

<213> Homo sapiens

<220>

<221> SITE

<222> (355)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 915

Val Cys Ala His Gly Gln Gly Leu Leu Arg Tyr Phe Tyr Ser Arg Arg
1 5 10 15

Ile Asp Ile Thr Leu Ser Ser Val Lys Cys Phe His Lys Leu Ala Ser
20 25 30

Ala Tyr Gly Ala Arg Gln Leu Gln Gly Tyr Cys Ala Ser Leu Phe Ala
35 40 45

Ile Leu Leu Pro Gln Asp Pro Ser Phe Gln Met Pro Leu Asp Leu Tyr
50 55 60

Ala Tyr Ala Val Ala Thr Gly Asp Ala Leu Leu Glu Lys Leu Cys Leu
65 70 75 80

Gln Phe Leu Ala Trp Asn Phe Glu Ala Leu Thr Gln Ala Glu Ala Trp
85 90 95

Pro Ser Val Pro Thr Asp Leu Leu Gln Leu Leu Leu Pro Arg Ser Asp
100 105 110

Leu Ala Val Pro Ser Glu Leu Ala Leu Leu Lys Ala Val Asp Thr Trp
115 120 125

Ser Trp Gly Glu Arg Ala Ser His Glu Glu Val Glu Gly Leu Val Glu
130 135 140

Lys Ile Arg Phe Pro Met Met Leu Pro Glu Glu Leu Phe Glu Leu Gln
145 150 155 160

Phe Asn Leu Ser Leu Tyr Trp Ser His Glu Ala Leu Phe Gln Lys Lys
165 170 175

Thr Leu Gln Ala Leu Glu Phe His Thr Val Pro Phe Gln Leu Leu Ala
180 185 190

Arg Tyr Lys Gly Leu Asn Leu Thr Glu Asp Thr Tyr Lys Pro Arg Ile
195 200 205

Tyr Thr Ser Pro Thr Trp Ser Ala Phe Val Thr Asp Ser Ser Trp Ser
210 215 220

Ala Arg Lys Ser Gln Leu Val Tyr Gln Ser Arg Arg Gly Pro Leu Val

867

225 230 235 240
 Lys Tyr Ser Ser Asp Tyr Phe Gln Ala Pro Ser Asp Tyr Arg Tyr Tyr
 245 250 255
 Pro Tyr Gln Ser Phe Gln Thr Pro Gln His Pro Ser Phe Leu Phe Gln
 260 265 270
 Asp Lys Arg Val Ser Trp Ser Leu Val Tyr Leu Pro Thr Ile Gln Ser
 275 280 285
 Cys Trp Asn Tyr Gly Phe Ser Cys Ser Ser Asp Glu Leu Pro Val Leu
 290 295 300
 Gly Leu Thr Lys Ser Gly Gly Ser Asp Arg Thr Ile Ala Tyr Glu Asn
 305 310 315 320
 Lys Ala Leu Met Leu Cys Glu Gly Leu Phe Val Ala Asp Val Thr Asp
 325 330 335
 Phe Glu Gly Trp Lys Ala Ala Ile Pro Ser Ala Leu Asp Thr Asn Ser
 340 345 350
 Ser Lys Xaa Thr Ser Ser Phe Pro Cys Pro Ala Gly Thr Ser Thr Ala
 355 360 365
 Ser Ala Arg Ser Ser Ala Pro Ser Thr
 370 375

<210> 916

<211> 100

<212> PRT

<213> Homo sapiens

<400> 916

Arg Val Gln Arg Asp Thr Cys Leu Pro Pro Met Ser Leu Ser Phe His
 1 5 10 15
 Leu Pro Ser Arg Arg Met Lys Asn Pro Ser Ile Val Gly Val Leu Cys
 20 25 30
 Thr Asp Ser Gln Gly Leu Asn Leu Gly Cys Arg Gly Thr Leu Ser Asp
 35 40 45
 Glu His Ala Gly Val Ile Ser Val Leu Ala Gln Gln Ala Ala Lys Leu
 50 55 60
 Thr Ser Asp Pro Thr Asp Ile Pro Val Val Cys Leu Glu Ser Asp Asn
 65 70 75 80

868

Gly Asn Ile Met Ile Gln Lys His Asp Gly Ile Thr Val Ala Val His
 85 90 95

Lys Met Ala Ser
 100

<210> 917

<211> 245

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (44)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (64)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (87)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (172)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (240)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (242)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 917

Leu Pro Pro Arg Ser Val Gly Gly Leu Lys Met Arg Arg Lys Leu
 1 5 10 15

Gly Leu Val Gln Val Glu Leu Glu Glu Asp Gly Ala Leu Val Ser Lys
 20 25 30

869

Leu Leu Glu Thr Met His Leu Thr Gly Ala Asp Xaa Thr Asn Thr Phe
 35 40 45
 Tyr Leu Leu Ser Ser Phe Pro Val Glu Leu Glu Ser Pro Gly Leu Xaa
 50 55 60
 Glu Phe Leu Ala Arg Leu Met Glu Gln Cys Ala Ser Leu Glu Glu Leu
 65 70 75 80
 Arg Leu Ala Phe Arg Pro Xaa Met Asp Pro Arg Gln Leu Ser Met Met
 85 90 95
 Leu Met Leu Ala Gln Ser Asn Pro Gln Leu Phe Ala Leu Met Gly Thr
 100 105 110
 Arg Ala Gly Ile Ala Arg Glu Leu Glu Arg Val Glu Gln Gln Ser Arg
 115 120 125
 Leu Glu Gln Leu Ser Ala Ala Glu Leu Gln Ser Arg Asn Gln Gly His
 130 135 140
 Trp Ala Asp Trp Leu Gln Ala Tyr Arg Ala Arg Leu Asp Lys Asp Leu
 145 150 155 160
 Glu Gly Ala Gly Asp Ala Ala Ala Trp Gln Ala Xaa Ala Arg Ala Arg
 165 170 175
 Asp Ala Arg Gln Gln Pro Glu Val Arg Ala Glu Glu Leu His Ser Arg
 180 185 190
 Arg Met Pro Phe Glu Val Ala Glu Arg Gly Asp Phe Ser Glu Val Arg
 195 200 205
 Arg Val Leu Lys Leu Phe Glu Thr Leu Tyr His Cys Glu Ala Gly Ala
 210 215 220
 Ala Thr Arg Arg Pro Arg Pro Arg Glu Ala Asp Gly Gly Gly Arg Xaa
 225 230 235 240
 Gly Xaa Phe Leu Thr
 245

<210> 918

<211> 44

<212> PRT

<213> Homo sapiens

<400> 918

Asn Ser Ala Arg Arg Ile Ser Leu Lys Glu Gly Glu Gly Lys Thr Asp

870

1 5 10 15
 Phe Leu Cys Gly Thr Lys Thr Lys Pro Ser Val Ser Leu Cys Glu Gln
 20 25 30
 Arg Cys Lys Lys Glu Glu Thr Gln Phe Thr His Gly
 35 40

 <210> 919
 <211> 160
 <212> PRT
 <213> Homo sapiens

 <400> 919
 Phe Gly Thr Arg Val Thr Ser Gly Gly Ser Arg Asp Ala Val Pro Gly
 1 5 10 15
 Ala Glu Pro Pro Lys Met Ala Val Cys Ile Ala Val Ile Ala Lys Glu
 20 25 30
 Asn Tyr Pro Leu Tyr Ile Arg Ser Thr Pro Thr Glu Asn Glu Leu Lys
 35 40 45
 Phe His Tyr Met Val His Thr Ser Leu Asp Val Val Asp Glu Lys Ile
 50 55 60
 Ser Ala Met Gly Lys Ala Leu Val Asp Gln Arg Glu Leu Tyr Leu Gly
 65 70 75 80
 Leu Leu Tyr Pro Thr Glu Asp Tyr Lys Val Tyr Gly Tyr Val Thr Asn
 85 90 95
 Ser Lys Val Lys Phe Val Met Val Val Asp Ser Ser Asn Thr Ala Leu
 100 105 110
 Arg Asp Asn Glu Ile Arg Ser Met Phe Arg Lys Leu His Asn Ser Tyr
 115 120 125
 Thr Asp Val Met Cys Asn Pro Phe Tyr Asn Pro Gly Asp Arg Ile Gln
 130 135 140
 Ser Arg Ala Phe Asp Asn Met Val Thr Ser Met Met Ile Gln Val Cys
 145 150 155 160

871

<210> 920

<211> 40

<212> PRT

<213> Homo sapiens

<400> 920

Leu Ala Phe Phe Leu Thr Ser Glu Gly Glu Lys Lys Val Ala Thr Tyr
1 5 10 15

Met Phe Glu Lys Pro Leu Lys Ser Thr Gln Ser Lys Asp Phe Met Leu
20 25 30

Gln Phe Gly His Met Leu Arg Val
35 40

<210> 921

<211> 372

<212> PRT

<213> Homo sapiens

<400> 921

Leu Leu Gly Pro Ala Gly Gln Arg Ser His Ala Ala Pro Met Arg Pro
1 5 10 15

Leu Pro Pro Val Gly Asp Val Arg Leu Glu Leu Ser Pro Pro Pro Pro
20 25 30

Leu Leu Pro Val Pro Val Val Ser Gly Ser Pro Val Gly Ser Ser Gly
35 40 45

Arg Leu Met Ala Ser Ser Ser Ser Leu Val Pro Asp Arg Leu Arg Leu
50 55 60

Pro Leu Cys Phe Leu Gly Val Phe Val Cys Tyr Phe Tyr Tyr Gly Ile
65 70 75 80

Leu Gln Glu Lys Ile Thr Arg Gly Lys Tyr Gly Glu Gly Ala Lys Gln
85 90 95

Glu Thr Phe Thr Phe Ala Leu Thr Leu Val Phe Ile Gln Cys Val Ile
100 105 110

Asn Ala Val Phe Ala Lys Ile Leu Ile Gln Phe Phe Asp Thr Ala Arg
115 120 125

Val Asp Arg Thr Arg Ser Trp Leu Tyr Ala Ala Cys Ser Ile Ser Tyr
130 135 140

Leu Gly Ala Met Val Ser Ser Asn Ser Ala Leu Gln Phe Val Asn Tyr

872

145	150	155	160
Pro Thr Gln Val Leu Gly Lys Ser Cys Lys Pro Ile Pro Val Met Leu			
	165	170	175
Leu Gly Val Thr Leu Leu Lys Lys Lys Tyr Pro Leu Ala Lys Tyr Leu			
	180	185	190
Cys Val Leu Leu Ile Val Ala Gly Val Ala Leu Phe Met Tyr Lys Pro			
	195	200	205
Lys Lys Val Val Gly Ile Glu Glu His Thr Val Gly Tyr Gly Glu Leu			
	210	215	220
Leu Leu Leu Leu Ser Leu Thr Leu Asp Gly Leu Thr Gly Val Ser Gln			
	225	230	235
Asp His Met Arg Ala His Tyr Gln Thr Gly Ser Asn His Met Met Leu			
	245	250	255
Asn Ile Asn Leu Trp Ser Thr Leu Leu Leu Gly Met Gly Ile Leu Phe			
	260	265	270
Thr Gly Glu Leu Trp Glu Phe Leu Ser Phe Ala Glu Arg Tyr Pro Ala			
	275	280	285
Ile Ile Tyr Asn Ile Leu Leu Phe Gly Leu Thr Ser Ala Leu Gly Gln			
	290	295	300
Ser Phe Ile Phe Met Thr Val Val Tyr Phe Gly Pro Leu Thr Cys Ser			
	305	310	315
Ile Ile Thr Thr Thr Arg Lys Phe Phe Thr Ile Leu Ala Ser Val Ile			
	325	330	335
Leu Phe Ala Asn Pro Ile Ser Pro Met Gln Trp Val Gly Thr Val Leu			
	340	345	350
Val Phe Leu Gly Leu Gly Leu Asp Ala Lys Phe Gly Lys Gly Ala Lys			
	355	360	365
Lys Thr Ser His			
	370		

<210> 922

<211> 363

<212> PRT

<213> Homo sapiens

873

<400> 922

Pro Ala Arg Thr Met Phe Tyr Ala His Phe Val Leu Ser Lys Arg Gly
1 5 10 15

Pro Leu Ala Lys Ile Trp Leu Ala Ala His Trp Asp Lys Lys Leu Thr
20 25 30

Lys Ala His Val Phe Glu Cys Asn Leu Glu Ser Ser Val Glu Ser Ile
35 40 45

Ile Ser Pro Lys Val Lys Met Ala Leu Arg Thr Ser Gly His Leu Leu
50 55 60

Leu Gly Val Val Arg Ile Tyr His Arg Lys Ala Lys Tyr Leu Leu Ala
65 70 75 80

Asp Cys Asn Glu Ala Phe Ile Lys Ile Lys Met Ala Phe Arg Pro Gly
85 90 95

Val Val Asp Leu Pro Glu Glu Asn Arg Glu Ala Ala Tyr Asn Ala Ile
100 105 110

Thr Leu Pro Glu Glu Phe His Asp Phe Asp Gln Pro Leu Pro Asp Leu
115 120 125

Asp Asp Ile Asp Val Ala Gln Gln Phe Ser Leu Asn Gln Ser Arg Val
130 135 140

Glu Glu Ile Thr Met Arg Glu Glu Val Gly Asn Ile Ser Ile Leu Gln
145 150 155 160

Glu Asn Asp Phe Gly Asp Phe Gly Met Asp Asp Arg Glu Ile Met Arg
165 170 175

Glu Gly Ser Ala Phe Glu Asp Asp Asp Met Leu Val Ser Thr Thr Thr
180 185 190

Ser Asn Leu Leu Leu Glu Ser Glu Gln Ser Thr Ser Asn Leu Asn Glu
195 200 205

Lys Ile Asn His Leu Glu Tyr Glu Asp Gln Tyr Lys Asp Asp Asn Phe
210 215 220

Gly Glu Gly Asn Asp Gly Gly Ile Leu Asp Asp Lys Leu Ile Ser Asn
225 230 235 240

Asn Asp Gly Gly Ile Phe Asp Asp Pro Pro Ala Leu Ser Glu Ala Gly
245 250 255

Val Met Leu Pro Glu Gln Pro Ala His Asp Asp Met Asp Glu Asp Asp
260 265 270

874

Asn Val Ser Met Gly Gly Pro Asp Ser Pro Asp Ser Val Asp Pro Val
 275 280 285

Glu Pro Met Pro Thr Met Thr Asp Gln Thr Thr Leu Val Pro Asn Glu
 290 295 300

Glu Glu Ala Phe Ala Leu Glu Pro Ile Asp Ile Thr Val Lys Glu Thr
 305 310 315 320

Lys Ala Lys Arg Lys Arg Lys Leu Ile Val Asp Ser Val Lys Glu Leu
 325 330 335

Asp Ser Lys Thr Ile Arg Ala Gln Leu Ser Asp Tyr Ser Asp Ile Val
 340 345 350

Thr Thr Leu Asp Leu Ala Pro Pro Pro Arg Asn
 355 360

<210> 923

<211> 296

<212> PRT

<213> Homo sapiens

<400> 923

Val Ala Val Ile Trp Ala Tyr Trp Leu Gly Leu Lys Val Arg Arg Glu
 1 5 10 15

Tyr Arg Lys Phe Phe Arg Ala Asn Ala Gly Lys Lys Ile Tyr Glu Phe
 20 25 30

Thr Leu Gln Arg Ile Val Gln Lys Tyr Phe Leu Glu Met Lys Asn Lys
 35 40 45

Met Pro Ser Leu Ser Pro Ile Asp Lys Asn Trp Pro Ser Arg Pro Tyr
 50 55 60

Leu Phe Leu Asp Ser Thr His Lys Glu Leu Lys Arg Ile Phe His Leu
 65 70 75 80

Trp Arg Cys Lys Lys Tyr Arg Asp Gln Phe Thr Asp Gln Gln Lys Leu
 85 90 95

Ile Tyr Glu Glu Lys Leu Glu Ala Ser Glu Leu Phe Lys Asp Lys Lys
 100 105 110

Ala Leu Tyr Pro Ser Ser Val Gly Gln Pro Phe Gln Gly Ala Tyr Leu
 115 120 125

875

Glu Ile Asn Lys Asn Pro Lys Tyr Lys Lys Leu Lys Asp Ala Ile Glu
130 135 140

Glu Lys Ile Ile Ile Ala Glu Val Val Asn Lys Ile Asn Arg Ala Asn
145 150 155 160

Gly Lys Ser Thr Ser Arg Ile Phe Leu Leu Thr Asn Asn Asn Leu Leu
165 170 175

Leu Ala Asp Gln Lys Ser Gly Gln Ile Lys Ser Glu Val Pro Leu Val
180 185 190

Asp Val Thr Lys Val Ser Met Ser Ser Gln Asn Asp Gly Phe Phe Ala
195 200 205

Val His Leu Lys Glu Gly Ser Glu Ala Ala Ser Lys Gly Asp Phe Leu
210 215 220

Phe Ser Ser Asp His Leu Ile Glu Met Ala Thr Lys Leu Tyr Arg Thr
225 230 235 240

Thr Leu Ser Gln Thr Lys Gln Lys Leu Asn Ile Glu Ile Ser Asp Glu
245 250 255

Phe Leu Val Gln Phe Arg Gln Asp Lys Val Cys Val Lys Phe Ile Gln
260 265 270

Gly Asn Gln Lys Asn Gly Ser Val Pro Thr Cys Lys Arg Lys Asn Asn
275 280 285

Arg Leu Leu Glu Val Ala Val Pro
290 295

<210> 924

<211> 91

<212> PRT

<213> Homo sapiens

<400> 924

His Phe Ser Ile Asn Tyr Asn Gln Lys Ser Asp Leu Leu Lys Glu Lys
1 5 10 15

Ser Asp Cys Lys Ser Phe Gln Gly Gln Thr Ala Thr Glu Pro Pro Thr
20 25 30

Pro Lys Gln Glu Thr Leu Val Lys Val Gln Glu Ala Arg Arg Phe Ser
35 40 45

Pro Thr Lys Val Gln Leu Gly Asn Asp Ala Glu Arg Met Thr Thr Thr

876

50 55 60
Cys Asn Ser Arg Lys Met Leu Ala Ser Arg Val Arg Val Thr Ser Glu
65 70 75 80
Cys His Lys Ser Ser Leu Ser His Cys Leu Ile
85 90
<210> 925
<211> 159
<212> PRT
<213> Homo sapiens
<400> 925
Asn Ser Ala Arg Ala Gly Gly Arg Ala Val Leu Ser Gly Glu Pro Glu
1 5 10 15
Ala Asn Met Asp Gln Glu Thr Val Gly Asn Val Val Leu Leu Ala Ile
20 25 30
Val Thr Leu Ile Ser Val Val Gln Asn Gly Phe Phe Ala His Lys Val
35 40 45
Glu His Glu Ser Arg Thr Gln Asn Gly Arg Ser Phe Gln Arg Thr Gly
50 55 60
Thr Leu Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp
65 70 75 80
Ala Tyr Pro Thr Phe Leu Ala Val Leu Trp Ser Ala Gly Leu Leu Cys
85 90 95
Ser Gln Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg
100 105 110
Gln Lys Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro
115 120 125
Gly Tyr Ile Phe Gly Glu Thr His His Thr Leu Pro Val Pro His Val
130 135 140
Arg Cys Trp His Ile Gln Leu Leu Pro His Leu Leu Phe Arg Lys
145 150 155

<210> 926
<211> 303
<212> PRT

877

<213> Homo sapiens

<400> 926

Gly Ser Leu Ala Ser Pro Pro Ser Leu Gly Ser Met Gly Glu Lys Ser
 1 5 10 15

Glu Asn Cys Gly Val Pro Glu Asp Leu Leu Asn Gly Leu Lys Val Thr
 20 25 30

Asp Thr Gln Glu Ala Glu Cys Ala Gly Pro Pro Val Pro Asp Pro Lys
 35 40 45

Asn Gln His Ser Gln Ser Lys Leu Leu Arg Asp Asp Glu Ala His Leu
 50 55 60

Gln Glu Asp Gln Gly Glu Glu Glu Cys Phe His Asp Cys Ser Ala Ser
 65 70 75 80

Phe Glu Glu Glu Pro Gly Ala Asp Lys Val Glu Asn Lys Ser Asn Glu
 85 90 95

Asp Val Asn Ser Ser Glu Leu Asp Glu Glu Tyr Leu Ile Glu Leu Glu
 100 105 110

Lys Asn Met Ser Asp Glu Glu Lys Gln Lys Arg Arg Glu Glu Ser Thr
 115 120 125

Arg Leu Lys Glu Glu Gly Asn Glu Gln Phe Lys Lys Gly Asp Tyr Ile
 130 135 140

Glu Ala Glu Ser Ser Tyr Ser Arg Ala Leu Glu Met Cys Pro Ser Cys
 145 150 155 160

Phe Gln Lys Glu Arg Ser Ile Leu Phe Ser Asn Arg Ala Ala Ala Arg
 165 170 175

Met Lys Gln Asp Lys Lys Glu Met Ala Ile Asn Asp Cys Ser Lys Ala
 180 185 190

Ile Gln Leu Asn Pro Ser Tyr Ile Arg Ala Ile Leu Arg Arg Ala Glu
 195 200 205

Leu Tyr Glu Lys Thr Asp Lys Leu Asp Glu Ala Leu Glu Asp Tyr Lys
 210 215 220

Ser Ile Leu Glu Lys Asp Pro Ser Ile His Gln Ala Arg Glu Ala Cys
 225 230 235 240

Met Arg Leu Pro Lys Gln Ile Glu Glu Arg Asn Glu Arg Leu Lys Glu
 245 250 255

878

Glu Met Leu Gly Lys Leu Lys Asp Leu Gly Asn Leu Val Leu Arg Pro
260 265 270

Phe Gly Leu Ser Thr Glu Asn Phe Gln Ile Lys Gln Asp Ser Ser Thr
275 280 285

Gly Ser Tyr Ser Ile Asn Phe Val Gln Asn Pro Asn Asn Asn Arg
290 295 300

<210> 927

<211> 329

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 927

Xaa Gly Gly Cys Cys Ser Gly Pro Gly His Ser Lys Arg Arg Arg Gln
1 5 10 15

Ala Pro Gly Val Gly Ala Val Gly Gly Gly Ser Pro Glu Arg Glu Glu
20 25 30

Val Gly Ala Gly Tyr Asn Ser Glu Asp Glu Tyr Glu Ala Ala Ala Ala
35 40 45

Arg Ile Glu Ala Met Asp Pro Ala Thr Val Glu Gln Gln Glu His Trp
50 55 60

Phe Glu Lys Ala Leu Arg Asp Lys Lys Gly Phe Ile Ile Lys Gln Met
65 70 75 80

Lys Glu Asp Gly Ala Cys Leu Phe Arg Ala Val Ala Asp Gln Val Tyr
85 90 95

Gly Asp Gln Asp Met His Glu Val Val Arg Lys His Cys Met Asp Tyr
100 105 110

Leu Met Lys Asn Ala Asp Tyr Phe Ser Asn Tyr Val Thr Glu Asp Phe
115 120 125

Thr Thr Tyr Ile Asn Arg Lys Arg Lys Asn Asn Cys His Gly Asn His
130 135 140

Ile Glu Met Gln Ala Met Ala Glu Met Tyr Asn Arg Pro Val Glu Val
145 150 155 160

Tyr Gln Tyr Ser Thr Glu Pro Ile Asn Thr Phe His Gly Ile His Gln
165 170 175

Asn Glu Asp Glu Pro Ile Arg Val Ser Tyr His Arg Asn Ile His Tyr
180 185 190

Asn Ser Val Val Asn Pro Asn Lys Ala Thr Ile Gly Val Gly Leu Gly
195 200 205

Leu Pro Ser Phe Lys Pro Gly Phe Ala Glu Gln Ser Leu Met Lys Asn
210 215 220

Ala Ile Lys Thr Ser Glu Glu Ser Trp Ile Glu Gln Gln Met Leu Glu
225 230 235 240

Asp Lys Lys Arg Ala Thr Asp Trp Glu Ala Thr Asn Glu Ala Ile Glu
245 250 255

Glu Gln Val Ala Arg Glu Ser Tyr Leu Gln Trp Leu Arg Asp Gln Glu
260 265 270

Lys Gln Ala Arg Gln Val Arg Gly Pro Ser Gln Pro Arg Lys Ala Ser
275 280 285

Ala Thr Cys Ser Ser Ala Thr Ala Ala Ala Ser Ser Gly Leu Glu Glu
290 295 300

Trp Thr Ser Arg Ser Pro Arg Gln Glu Phe Gln Pro Arg His Leu Ser
305 310 315 320

Thr Leu Ser Cys Met Leu Asn Trp Ala
325

<210> 928

<211> 436

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (210)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (217)

<223> Xaa equals any of the naturally occurring L-amino acids

880

<220>

<221> SITE

<222> (262)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 928

Lys Arg Phe Leu Arg Asn Phe Lys Leu Leu Thr Lys Arg Glu Phe Trp
 1 5 10 15

Lys Glu Asn Gln Glu His Tyr His Ile Val Gln Lys Phe Leu Ile Leu
 20 25 30

Gly Asp Ile Asp Gly Leu Met Asp Glu Phe Ser Lys Trp Leu Ser Lys
 35 40 45

Ser Arg Asn Asn Leu Pro Gly His Leu Leu Arg Phe Met Thr His Leu
 50 55 60

Ile Leu Phe Phe Arg Thr Leu Gly Leu Gln Thr Lys Glu Glu Val Ser
 65 70 75 80

Ile Glu Val Leu Lys Thr Tyr Ile Gln Leu Leu Ile Arg Glu Lys His
 85 90 95

Thr Asn Leu Ile Ala Phe Tyr Thr Cys His Leu Pro Gln Asp Leu Ala
 100 105 110

Val Ala Gln Tyr Ala Leu Phe Leu Glu Ser Val Thr Glu Phe Glu Gln
 115 120 125

Arg His His Cys Leu Glu Leu Ala Lys Glu Ala Asp Leu Asp Val Ala
 130 135 140

Thr Ile Thr Lys Thr Val Val Glu Asn Ile Arg Lys Lys Asp Asn Gly
 145 150 155 160

Glu Phe Ser His His Asp Leu Ala Pro Ala Leu Asp Thr Gly Thr Thr
 165 170 175

Glu Glu Asp Arg Leu Lys Ile Asp Val Ile Asp Trp Leu Val Phe Asp
 180 185 190

Pro Ala Gln Arg Ala Glu Ala Leu Lys Gln Gly Asn Ala Ile Met Arg
 195 200 205

Lys Xaa Leu Ala Ser Lys Lys His Xaa Ala Ala Lys Glu Val Phe Val
 210 215 220

Lys Ile Pro Gln Asp Ser Ile Ala Glu Ile Tyr Asn Gln Cys Glu Glu
 225 230 235 240

881

Gln Gly Met Glu Ser Pro Leu Pro Ala Glu Asp Asp Asn Ala Ile Arg
245 250 255

Glu His Leu Cys Ile Xaa Ala Tyr Leu Glu Ala His Glu Thr Phe Asn
260 265 270

Glu Trp Phe Lys His Met Asn Ser Val Pro Gln Lys Pro Ala Leu Ile
275 280 285

Pro Gln Pro Thr Phe Thr Glu Lys Val Ala His Glu His Lys Glu Lys
290 295 300

Lys Tyr Glu Met Asp Phe Gly Ile Trp Lys Gly His Leu Asp Ala Leu
305 310 315 320

Thr Ala Asp Val Lys Glu Lys Met Tyr Asn Val Leu Leu Phe Val Asp
325 330 335

Gly Gly Trp Met Val Asp Val Arg Glu Asp Ala Lys Glu Asp His Glu
340 345 350

Arg Thr His Gln Met Val Leu Leu Arg Lys Leu Cys Leu Pro Met Leu
355 360 365

Cys Phe Leu Leu His Thr Ile Leu His Ser Thr Gly Gln Tyr Gln Glu
370 375 380

Cys Leu Gln Leu Ala Asp Met Val Ser Ser Glu Arg His Lys Leu Tyr
385 390 395 400

Leu Val Phe Ser Lys Glu Glu Leu Arg Lys Leu Leu Gln Lys Leu Arg
405 410 415

Glu Ser Ser Leu Met Leu Leu Asp Gln Gly Leu Asp Pro Leu Gly Tyr
420 425 430

Glu Ile Gln Leu
435

<210> 929

<211> 161

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (159)

<223> Xaa equals any of the naturally occurring L-amino acids

882

<400> 929

Asp Ala Asp Val Gln Phe Leu Ala Ser Val Leu Pro Pro Asp Thr Asp
 1 5 10 15

Pro Ala Phe Phe Glu His Leu Arg Ala Leu Asp Cys Ser Glu Val Thr
 20 25 30

Val Arg Ala Leu Pro Glu Gly Ser Leu Ala Phe Pro Gly Val Pro Leu
 35 40 45

Leu Gln Val Ser Gly Pro Leu Leu Val Val Gln Leu Leu Glu Thr Pro
 50 55 60

Leu Leu Cys Leu Val Ser Tyr Ala Ser Leu Val Ala Thr Asn Ala Ala
 65 70 75 80

Arg Leu Arg Leu Ile Ala Gly Pro Glu Lys Arg Leu Leu Glu Met Gly
 85 90 95

Leu Arg Arg Ala Gln Gly Pro Asp Gly Gly Leu Thr Ala Ser Thr Tyr
 100 105 110

Ser Tyr Leu Gly Gly Phe Asp Ser Ser Ser Asn Val Leu Ala Gly Gln
 115 120 125

Leu Arg Gly Val Pro Val Ala Gly Thr Leu Ala His Ser Phe Val Thr
 130 135 140

Ser Phe Ser Gly Ser Glu Val Pro Leu Thr Arg Cys Trp Gly Xaa Ser
 145 150 155 160

Leu

<210> 930

<211> 741

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

883

<220>

<221> SITE

<222> (282)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 930

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Leu Met Lys Ile Glu Ala Asn Xaa Asp His Met Gly Phe His Phe Thr
 1             5             10             15

Thr Gly Xaa Pro Ala Pro Ser Thr Glu Thr Glu Leu Asp Val Leu Leu
          20             25             30

Pro Thr Ala Thr Ser Leu Pro Ile Pro Arg Lys Ser Ala Thr Val Ile
          35             40             45

Pro Glu Ile Glu Gly Ile Lys Ala Glu Ala Lys Ala Leu Asp Asp Met
 50             55             60

Phe Glu Ser Ser Thr Leu Ser Asp Gly Gln Ala Ile Ala Asp Gln Ser
 65             70             75             80

Glu Ile Ile Pro Thr Leu Gly Gln Phe Glu Arg Thr Gln Glu Glu Tyr
          85             90             95

Glu Asp Lys Lys His Ala Gly Pro Ser Phe Gln Pro Glu Phe Ser Ser
          100             105             110

Gly Ala Glu Glu Ala Leu Val Asp His Thr Pro Tyr Leu Ser Ile Ala
          115             120             125

Thr Thr His Leu Met Asp Gln Ser Val Thr Glu Val Pro Asp Val Met
          130             135             140

Glu Gly Ser Asn Pro Pro Tyr Tyr Thr Asp Thr Thr Leu Ala Val Ser
          145             150             155             160

Thr Phe Ala Lys Leu Ser Ser Gln Thr Pro Ser Ser Pro Leu Thr Ile
          165             170             175

Tyr Ser Gly Ser Glu Ala Ser Gly His Thr Glu Ile Pro Gln Pro Ser
          180             185             190

Ala Leu Pro Gly Ile Asp Val Gly Ser Ser Val Met Ser Pro Gln Asp
          195             200             205

Ser Phe Lys Glu Ile His Val Asn Ile Glu Ala Thr Phe Lys Pro Ser
          210             215             220

Ser Glu Glu Tyr Leu His Ile Thr Glu Pro Pro Ser Leu Ser Pro Asp
          225             230             235             240

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884

Thr Lys Leu Glu Pro Ser Glu Asp Asp Gly Lys Pro Glu Leu Leu Glu
 245 250 255
 Glu Met Glu Ala Ser Pro Thr Glu Leu Ile Ala Val Glu Gly Thr Glu
 260 265 270
 Ile Leu Gln Asp Phe Gln Asn Lys Thr Xaa Gly Gln Val Ser Gly Glu
 275 280 285
 Ala Ile Lys Met Phe Pro Thr Ile Lys Thr Pro Glu Ala Gly Thr Val
 290 295 300
 Ile Thr Thr Ala Asp Glu Ile Glu Leu Glu Gly Ala Thr Gln Trp Pro
 305 310 315 320
 His Ser Thr Ser Ala Ser Ala Thr Tyr Gly Val Glu Ala Gly Val Val
 325 330 335
 Pro Trp Leu Ser Pro Gln Thr Ser Glu Arg Pro Thr Leu Ser Ser Ser
 340 345 350
 Pro Glu Ile Asn Pro Glu Thr Gln Ala Ala Leu Ile Arg Gly Gln Asp
 355 360 365
 Ser Thr Ile Ala Ala Ser Glu Gln Gln Val Ala Ala Arg Ile Leu Asp
 370 375 380
 Ser Asn Asp Gln Ala Thr Val Asn Pro Val Glu Phe Asn Thr Glu Val
 385 390 395 400
 Ala Thr Pro Pro Phe Ser Leu Leu Glu Thr Ser Asn Glu Thr Asp Phe
 405 410 415
 Leu Ile Gly Ile Asn Glu Glu Ser Val Glu Gly Thr Ala Ile Tyr Leu
 420 425 430
 Pro Gly Pro Asp Arg Cys Lys Met Asn Pro Cys Leu Asn Gly Gly Thr
 435 440 445
 Cys Tyr Pro Thr Glu Thr Ser Tyr Val Cys Thr Cys Val Pro Gly Tyr
 450 455 460
 Ser Gly Asp Gln Cys Glu Leu Asp Phe Asp Glu Cys His Ser Asn Pro
 465 470 475 480
 Cys Arg Asn Gly Ala Thr Cys Val Asp Gly Phe Asn Thr Phe Arg Cys
 485 490 495
 Leu Cys Leu Pro Ser Tyr Val Gly Ala Leu Cys Glu Gln Asp Thr Glu
 500 505 510

885

Thr Cys Asp Tyr Gly Trp His Lys Phe Gln Gly Gln Cys Tyr Lys Tyr
 515 520 525

Phe Ala His Arg Arg Thr Trp Asp Ala Ala Glu Arg Glu Cys Arg Leu
 530 535 540

Gln Gly Ala His Leu Thr Ser Ile Leu Ser His Glu Glu Gln Met Phe
 545 550 555 560

Val Asn Arg Val Gly His Asp Tyr Gln Trp Ile Gly Leu Asn Asp Lys
 565 570 575

Met Phe Glu His Asp Phe Arg Trp Thr Asp Gly Ser Thr Leu Gln Tyr
 580 585 590

Glu Asn Trp Arg Pro Asn Gln Pro Asp Ser Phe Phe Ser Ala Gly Glu
 595 600 605

Asp Cys Val Val Ile Ile Trp His Glu Asn Gly Gln Trp Asn Asp Val
 610 615 620

Pro Cys Asn Tyr His Leu Thr Tyr Thr Cys Lys Lys Gly Thr Val Ala
 625 630 635 640

Cys Gly Gln Pro Pro Val Val Glu Asn Ala Lys Thr Phe Gly Lys Met
 645 650 655

Lys Pro Arg Tyr Glu Ile Asn Ser Leu Ile Arg Tyr His Cys Lys Asp
 660 665 670

Gly Phe Ile Gln Arg His Leu Pro Thr Ile Arg Cys Leu Gly Asn Gly
 675 680 685

Arg Trp Ala Ile Pro Lys Ile Thr Cys Met Asn Pro Ser Ala Tyr Gln
 690 695 700

Arg Thr Tyr Ser Met Lys Tyr Phe Lys Asn Ser Ser Ser Ala Lys Asp
 705 710 715 720

Asn Ser Ile Asn Thr Ser Lys His Asp His Arg Trp Ser Arg Arg Trp
 725 730 735

Gln Glu Ser Arg Arg
 740

<210> 931

<211> 209

<212> PRT

<213> Homo sapiens

886

<220>

<221> SITE

<222> (28)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 931

Gly Lys Ala Gly Asp Gln Leu Val Pro Asp Asn Leu Lys Glu Thr Asp
1 5 10 15

Lys Glu Lys Gly Asn Val Val Leu Lys Gly Glu Xaa Ser Ala Arg Met
20 25 30

Lys Ile Pro Ser Asn Met Trp Val Glu Ala Trp Glu Thr Ala Lys Pro
35 40 45

Ile Pro Ala Arg Arg Gln Arg Arg Leu Phe Asp Asp Thr Arg Glu Ala
50 55 60

Glu Lys Val Leu His Tyr Leu Ala Ile Gln Lys Pro Ala Asp Leu Ala
65 70 75 80

Arg His Leu Leu Pro Cys Val Ile His Ala Ala Val Leu Lys Val Lys
85 90 95

Glu Glu Glu Ser Leu Glu Asn Ile Ser Ser Val Lys Lys Ile Ile Lys
100 105 110

Gln Ile Ile Ser His Ser Ser Lys Val Leu His Phe Pro Asn Pro Glu
115 120 125

Asp Lys Lys Leu Glu Glu Ile Ile His Gln Ile Thr Asn Val Glu Ala
130 135 140

Leu Ile Ala Arg Ala Arg Ser Leu Lys Ala Lys Phe Gly Thr Glu Lys
145 150 155 160

Cys Glu Gln Glu Glu Lys Glu Asp Leu Glu Arg Phe Val Ser Cys
165 170 175

Leu Leu Glu Gln Pro Glu Val Leu Val Thr Gly Ala Gly Arg Gly His
180 185 190

Ala Gly Arg Ile Ile His Lys Leu Phe Val Asn Ala Gln Arg Cys Gln
195 200 205

Leu

887

<210> 932
<211> 57
<212> PRT
<213> Homo sapiens

<400> 932
Leu Leu Glu Val Pro Glu Met Gly Leu Thr Phe Ile Lys Gln Ile Ala
1 5 10 15
Tyr Tyr Asp Leu Ala Ala Ala Thr Val Gln Leu His Ile Asn Ser Thr
20 25 30
Asp Gln Thr Ile Cys Ile Trp His His Leu Leu Thr His Asp Met Arg
35 40 45
Leu Phe Cys Ile Asn Cys Tyr Asp Gly
50 55

<210> 933
<211> 125
<212> PRT
<213> Homo sapiens

<400> 933
Ile Lys Glu Glu Ser Asp Tyr His Asp Leu Glu Ser Val Val Gln Gln
1 5 10 15
Val Glu Gln Asn Leu Glu Leu Met Thr Lys Arg Ala Val Lys Ala Glu
20 25 30
Asn His Val Val Lys Leu Lys Gln Glu Ile Ser Leu Leu Gln Ala Gln
35 40 45
Val Ser Asn Phe Gln Arg Glu Asn Glu Ala Leu Arg Cys Gly Gln Gly
50 55 60
Ala Ser Leu Thr Val Val Lys Gln Asn Ala Asp Val Ala Leu Gln Asn
65 70 75 80
Leu Arg Val Val Met Asn Ser Ala Gln Ala Ser Ile Lys Gln Leu Val
85 90 95
Ser Gly Ala Glu Thr Leu Asn Leu Val Ala Glu Ile Leu Lys Ser Ile
100 105 110
Asp Arg Ile Ser Glu Val Lys Asp Glu Glu Glu Asp Ser
115 120 125

888

<210> 934

<211> 306

<212> PRT

<213> Homo sapiens

<400> 934

Pro Thr Phe Ser Arg Ala Val Ala Thr Met Phe Ser Arg Ala Gly Val
1 5 10 15

Ala Gly Leu Ser Ala Trp Thr Leu Gln Pro Gln Trp Ile Gln Val Arg
20 25 30

Asn Met Ala Thr Leu Lys Asp Ile Thr Arg Arg Leu Lys Ser Ile Lys
35 40 45

Asn Ile Gln Lys Ile Thr Lys Ser Met Lys Met Val Ala Ala Ala Lys
50 55 60

Tyr Ala Arg Ala Glu Arg Glu Leu Lys Pro Ala Arg Ile Tyr Gly Leu
65 70 75 80

Gly Ser Leu Ala Leu Tyr Glu Lys Ala Asp Ile Lys Gly Pro Glu Asp
85 90 95

Lys Lys Lys His Leu Leu Ile Gly Val Ser Ser Asp Arg Gly Leu Cys
100 105 110

Gly Ala Ile His Ser Ser Ile Ala Lys Gln Met Lys Ser Glu Val Ala
115 120 125

Thr Leu Thr Ala Ala Gly Lys Glu Val Met Leu Val Gly Ile Gly Asp
130 135 140

Lys Ile Arg Gly Ile Leu Tyr Arg Thr His Ser Asp Gln Phe Leu Val
145 150 155 160

Ala Phe Lys Glu Val Gly Arg Lys Pro Pro Thr Phe Gly Asp Ala Ser
165 170 175

Val Ile Ala Leu Glu Leu Leu Asn Ser Gly Tyr Glu Phe Asp Glu Gly
180 185 190

Ser Ile Ile Phe Asn Lys Phe Arg Ser Val Ile Ser Tyr Lys Thr Glu
195 200 205

Glu Lys Pro Ile Phe Ser Leu Asn Thr Val Ala Ser Ala Asp Ser Met
210 215 220

Ser Ile Tyr Asp Asp Ile Asp Ala Asp Val Leu Gln Asn Tyr Gln Glu
225 230 235 240

889

Tyr Asn Leu Ala Asn Ile Ile Tyr Tyr Ser Leu Lys Glu Ser Thr Thr
245 250 255

Ser Glu Gln Ser Ala Arg Met Thr Ala Met Asp Asn Ala Ser Lys Asn
260 265 270

Ala Ser Glu Met Ile Asp Lys Leu Thr Leu Thr Phe Asn Arg Thr Arg
275 280 285

Gln Ala Val Ile Thr Lys Glu Leu Ile Glu Ile Ile Ser Gly Ala Ala
290 295 300

Ala Leu
305

<210> 935

<211> 135

<212> PRT

<213> Homo sapiens

<400> 935

Gly Ala Leu Cys Ala Ala Ser Val Pro Arg Cys Val Trp Ser Ser Ala
1 5 10 15

Gly Val Val Ala Leu Phe Glu Glu His Cys Ala Pro Leu Val Trp Val
20 25 30

Tyr Thr Tyr Glu Cys Cys His Tyr Met Cys Ser Ala Leu Leu Ser Leu
35 40 45

Ser Cys Pro Cys Pro Ala Pro Ser Glu Arg Ala Ala Gly Leu Cys Cys
50 55 60

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
65 70 75 80

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
85 90 95

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
100 105 110

Met Leu Arg Leu Asn Tyr Ser Leu Ile Ser Phe Pro Val Trp Lys Ile
115 120 125

Pro Asn Thr Lys Asp Gly Arg
130 135

890

<210> 936

<211> 284

<212> PRT

<213> Homo sapiens

<400> 936

Leu Ser Gly Thr Thr Tyr Ala Arg Ala Cys Arg Ser Gln Cys Ala Ser
 1 5 10 15

Ala Ala Gly Gly Cys Thr Gly Gly Ala Gly Gly Gly Gly Gly Gly Gly
 20 25 30

Gly Gly Trp Gly Gly Ala Gly Gly Lys Cys Cys Asp Ala Val Pro Gly
 35 40 45

Arg Gly Arg Arg Val Glu Ala Glu Tyr Gln Phe Pro Ser Gly Lys Ala
 50 55 60

Ala Met Ala Ile Phe Ser Val Tyr Val Val Asn Lys Ala Gly Gly Leu
 65 70 75 80

Ile Tyr Gln Leu Asp Ser Tyr Ala Pro Arg Ala Glu Ala Glu Lys Thr
 85 90 95

Phe Ser Tyr Pro Leu Asp Leu Leu Leu Lys Leu His Asp Glu Arg Val
 100 105 110

Leu Val Ala Phe Gly Gln Arg Asp Gly Ile Arg Val Gly His Ala Val
 115 120 125

Leu Ala Ile Asn Gly Met Asp Val Asn Gly Arg Tyr Thr Ala Asp Gly
 130 135 140

Lys Glu Val Leu Glu Tyr Leu Gly Asn Pro Ala Asn Tyr Pro Val Ser
 145 150 155 160

Ile Arg Phe Gly Arg Pro Arg Leu Thr Ser Asn Glu Lys Leu Met Leu
 165 170 175

Ala Ser Met Phe His Ser Leu Phe Ala Ile Gly Ser Gln Leu Ser Pro
 180 185 190

Glu Gln Gly Ser Ser Gly Ile Glu Met Leu Glu Thr Asp Thr Phe Lys
 195 200 205

Leu His Cys Tyr Gln Thr Leu Thr Gly Ile Lys Phe Val Val Leu Ala
 210 215 220

Asp Pro Arg Gln Ala Gly Ile Asp Ser Leu Leu Arg Lys Ile Tyr Glu

891

225 230 235 240
Ile Tyr Ser Asp Phe Ala Leu Lys Asn Pro Phe Tyr Ser Leu Glu Met
 245 250 255
Pro Ile Arg Cys Glu Leu Phe Asp Gln Asn Leu Lys Leu Ala Leu Glu
 260 265 270
Val Ala Glu Lys Ala Gly Thr Phe Gly Pro Gly Ser
 275 280

<210> 937
<211> 338
<212> PRT
<213> Homo sapiens

<400> 937
Pro Val Ser Pro Leu His Arg Glu Glu Gly Asp Lys Trp Gly Glu Val
1 5 10 15
Trp Cys Gln Met Gly Trp Arg Arg Lys Arg Val Pro Gln Arg Gly Arg
 20 25 30
Lys Ala Pro Pro Pro Gln Leu His Gly Asn Ile Asn Asn Leu Tyr Phe
 35 40 45
Pro Ile Arg Trp Arg Asp Arg Leu His Trp Asp Ser Pro Asn Pro Ala
 50 55 60
Ala Glu Cys Gln Arg Pro Arg Ser Thr Leu Val Ser Arg Lys Pro Gly
65 70 75 80
Pro Gly Arg Ile Thr Trp Asp Glu Leu Ala Ala Ser Gly Leu Pro Ser
 85 90 95
Cys Asp Ala Ala Val Asn Leu Ala Gly Glu Asn Ile Leu Asn Pro Leu
 100 105 110
Arg Arg Trp Asn Glu Thr Phe Gln Lys Glu Val Leu Gly Ser Arg Leu
 115 120 125
Glu Thr Thr Gln Leu Leu Ala Lys Ala Ile Thr Lys Ala Pro Gln Pro
130 135 140
Pro Lys Ala Trp Val Leu Val Thr Gly Val Ala Tyr Tyr Gln Pro Ser
145 150 155 160
Leu Thr Ala Glu Tyr Asp Glu Asp Ser Pro Gly Gly Asp Phe Asp Phe
 165 170 175

892

Phe Ser Asn Leu Val Thr Lys Trp Glu Ala Ala Arg Leu Pro Gly
180 185 190

Asp Ser Thr Arg Gln Val Val Val Arg Ser Gly Val Val Leu Gly Arg
195 200 205

Gly Gly Gly Ala Met Gly His Met Leu Leu Pro Phe Arg Leu Gly Leu
210 215 220

Gly Gly Pro Ile Gly Ser Gly His Gln Phe Phe Pro Trp Ile His Ile
225 230 235 240

Gly Asp Leu Ala Gly Ile Leu Thr His Ala Leu Glu Ala Asn His Val
245 250 255

His Gly Val Leu Asn Gly Val Ala Pro Ser Ser Ala Thr Asn Ala Glu
260 265 270

Phe Ala Gln Thr Phe Gly Ala Ala Leu Gly Arg Arg Ala Phe Ile Pro
275 280 285

Leu Pro Ser Ala Val Val Gln Ala Val Phe Gly Arg Gln Arg Ala Ile
290 295 300

Met Leu Leu Glu Gly Gln Lys Val Ile Pro Arg Arg Thr Leu Ala Thr
305 310 315 320

Gly Tyr Gln Tyr Ser Phe Pro Glu Leu Gly Ala Ala Leu Lys Glu Ile
325 330 335

Val Ala

<210> 938

<211> 321

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (31)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (164)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (220)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (221)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (238)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (263)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (267)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (268)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 938
 Cys Gln Glu Trp Val Pro Asp Arg Glu Ser Tyr Val Ser His Met Lys
 1 5 10 15
 Lys Ser His Gly Arg Thr Leu Lys Arg Tyr Pro Cys Arg Gln Xaa Glu
 20 25 30
 Gln Ser Phe His Thr Pro Asn Ser Leu Arg Lys His Ile Arg Asn Asn
 35 40 45
 His Asp Thr Val Lys Lys Phe Tyr Thr Cys Gly Tyr Cys Thr Glu Asp
 50 55 60
 Ser Pro Ser Phe Pro Arg Pro Ser Leu Leu Glu Ser His Ile Ser Leu
 65 70 75 80
 Met His Gly Ile Arg Asn Pro Asp Leu Ser Gln Thr Ser Lys Val Lys
 85 90 95
 Pro Pro Gly Gly His Ser Pro Gln Val Asn His Leu Lys Arg Pro Val
 100 105 110

894

Ser Gly Val Gly Asp Ala Pro Gly Thr Ser Asn Gly Ala Thr Val Ser
 115 120 125
 Ser Thr Lys Arg His Lys Ser Leu Phe Gln Cys Ala Lys Cys Ser Phe
 130 135 140
 Ala Thr Asp Ser Gly Leu Glu Phe Gln Ser His Ile Pro Gln His Gln
 145 150 155 160
 Val Gly Gln Xaa His Ser Pro Met Ser Pro Leu Trp Phe Val Leu His
 165 170 175
 Leu Cys Gln Leu Pro Gln Pro Pro Pro Leu His Cys Pro Gln Gly Glu
 180 185 190
 Arg Pro Gly Gly Gly Gly Gly Arg Gly Gly Gly Gly Thr Glu Met Ala
 195 200 205
 Val Glu Val Ala Glu Gln Arg Arg Ala Pro Gly Xaa Xaa Cys Pro Trp
 210 215 220
 Arg Leu Glu Arg Met Asp Trp Lys Asn Val Pro Val Ser Xaa Cys Gln
 225 230 235 240
 Leu Thr Gln Arg Arg Gly Asp Cys Trp Ala Arg Pro Leu Arg Thr Met
 245 250 255
 Val Ala Thr Met Ile Thr Xaa Asn His Arg Xaa Xaa Arg Thr Arg Thr
 260 265 270
 Ala Thr His Cys Pro Leu Arg Cys Asp Arg Arg Leu Cys Ser Val His
 275 280 285
 Gly Gln Gly Trp Cys Arg Ser Val Phe His Leu Pro Cys Gly Pro Trp
 290 295 300
 Lys Ile Lys Gly Ser Ala Pro Ser Val Ser Val Thr Gly Cys Thr Leu
 305 310 315 320
 Glu

<210> 939

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (71)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (81)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 939
Ala Ala Ser Xaa Gly Glu Gln Arg Glu Arg Ala Arg Leu Gln Thr Pro
1 5 10 15
Thr Arg Pro His Ser Thr Ser Ala Arg Pro Arg Arg Arg Gln Val Gln
20 25 30
Leu Leu Gln Leu Cys Gly Cys Ala Ala Lys Gly Xaa Ala His Gly Leu
35 40 45
Asp Val Thr Ser Pro Thr Val Ser Trp Leu Ala Cys Pro Cys Ala Arg
50 55 60
Pro Ser Xaa Ser Arg Gln Xaa Leu Gly Thr Ser Glu Glu Glu Pro Gly
65 70 75 80
Xaa Asn Gly Lys Gly Gly Ile Gly Val His His Ser Leu Leu Leu Trp
85 90 95
Ser Ser Thr Gly Gly Thr Xaa Met Glu Val Ser Cys Leu Thr Ser Leu
100 105 110

His Cys Thr Gly Pro Gly Met Pro Ile His Pro Leu Ala Glu Asp Thr
115 120 125

His Gln Val Ile Cys Glu Glu Thr Leu Gly Ser His His Leu Lys Ala
130 135 140

Arg Gly Ser Pro Ser His Arg
145 150

<210> 940
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 940
Arg Cys Gly Trp Ser Ser Arg Ser Arg Arg Ser Arg Cys Ala Arg Arg
1 5 10 15

Cys Pro Pro Ser Pro Cys Pro Thr Pro Arg His Val Pro Ser Ser Arg
20 25 30

His Pro Glu Val Cys Gly Leu Arg Thr Asn Ser His Arg Cys Leu Phe
35 40 45

Arg Pro Gln Leu Gln Ala Met Pro Ala Ala Gly Gly Val Leu Tyr Gln
50 55 60

Pro Ser Gly Pro Ala Ser Phe Pro Ser Thr Phe Ser Pro Ala Gly Ser
65 70 75 80

Val Glu Gly Ser Pro Met His Gly Val Tyr Met Ser Gln Pro Val Pro
85 90 95

Ala Ala Gly Pro Tyr Pro Xaa
100

<210> 941
<211> 136
<212> PRT
<213> Homo sapiens

<220>

897

<221> SITE

<222> (123)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 941

Thr Ala Gly Arg Ser Asp Val Leu Pro Val Ala Gly Gly Glu Val Arg
1 5 10 15

Ala Leu Gln Glu Gly Gly Cys Gly Asp Lys Met Lys Ile Phe Val Gly
20 25 30

Asn Val Asp Gly Ala Asp Thr Thr Pro Glu Glu Leu Ala Ala Leu Phe
35 40 45

Ala Pro Tyr Gly Thr Val Met Ser Cys Ala Val Met Lys Gln Phe Ala
50 55 60

Phe Val His Met Arg Glu Asn Ala Gly Ala Leu Arg Ala Ile Glu Ala
65 70 75 80

Leu His Gly His Glu Leu Arg Pro Gly Arg Ala Leu Val Val Glu Met
85 90 95

Ser Arg Pro Arg Pro Leu Asn Thr Trp Lys Ile Phe Val Gly Asn Val
100 105 110

Ser Ala Ala Cys Thr Ser Gln Glu Leu Arg Xaa Ser Ser Ser Ala Ala
115 120 125

Asp Ala Ser Ser Ser Val Thr Trp
130 135

<210> 942

<211> 61

<212> PRT

<213> Homo sapiens

<400> 942

Ile Met Lys Glu Ser Ser Ser Val Leu Ala Lys Cys Ser Ser Ile Ala
1 5 10 15

Gly Tyr Ile Gln Trp Ser Ser Ile Asn Ser Tyr Leu Ser Gly Leu Asn
20 25 30

Gln Asn Cys Val Ser Leu Asn Ser Tyr His Thr Glu Gly Ala Ser Gln
35 40 45

Ile Thr Ile Phe Leu Ser Ala Val Phe Leu Gln Lys Ser
50 55 60

<210> 943
<211> 580
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (73)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 943
Gly Ala Gln Ala Gln Ala Ser Ala Arg Pro Leu Gln Ala Phe Gly Ala
1 5 10 15
Arg Ala Arg Leu Gly Tyr Gly Pro Gly Arg Arg Arg Pro Pro Ser Ala
20 25 30
Arg Cys Leu Ser Gly Thr Ala Asn Arg Arg Glu Arg Arg Arg Val Gly
35 40 45
Leu Ser Ala Xaa Leu Gly Ala Gly Ala His Ala Arg Ala Pro Pro Gln
50 55 60
Ala Gly Ala Met Ala Ser Gly Ser Xaa Ala Glu Cys Leu Gln Gln Glu
65 70 75 80
Thr Thr Cys Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu
85 90 95
Asp Cys Gly His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly
100 105 110
Thr Ala Glu Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro
115 120 125
Gln Arg His Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu
130 135 140
Val Lys Gln Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met
145 150 155 160
Gly Val Cys Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu
165 170 175

899

Asp	Gln	Met	Pro	Ile	Cys	Val	Val	Cys	Asp	Arg	Ser	Arg	Glu	His	Arg			
			180						185					190				
Gly	His	Ser	Val	Leu	Pro	Leu	Glu	Glu	Ala	Val	Glu	Gly	Phe	Lys	Glu			
		195					200					205						
Gln	Ile	Gln	Asn	Gln	Leu	Asp	His	Leu	Lys	Arg	Val	Lys	Asp	Leu	Lys			
	210						215					220						
Lys	Arg	Arg	Arg	Ala	Gln	Gly	Glu	Gln	Ala	Arg	Ala	Glu	Leu	Leu	Ser			
225					230					235					240			
Leu	Thr	Gln	Met	Glu	Arg	Glu	Lys	Ile	Val	Trp	Glu	Phe	Glu	Gln	Leu			
				245					250					255				
Tyr	His	Ser	Leu	Lys	Glu	His	Glu	Tyr	Arg	Leu	Leu	Ala	Arg	Leu	Glu			
			260					265					270					
Glu	Leu	Asp	Leu	Ala	Ile	Tyr	Asn	Ser	Ile	Asn	Gly	Ala	Ile	Thr	Gln			
		275						280				285						
Phe	Ser	Cys	Asn	Ile	Ser	His	Leu	Ser	Ser	Leu	Ile	Ala	Gln	Leu	Glu			
		290				295					300							
Glu	Lys	Gln	Gln	Gln	Pro	Thr	Arg	Glu	Leu	Leu	Gln	Asp	Ile	Gly	Asp			
305					310					315					320			
Thr	Leu	Ser	Arg	Ala	Glu	Arg	Ile	Arg	Ile	Pro	Glu	Pro	Trp	Ile	Thr			
				325					330					335				
Pro	Pro	Asp	Leu	Gln	Glu	Lys	Ile	His	Ile	Phe	Ala	Gln	Lys	Cys	Leu			
			340					345					350					
Phe	Leu	Thr	Glu	Ser	Leu	Lys	Gln	Phe	Thr	Glu	Lys	Met	Gln	Ser	Asp			
		355					360					365						
Met	Glu	Lys	Ile	Gln	Glu	Leu	Arg	Glu	Ala	Gln	Leu	Tyr	Ser	Val	Asp			
	370					375					380							
Val	Thr	Leu	Asp	Pro	Asp	Thr	Ala	Tyr	Pro	Ser	Leu	Ile	Leu	Ser	Asp			
385					390					395					400			
Asn	Leu	Arg	Gln	Val	Arg	Tyr	Ser	Tyr	Leu	Gln	Gln	Asp	Leu	Pro	Asp			
			405						410				415					
Asn	Pro	Glu	Arg	Phe	Asn	Leu	Phe	Pro	Cys	Val	Leu	Gly	Ser	Pro	Cys			
		420					425						430					
Phe	Ile	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	Glu	Val	Gly	Asp	Lys	Ala			
	435						440					445						

900

Lys Trp Thr Ile Gly Val Cys Glu Asp Ser Val Cys Arg Lys Gly Gly
450 455 460

Val Thr Ser Ala Pro Gln Asn Gly Phe Trp Ala Val Ser Leu Trp Tyr
465 470 475 480

Gly Lys Glu Tyr Trp Ala Leu Thr Ser Pro Met Thr Ala Leu Pro Leu
485 490 495

Arg Thr Pro Leu Gln Arg Val Gly Ile Phe Leu Asp Tyr Asp Ala Gly
500 505 510

Glu Val Ser Phe Tyr Asn Val Thr Glu Arg Cys His Thr Phe Thr Phe
515 520 525

Ser His Ala Thr Phe Cys Gly Pro Val Arg Pro Tyr Phe Ser Leu Ser
530 535 540

Tyr Ser Gly Gly Lys Ser Ala Ala Pro Leu Ile Ile Cys Pro Met Ser
545 550 555 560

Gly Ile Asp Gly Phe Ser Gly His Val Gly Asn His Gly His Ser Met
565 570 575

Glu Thr Ser Pro
580

<210> 944

<211> 437

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (68)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (166)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (317)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 944

901

Ser Ala Thr Gly Ser Gly Glu Lys Glu Cys Gly Val Thr Ala Thr Phe
1 5 10 15

Asp Ala Ser Arg Thr Thr Phe Thr Arg Glu Gly Ser Phe Arg Val Thr
20 25 30

Thr Ala Thr Glu Gln Ala Glu Arg Glu Glu Ile Met Lys Gln Met Gln
35 40 45

Asp Ala Lys Lys Ala Glu Thr Asp Lys Ile Val Val Gly Ser Ser Val
50 55 60

Ala Pro Gly Xaa Thr Ala Pro Ser Pro Ser Ser Pro Thr Ser Pro Thr
65 70 75 80

Ser Asp Ala Thr Thr Ser Leu Glu Met Asn Asn Pro His Ala Ile Pro
85 90 95

Arg Arg His Ala Pro Ile Glu Gln Leu Ala Arg Gln Gly Ser Phe Arg
100 105 110

Gly Phe Pro Ala Leu Ser Gln Lys Met Ser Pro Phe Lys Arg Gln Leu
115 120 125

Ser Leu Arg Ile Asn Glu Leu Pro Ser Thr Met Gln Arg Lys Thr Asp
130 135 140

Phe Pro Ile Lys Asn Ala Val Pro Glu Val Glu Gly Glu Ala Glu Ser
145 150 155 160

Ile Ser Ser Leu Cys Xaa Gln Ile Thr Asn Ala Phe Ser Thr Pro Glu
165 170 175

Asp Pro Phe Ser Ser Ala Pro Met Thr Lys Pro Val Thr Val Val Ala
180 185 190

Pro Gln Ser Pro Thr Phe Gln Gly Thr Glu Trp Gly Gln Ser Ser Gly
195 200 205

Ala Ala Ser Pro Gly Leu Phe Gln Ala Gly His Arg Arg Thr Pro Ser
210 215 220

Glu Ala Asp Arg Trp Leu Glu Glu Val Ser Lys Ser Val Arg Ala Gln
225 230 235 240

Gln Pro Gln Ala Ser Ala Ala Pro Leu Gln Pro Val Leu Gln Pro Pro
245 250 255

Pro Pro Thr Ala Ile Ser Gln Pro Ala Ser Pro Phe Gln Gly Asn Ala
260 265 270

Phe Leu Thr Ser Gln Pro Val Pro Val Gly Val Val Pro Ala Leu Gln
275 280 285

Pro Ala Phe Val Pro Ala Gln Ser Tyr Pro Val Ala Asn Gly Met Pro
290 295 300

Tyr Pro Ala Pro Asn Val Pro Val Val Gly Ile Thr Xaa Ser Gln Met
305 310 315 320

Val Ala Asn Val Phe Gly Thr Ala Gly His Pro Gln Ala Ala His Pro
325 330 335

His Gln Ser Pro Ser Leu Val Arg Gln Gln Thr Phe Pro His Tyr Glu
340 345 350

Ala Ser Ser Ala Thr Thr Ser Pro Phe Phe Lys Pro Pro Ala Gln His
355 360 365

Leu Asn Gly Ser Ala Ala Phe Asn Gly Val Asp Asp Gly Arg Leu Ala
370 375 380

Ser Ala Asp Arg His Thr Glu Val Pro Thr Gly Thr Cys Pro Val Asp
385 390 395 400

Pro Phe Glu Ala Gln Trp Ala Ala Leu Glu Asn Lys Ser Lys Gln Arg
405 410 415

Thr Asn Pro Ser Pro Thr Asn Pro Phe Ser Ser Asp Leu Gln Lys Thr
420 425 430

Phe Glu Ile Glu Leu
435

<210> 945

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (119)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 945

His Gly Ser Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
1 5 10 15

Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly
20 25 30

Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp
 35 40 45
 Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro
 50 55 60
 Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys
 65 70 75 80
 Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly
 85 90 95
 Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys
 100 105 110
 Val Leu Gly Arg Leu Val Xaa Cys Pro Ile Glu Thr Gln Val Leu Arg
 115 120 125
 Glu Thr Gln Cys Leu Arg Val Gln Arg Ala Gly Glu Asp Pro His Ser
 130 135 140
 Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser Lys Ala Leu Pro Arg Ser
 145 150 155 160

<210> 946

<211> 221

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (198)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 946

Gly Gly Asp Pro Pro Gly Asp Leu Ser Ser Leu Ser Ser Lys Leu Leu
 1 5 10 15
 Pro Gly Phe Thr Thr Leu Gly Phe Lys Asp Glu Arg Arg Asn Lys Val
 20 25 30
 Thr Phe Leu Ser Ser Ala Thr Thr Ala Leu Ser Met Gln Asn Asn Ser
 35 40 45
 Val Phe Gly Asp Leu Lys Ser Asp Glu Met Glu Leu Leu Tyr Ser Ala

904

50	55	60
Tyr Gly Asp Glu Thr Gly Val Gln Cys Ala Leu Ser Leu Gln Glu Phe		
65	70	75 80
Val Lys Asp Ala Gly Ser Tyr Ser Lys Lys Val Val Asp Asp Leu Leu		
	85	90 95
Asp Gln Ile Thr Gly Gly Asp His Ser Arg Thr Leu Phe Gln Leu Lys		
	100	105 110
Gln Arg Arg Asn Val Pro Met Lys Pro Pro Asp Glu Ala Lys Val Gly		
	115	120 125
Asp Thr Leu Gly Asp Ser Ser Ser Ser Val Leu Glu Phe Met Ser Met		
	130	135 140
Lys Ser Tyr Pro Asp Val Ser Val Asp Ile Ser Met Leu Ser Ser Leu		
	145	150 155 160
Gly Lys Val Lys Lys Glu Leu Asp Pro Asp Asp Ser His Leu Asn Leu		
	165	170 175
Asp Glu Thr Thr Lys Leu Leu Gln Asp Leu His Glu Ala Gln Ala Asp		
	180	185 190
Ala Ala Ala Leu Gly Xaa Arg Pro Thr Ser Ala Pro Cys Pro Thr Pro		
	195	200 205
Pro Arg Gly Thr Ser Thr Thr Trp Glu Ala Leu Leu Ala		
	210	215 220

<210> 947

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (293)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (312)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 947

Glu Gln Tyr Val Cys Ala Gln Arg Asp Glu Tyr Leu Glu Ser Phe Cys

905

1	5	10	15
Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly Pro Val	20	25	30
Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn Glu Lys	35	40	45
Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg Leu Ile	50	55	60
Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe Phe Met	65	70	75
Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu Val Pro	85	90	95
Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln Ser Arg	100	105	110
Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys Lys Glu	115	120	125
Asp Lys Lys Gln Ser Leu Glu Asn Phe Leu Ser Arg Phe Arg Trp Arg	130	135	140
Arg Arg Leu Leu Val Ile Ser Ala Pro Asn Asp Glu Asp Trp Ala Tyr	145	150	155
Ser Gln Gln Leu Ser Ala Leu Ser Gly Gln Ala Cys Asn Phe Gly Leu	165	170	175
Arg His Ile Thr Ile Leu Lys Leu Leu Gly Val Gly Glu Glu Val Gly	180	185	190
Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser Ser Val Val Glu Arg	195	200	205
Glu Asp Val Pro Ala His Leu Val Lys Asp Ile Arg Asn Tyr Phe Gln	210	215	220
Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val Gly Lys Asp Gly Asn	225	230	235
Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser Met Val Ile Val Tyr	245	250	255
Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln Glu Met Ala Ile Gln	260	265	270
Gln Ser Leu Gly Met Arg Cys Pro Glu Asp Glu Tyr Ala Gly Tyr Gly			

906

275 280 285

Tyr His Ser Tyr Xaa Gln Gly Tyr Gln Asp Gly Tyr Gln Asp Asp Tyr
290 295 300

Arg His His Glu Ser Tyr His Xaa Gly Tyr Pro Tyr
305 310 315

<210> 948
<211> 162
<212> PRT
<213> Homo sapiens

<400> 948

Ser Thr His Ala Ser Ala His Ala Ser Gly Lys Gln Cys Gln Asp Ser
1 5 10 15

Lys Asp Ser Asn His Leu Pro Lys Met Ser Leu Ser Ala Phe Thr Leu
20 25 30

Phe Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Tyr Asp
35 40 45

Phe Pro Leu Ser Ile Tyr Gly Gln Ser Ser Pro Asn Cys Ala Pro Glu
50 55 60

Cys Asn Cys Pro Glu Ser Tyr Pro Ser Ala Met Tyr Cys Asp Glu Leu
65 70 75 80

Lys Leu Lys Ser Val Pro Met Val Pro Pro Gly Ile Lys Tyr Leu Tyr
85 90 95

Leu Arg Asn Asn Gln Ile Asp His Ile Asp Glu Lys Ala Phe Glu Asn
100 105 110

Val Thr Asp Leu Gln Trp Leu Ile Leu Asp His Asn Leu Leu Glu Asn
115 120 125

Ser Lys Ile Lys Gly Arg Val Phe Ser Lys Leu Lys Gln Leu Lys Lys
130 135 140

Leu His Ile Asn His Asn Asn Leu Thr Glu Ser Val Gly Pro Leu Pro
145 150 155 160

Lys Ser

907

<210> 949
 <211> 185
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (114)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 949

Leu Gly Phe Asn Tyr Tyr Tyr Lys Tyr Ser Asn Glu Gly Asp Ser His
 1 5 10 15

Leu Gly Gly Gly Ser Arg Glu Gly Ser Phe Lys Glu Thr Ile Thr Leu
 20 25 30

Lys Trp Cys Thr Pro Arg Thr Asn Asn Ile Glu Leu His Tyr Cys Thr
 35 40 45

Gly Ala Tyr Arg Ile Ser Pro Val Asp Val Asn Ser Arg Pro Ser Ser
 50 55 60

Cys Leu Thr Asn Phe Leu Leu Asn Gly Arg Ser Val Leu Leu Glu Gln
 65 70 75 80

Pro Arg Lys Ser Gly Ser Lys Val Ile Ser His Met Leu Ser Ser His
 85 90 95

Gly Gly Glu Ile Phe Leu His Val Leu Ser Ser Ser Arg Ser Ile Leu
 100 105 110

Glu Xaa Pro Pro Ser Ile Ser Glu Gly Cys Gly Gly Arg Val Thr Asp
 115 120 125

Tyr Arg Ile Thr Asp Phe Gly Glu Phe Met Arg Glu Asn Arg Leu Thr
 130 135 140

Pro Phe Leu Asp Pro Arg Tyr Lys Ile Asp Gly Ser Leu Glu Val Pro
 145 150 155 160

Leu Glu Arg Ala Lys Asp Gln Leu Glu Lys His Thr Arg Tyr Trp Pro
 165 170 175

Met Asp His Phe Thr Asn His His Phe
 180 185

<210> 950
 <211> 169

908

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (161)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 950

Pro Arg Arg Pro His Arg Ser Cys Asp Met Pro Ala Ser Gly Glu Pro
1 5 10 15

Leu Gly Cys Thr Pro Leu Leu Pro Asn Asp Ser Gly His Pro Ser Glu
20 25 30

Leu Gly Gly Thr Arg Arg Ala Gly Asn Gly Ala Leu Gly Gly Pro Lys
35 40 45

Ala His Arg Lys Leu Gln Thr His Pro Ser Leu Ala Ser Gln Gly Ser
50 55 60

Lys Lys Ser Lys Ser Ser Ser Lys Ser Thr Thr Ser Gln Ile Pro Leu
65 70 75 80

Gln Ala Gln Glu Asp Cys Cys Val His Cys Ile Leu Ser Cys Leu Phe
85 90 95

Cys Glu Phe Leu Thr Leu Cys Asn Ile Val Leu Asp Cys Ala Thr Cys
100 105 110

Gly Ser Cys Ser Ser Glu Asp Ser Cys Leu Cys Cys Cys Cys Gly
115 120 125

Ser Gly Glu Cys Ala Asp Cys Asp Leu Pro Cys Asp Leu Asp Cys Gly
130 135 140

Ile Leu Asp Ala Cys Cys Glu Ser Ala Asp Cys Leu Glu Ile Cys Met
145 150 155 160

Xaa Cys Cys Gly Leu Cys Phe Ser Ser
165

<210> 951

<211> 288

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (161)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (234)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 951

Met Ser Asp Glu Thr Gly Arg Val Pro Glu Arg Asp Thr Lys Arg Met
 1 5 10 15

Gln Val Cys Leu Leu Ser Ala Met Pro Leu Pro Val Ala Leu Gln Thr
 20 25 30

Arg Leu Ala Lys Arg Gly Ile Leu Lys His Leu Glu Pro Glu Pro Glu
 35 40 45

Glu Glu Ile Ile Ala Glu Asp Tyr Asp Asp Asp Pro Val Asp Tyr Glu
 50 55 60

Ala Thr Arg Leu Glu Gly Leu Pro Pro Ser Trp Tyr Lys Val Phe Asp
 65 70 75 80

Pro Ser Cys Gly Leu Pro Tyr Tyr Trp Asn Ala Asp Thr Asp Leu Val
 85 90 95

Ser Trp Leu Ser Pro His Asp Pro Asn Ser Val Val Thr Lys Ser Ala
 100 105 110

Lys Lys Leu Arg Ser Ser Asn Ala Asp Ala Glu Glu Lys Leu Asp Arg
 115 120 125

Ser His Asp Lys Ser Asp Arg Gly His Asp Lys Ser Asp Arg Ser His
 130 135 140

Glu Lys Leu Asp Arg Gly His Asp Lys Ser Asp Arg Gly His Asp Lys
 145 150 155 160

Xaa Asp Arg Asp Arg Glu Arg Gly Tyr Asp Lys Val Asp Arg Glu Arg
 165 170 175

Glu Arg Asp Arg Glu Arg Asp Arg Asp Arg Gly Tyr Asp Lys Ala Asp
 180 185 190

Arg Glu Glu Gly Lys Glu Arg Arg His His Arg Arg Glu Glu Leu Ala
 195 200 205

Pro Tyr Pro Lys Ser Lys Lys Ala Val Ser Arg Lys Asp Glu Glu Leu
 210 215 220

Asp Pro Met Asp Pro Ser Ser Tyr Ser Xaa Arg Pro Arg Gly Thr Trp
225 230 235 240

Ser Thr Gly Leu Pro Lys Arg Asn Glu Ala Lys Thr Gly Ala Asp Thr
245 250 255

Thr Ala Ala Gly Pro Leu Phe Gln Gln Arg Pro Tyr Pro Ser Pro Gly
260 265 270

Ala Val Leu Arg Ala Asn Ala Glu Ala Ser Arg Thr Lys Gln Gln Asp
275 280 285

<210> 952

<211> 323

<212> PRT

<213> Homo sapiens

<400> 952

Val Gly Gly Val Leu Pro Gly Trp Lys Leu Arg Pro Arg Ser Asp Gly
1 5 10 15

Gly Leu Ser Glu Asp Gly Pro Gly Arg Asp His Gly Gly Gly Ser Arg
20 25 30

Gly Gly Arg Gly Gly Ala Ala Gly Gly Arg Gly Gly Cys Gly Pro Gln
35 40 45

Gly Ala Val Gly Gly Gly Met Ala Arg Ala Ser Ser Gly Asn Gly Ser
50 55 60

Glu Glu Ala Trp Gly Ala Leu Arg Ala Pro Gln Gln Gln Leu Arg Glu
65 70 75 80

Leu Cys Pro Gly Val Asn Asn Gln Pro Tyr Leu Cys Glu Ser Gly His
85 90 95

Cys Cys Gly Glu Thr Gly Cys Cys Thr Tyr Tyr Tyr Glu Leu Trp Trp
100 105 110

Phe Trp Leu Leu Trp Thr Val Leu Ile Leu Phe Ser Cys Cys Cys Ala
115 120 125

Phe Arg His Arg Arg Ala Lys Leu Arg Leu Gln Gln Gln Arg Gln
130 135 140

Arg Glu Ile Asn Leu Leu Ala Tyr His Gly Ala Cys His Gly Ala Gly

911

145 150 155 160
 Pro Phe Pro Thr Gly Ser Leu Leu Asp Leu Arg Phe Leu Ser Thr Phe
 165 170 175
 Lys Pro Pro Ala Tyr Glu Asp Val Val His Arg Pro Gly Thr Pro Pro
 180 185 190
 Pro Pro Tyr Thr Val Ala Pro Gly Arg Pro Leu Thr Ala Ser Ser Glu
 195 200 205
 Gln Thr Cys Cys Ser Ser Ser Ser Ser Cys Pro Ala His Phe Glu Gly
 210 215 220
 Thr Asn Val Glu Gly Val Ser Ser His Gln Ser Ala Pro Pro His Gln
 225 230 235 240
 Glu Gly Glu Pro Gly Ala Gly Val Thr Pro Ala Ser Thr Pro Pro Ser
 245 250 255
 Cys Arg Tyr Arg Arg Leu Thr Gly Asp Ser Gly Ile Glu Leu Cys Pro
 260 265 270
 Cys Pro Ala Ser Gly Glu Gly Glu Pro Val Lys Glu Val Arg Val Ser
 275 280 285
 Ala Thr Leu Pro Asp Leu Glu Asp Tyr Ser Pro Cys Ala Leu Pro Pro
 290 295 300
 Glu Ser Val Pro Gln Ile Phe Pro Met Gly Leu Ser Ser Ser Glu Gly
 305 310 315 320
 Asp Ile Pro

<210> 953

<211> 433

<212> PRT

<213> Homo sapiens

<400> 953

Ala Lys Met Ser Val Asn Val Asn Arg Ser Val Ser Asp Gln Phe Tyr
 1 5 10 15
 Arg Tyr Lys Met Pro Arg Leu Ile Ala Lys Val Glu Gly Lys Gly Asn
 20 25 30
 Gly Ile Lys Thr Val Ile Val Asn Met Val Asp Val Ala Lys Ala Leu
 35 40 45

Asn Arg Pro Pro Thr Tyr Pro Thr Lys Tyr Phe Gly Cys Glu Leu Gly
 50 55 60

Ala Gln Thr Gln Phe Asp Val Lys Asn Asp Arg Tyr Ile Val Asn Gly
 65 70 75 80

Ser His Glu Ala Asn Lys Leu Gln Asp Met Leu Asp Gly Phe Ile Lys
 85 90 95

Lys Phe Val Leu Cys Pro Glu Cys Glu Asn Pro Glu Thr Asp Leu His
 100 105 110

Val Asn Pro Lys Lys Gln Thr Ile Gly Asn Ser Cys Lys Ala Cys Gly
 115 120 125

Tyr Arg Gly Met Leu Asp Thr His His Lys Leu Cys Thr Phe Ile Leu
 130 135 140

Lys Asn Pro Pro Glu Asn Ser Asp Ser Gly Thr Gly Lys Lys Glu Lys
 145 150 155 160

Glu Lys Lys Asn Arg Lys Gly Lys Asp Lys Glu Asn Gly Ser Val Ser
 165 170 175

Ser Ser Glu Thr Pro Pro Pro Pro Pro Pro Pro Asn Glu Ile Asn Pro
 180 185 190

Pro Pro His Thr Met Glu Glu Glu Glu Asp Asp Asp Trp Gly Glu Asp
 195 200 205

Thr Thr Glu Glu Ala Gln Arg Arg Arg Met Asp Glu Ile Ser Asp His
 210 215 220

Ala Lys Val Leu Thr Leu Ser Asp Asp Leu Glu Arg Thr Ile Glu Glu
 225 230 235 240

Arg Val Asn Ile Leu Phe Asp Phe Val Lys Lys Lys Lys Glu Glu Gly
 245 250 255

Val Ile Asp Ser Ser Asp Lys Glu Ile Val Ala Glu Ala Glu Arg Leu
 260 265 270

Asp Val Lys Ala Met Gly Pro Leu Val Leu Thr Glu Val Leu Phe Asn
 275 280 285

Glu Lys Ile Arg Glu Gln Ile Lys Lys Tyr Arg Arg His Phe Leu Arg
 290 295 300

Phe Cys His Asn Asn Lys Lys Ala Gln Arg Tyr Leu Leu His Gly Leu
 305 310 315 320

913

Glu Cys Val Val Ala Met His Gln Ala Gln Leu Ile Ser Lys Ile Pro
 325 330 335

His Ile Leu Lys Glu Met Tyr Asp Ala Asp Leu Leu Glu Glu Glu Val
 340 345 350

Ile Ile Ser Trp Ser Glu Lys Ala Ser Lys Lys Tyr Val Ser Lys Glu
 355 360 365

Leu Ala Lys Glu Ile Arg Val Lys Ala Glu Pro Phe Ile Lys Trp Leu
 370 375 380

Lys Glu Ala Glu Glu Glu Ser Ser Gly Gly Glu Glu Glu Asp Glu Asp
 385 390 395 400

Glu Asn Ile Glu Val Val Tyr Ser Lys Ala Ala Ser Val Pro Lys Val
 405 410 415

Glu Thr Val Lys Ser Asp Asn Lys Asp Asp Asp Ile Asp Ile Asp Ala
 420 425 430

Ile

<210> 954

<211> 428

<212> PRT

<213> Homo sapiens

<400> 954

Gly Tyr Gln Ile Gly Met Ala Leu Ala Ser Gly Pro Ala Arg Arg Ala
 1 5 10 15

Leu Ala Gly Ser Gly Gln Leu Gly Leu Gly Gly Phe Gly Ala Pro Arg
 20 25 30

Arg Gly Ala Tyr Glu Trp Gly Val Arg Ser Thr Arg Lys Ser Glu Pro
 35 40 45

Pro Pro Leu Asp Arg Val Tyr Glu Ile Pro Gly Leu Glu Pro Ile Thr
 50 55 60

Phe Ala Gly Lys Met His Phe Val Pro Trp Leu Ala Arg Pro Ile Phe
 65 70 75 80

Pro Pro Trp Asp Arg Gly Tyr Lys Asp Pro Arg Phe Tyr Arg Ser Pro
 85 90 95

Pro Leu His Glu His Pro Leu Tyr Lys Asp Gln Ala Cys Tyr Ile Phe
 100 105 110
 His His Arg Cys Arg Leu Leu Glu Gly Val Lys Gln Ala Leu Trp Leu
 115 120 125
 Thr Lys Thr Lys Leu Ile Glu Gly Leu Pro Glu Lys Val Leu Ser Leu
 130 135 140
 Val Asp Asp Pro Arg Asn His Ile Glu Asn Gln Asp Glu Cys Val Leu
 145 150 155 160
 Asn Val Ile Ser His Ala Arg Leu Trp Gln Thr Thr Glu Glu Ile Pro
 165 170 175
 Lys Arg Glu Thr Tyr Cys Pro Val Ile Val Asp Asn Leu Ile Gln Leu
 180 185 190
 Cys Lys Ser Gln Ile Leu Lys His Pro Ser Leu Ala Arg Arg Ile Cys
 195 200 205
 Val Gln Asn Ser Thr Phe Ser Ala Thr Trp Asn Arg Glu Ser Leu Leu
 210 215 220
 Leu Gln Val Arg Gly Ser Gly Gly Ala Arg Leu Ser Thr Lys Asp Pro
 225 230 235 240
 Leu Pro Thr Ile Ala Ser Arg Glu Glu Ile Glu Ala Thr Lys Asn His
 245 250 255
 Val Leu Glu Thr Phe Tyr Pro Ile Ser Pro Ile Ile Asp Leu His Glu
 260 265 270
 Cys Asn Ile Tyr Asp Val Lys Asn Asp Thr Gly Phe Gln Glu Gly Tyr
 275 280 285
 Pro Tyr Pro Tyr Pro His Thr Leu Tyr Leu Leu Asp Lys Ala Asn Leu
 290 295 300
 Arg Pro His Arg Leu Gln Pro Asp Gln Leu Arg Ala Lys Met Ile Leu
 305 310 315 320
 Phe Ala Phe Gly Ser Ala Leu Ala Gln Ala Arg Leu Leu Tyr Gly Asn
 325 330 335
 Asp Ala Lys Val Leu Glu Gln Pro Val Val Val Gln Ser Val Gly Thr
 340 345 350
 Asp Gly Arg Val Phe His Phe Leu Val Phe Gln Leu Asn Thr Thr Asp
 355 360 365

915

Leu Asp Ser Asn Glu Gly Val Lys Asn Leu Ala Trp Val Asp Ser Asp
 370 375 380

Gln Leu Leu Tyr Gln His Phe Trp Cys Leu Pro Val Ile Lys Lys Arg
 385 390 395 400

Val Val Val Glu Pro Val Gly Pro Val Gly Phe Lys Pro Glu Thr Phe
 405 410 415

Arg Lys Phe Leu Ala Leu Tyr Leu His Gly Ala Ala
 420 425

<210> 955

<211> 169

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (131)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (140)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (166)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 955

Asp Pro Arg Val Arg Pro Arg Val Arg Pro Arg Val Arg Glu Pro Gly
 1 5 10 15

Asp Arg Met Leu Val Leu Val Leu Gly Asp Leu His Ile Pro His Arg
 20 25 30

Cys Asn Ser Leu Pro Ala Lys Phe Lys Lys Leu Leu Val Pro Gly Lys
 35 40 45

Ile Gln His Ile Leu Cys Thr Gly Asn Leu Cys Thr Lys Glu Ser Tyr
 50 55 60

Asp Tyr Leu Lys Thr Leu Ala Gly Asp Val His Ile Val Arg Gly Asp
 65 70 75 80

Phe Asp Glu Asn Leu Asn Tyr Pro Glu Gln Lys Val Val Thr Val Gly

916

85 90 95
Gln Phe Lys Ile Gly Leu Ile His Gly His Gln Val Ile Pro Trp Gly
100 105 110
Asp Met Ala Ser Leu Ala Leu Leu Gln Arg Gln Phe Asp Val Asp Ile
115 120 125
Leu Ile Xaa Gly His Thr His Lys Phe Glu Ala Xaa Glu His Glu Asn
130 135 140
Lys Phe Tyr Ile Asn Pro Gly Ser Ala Thr Gly Ala Tyr Asn Ala Leu
145 150 155 160
Glu Thr Asn Ile Ile Xaa Ser Leu Cys
165

<210> 956
<211> 39
<212> PRT
<213> Homo sapiens

<400> 956
Ser Pro Tyr Cys Gly Leu Gln Val Met Leu Phe Leu Leu His His Thr
1 5 10 15
Leu Trp Cys Leu Leu Pro Cys Ala Ser Ser Leu Arg Leu Ile Lys Lys
20 25 30
Val Ser Arg Leu Leu Gln Leu
35

<210> 957
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

917

<400> 957

Gln Gly His Cys Gly Cys Xaa Leu Xaa Ser Leu Leu Ala Asn Gly His
 1 5 10 15
 Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser Asn Pro Thr Ser Lys
 20 25 30
 His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser Lys Ala Glu Arg Ala
 35 40 45
 Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu Gln Gln Phe Ala Gln
 50 55 60
 Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu His Leu Pro Leu Met
 65 70 75 80
 Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu Ala Val Ala Gly Ala
 85 90 95
 Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr Leu Gly Ala Phe Pro
 100 105 110
 Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala Gly Val Phe Leu Ala
 115 120 125
 Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu Tyr Pro Met Gln Gly
 130 135 140
 Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys Lys Arg Lys Arg Cys
 145 150 155 160
 Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn Cys Glu Gln Cys Ser
 165 170 175
 Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile Cys Lys Phe Arg Lys
 180 185 190
 Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala Leu Glu Lys Val Met
 195 200 205
 Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
 210 215

<210> 958

<211> 259

<212> PRT

<213> Homo sapiens

<220>

918

<221> SITE

<222> (21)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (74)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 958

Leu Pro Gln Asn Ala Val Leu Glu Ala Asp Phe Ala Lys Arg Gly Tyr
 1 5 10 15

Lys Leu Pro Lys Xaa Arg Lys Thr Gly Thr Thr Ile Ala Gly Val Val
 20 25 30

Tyr Lys Asp Gly Ile Val Leu Gly Ala Asp Thr Arg Ala Thr Glu Gly
 35 40 45

Met Val Val Ala Asp Lys Asn Cys Ser Lys Ile His Phe Ile Ser Pro
 50 55 60

Asn Ile Tyr Cys Cys Gly Ala Gly Thr Xaa Ala Asp Thr Asp Met Thr
 65 70 75 80

Thr Gln Leu Ile Ser Ser Asn Leu Glu Leu His Ser Leu Ser Thr Gly
 85 90 95

Arg Leu Pro Arg Val Val Thr Ala Asn Arg Met Leu Lys Gln Met Leu
 100 105 110

Phe Arg Tyr Gln Gly Tyr Ile Gly Ala Ala Leu Val Leu Gly Gly Val
 115 120 125

Asp Val Thr Gly Pro His Leu Tyr Ser Ile Tyr Pro His Gly Ser Thr
 130 135 140

Asp Lys Leu Pro Tyr Val Thr Met Gly Ser Gly Ser Leu Ala Ala Met
 145 150 155 160

Ala Val Phe Glu Asp Lys Phe Arg Pro Asp Met Glu Glu Glu Glu Ala
 165 170 175

Lys Asn Leu Val Ser Glu Ala Ile Ala Ala Gly Ile Phe Asn Asp Leu
 180 185 190

Gly Ser Gly Ser Asn Ile Asp Leu Cys Val Ile Ser Lys Asn Lys Leu
 195 200 205

Asp Phe Leu Arg Pro Tyr Thr Val Pro Asn Lys Lys Gly Thr Arg Leu
 210 215 220

Gly Arg Tyr Arg Cys Glu Lys Gly Thr Thr Ala Val Leu Thr Glu Lys
225 230 235 240

Ile Thr Pro Leu Glu Ile Glu Val Leu Glu Glu Thr Val Gln Thr Met
245 250 255

Asp Thr Ser

<210> 959

<211> 75

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (36)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (41)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (53)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 959

Phe Trp Ser Ala Ala Lys Phe Asp Phe Thr Ser His Thr Pro Phe Leu
1 5 10 15

Pro Leu Glu Met Gln Phe Arg Gln Arg Pro Cys Gly Glu Ser Cys Asn
20 25 30

Ile Lys Phe Xaa Phe Arg Arg Ser Xaa Pro Gln Thr Ser Glu Pro Leu
35 40 45

Ala Val Leu Pro Xaa Asn Lys Asn Glu Leu Glu Lys Lys Val Ala Gln
50 55 60

Leu Gln Arg Ser Lys Ser Ser Tyr Phe Pro Thr
65 70 75

<210> 960

920

<211> 128

<212> PRT

<213> Homo sapiens

<400> 960

Gln Ser Arg Gly Leu Arg Leu Leu Gly Pro Gly Asp Gly Ala Gly Met
 1 5 10 15

Thr Pro Gly Val Val His Ala Ser Pro Pro Gln Ser Gln Arg Val Pro
 20 25 30

Arg Gln Ala Pro Cys Glu Trp Ala Ile Arg Asn Ile Gly Gln Lys Pro
 35 40 45

Lys Glu Pro Asn Cys His Asn Cys Gly Thr His Ile Gly Leu Arg Ser
 50 55 60

Lys Thr Leu Arg Gly Thr Pro Asn Tyr Leu Pro Ile Arg Gln Asp Thr
 65 70 75 80

His Pro Pro Ser Val Ile Phe Cys Leu Ala Gly Val Gly Val Pro Gly
 85 90 95

Gly Thr Cys Arg Pro Ala Pro Cys Val Pro Arg Phe Ala Ala Leu Pro
 100 105 110

Trp Ala Thr Asn His Pro Gly Pro Gly Cys Leu Ser Asp Leu Arg Ala
 115 120 125

<210> 961

<211> 564

<212> PRT

<213> Homo sapiens

<400> 961

Lys Met Lys Ser Val Lys Ile Ala Phe Ala Val Thr Leu Glu Thr Val
 1 5 10 15

Leu Ala Gly His Glu Asn Trp Val Asn Ala Val His Trp Gln Pro Val
 20 25 30

Phe Tyr Lys Asp Gly Val Leu Gln Gln Pro Val Arg Leu Leu Ser Ala
 35 40 45

Ser Met Asp Lys Thr Met Ile Leu Trp Ala Pro Asp Glu Glu Ser Gly
 50 55 60

Val Trp Leu Glu Gln Val Arg Val Gly Glu Val Gly Gly Asn Thr Leu			
65	70	75	80
Gly Phe Tyr Asp Cys Gln Phe Asn Glu Asp Gly Ser Met Ile Ile Ala			
	85	90	95
His Ala Phe His Gly Ala Leu His Leu Trp Lys Gln Asn Thr Val Asn			
	100	105	110
Pro Arg Glu Trp Thr Pro Glu Ile Val Ile Ser Gly His Phe Asp Gly			
	115	120	125
Val Gln Asp Leu Val Trp Asp Pro Glu Gly Glu Phe Ile Ile Thr Val			
	130	135	140
Gly Thr Asp Gln Thr Thr Arg Leu Phe Ala Pro Trp Lys Arg Lys Asp			
	145	150	155
Gln Ser Gln Val Thr Trp His Glu Ile Ala Arg Pro Gln Ile His Gly			
	165	170	175
Tyr Asp Leu Lys Cys Leu Ala Met Ile Asn Arg Phe Gln Phe Val Ser			
	180	185	190
Gly Ala Asp Glu Lys Val Leu Arg Val Phe Ser Ala Pro Arg Asn Phe			
	195	200	205
Val Glu Asn Phe Cys Ala Ile Thr Gly Gln Ser Leu Asn His Val Leu			
	210	215	220
Cys Asn Gln Asp Ser Asp Leu Pro Glu Gly Ala Thr Val Pro Ala Leu			
	225	230	235
Gly Leu Ser Asn Lys Ala Val Phe Gln Gly Asp Ile Ala Ser Gln Pro			
	245	250	255
Ser Asp Glu Glu Glu Leu Leu Thr Ser Thr Gly Phe Glu Tyr Gln Gln			
	260	265	270
Val Ala Phe Gln Pro Ser Ile Leu Thr Glu Pro Pro Thr Glu Asp His			
	275	280	285
Leu Leu Gln Asn Thr Leu Trp Pro Glu Val Gln Lys Leu Tyr Gly His			
	290	295	300
Gly Tyr Glu Ile Phe Cys Val Thr Cys Asn Ser Ser Lys Thr Leu Leu			
	305	310	315
Ala Ser Ala Cys Lys Ala Ala Lys Lys Glu His Ala Ala Ile Ile Leu			
	325	330	335

922

Trp Asn Thr Thr Ser Trp Lys Gln Val Gln Asn Leu Val Phe His Ser
340 345 350

Leu Thr Val Thr Gln Met Ala Phe Ser Pro Asn Glu Lys Phe Leu Leu
355 360 365

Ala Val Ser Arg Asp Arg Thr Trp Ser Leu Trp Lys Lys Gln Asp Thr
370 375 380

Ile Ser Pro Glu Phe Glu Pro Val Phe Ser Leu Phe Ala Phe Thr Asn
385 390 395 400

Lys Ile Thr Ser Val His Ser Arg Ile Ile Trp Ser Cys Asp Trp Ser
405 410 415

Pro Asp Ser Lys Tyr Phe Phe Thr Gly Ser Arg Asp Lys Lys Val Val
420 425 430

Val Trp Gly Glu Cys Asp Ser Thr Asp Asp Cys Ile Glu His Asn Ile
435 440 445

Gly Pro Cys Ser Ser Val Leu Asp Val Gly Gly Ala Val Thr Ala Val
450 455 460

Ser Val Cys Pro Val Leu His Pro Ser Gln Arg Tyr Val Val Ala Val
465 470 475 480

Gly Leu Glu Cys Gly Lys Ile Cys Leu Tyr Thr Trp Lys Lys Thr Asp
485 490 495

Gln Val Pro Glu Ile Asn Asp Trp Thr His Cys Val Glu Thr Ser Gln
500 505 510

Ser Gln Ser His Thr Leu Ala Ile Arg Lys Leu Cys Trp Lys Asn Cys
515 520 525

Ser Gly Lys Thr Glu Gln Lys Glu Ala Glu Gly Ala Glu Trp Leu His
530 535 540

Phe Ala Ser Cys Gly Glu Asp His Thr Val Lys Ile His Arg Val Asn
545 550 555 560

Lys Cys Ala Leu

<210> 962

<211> 43

<212> PRT

923

<213> Homo sapiens

<400> 962

Phe Lys Tyr Val Lys Cys Gly Ser Phe Thr Pro His His Ser Glu His
 1 5 10 15

Thr Gly Glu Met Cys Phe Phe Gly Lys Leu Lys Gly Ala Ser Ser Leu
 20 25 30

Ile Gln Arg Asn Ile Ser His Val Cys Ser Phe
 35 40

<210> 963

<211> 132

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (131)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 963

Glu Ser Arg Val Asp Pro Arg Val Arg Glu Arg Ser Ala Arg Thr Ala
 1 5 10 15

Gly Ala Thr Val Gly Pro Ala Ala Val Met Ser Val Leu Arg Pro Leu
 20 25 30

Asp Lys Leu Pro Gly Leu Asn Thr Ala Thr Ile Leu Leu Val Gly Thr
 35 40 45

Glu Asp Ala Leu Leu Gln Gln Leu Ala Asp Ser Met Leu Lys Glu Asp
 50 55 60

Cys Ala Ser Glu Leu Lys Val His Leu Ala Lys Ser Leu Pro Leu Pro
 65 70 75 80

Ser Ser Val Asn Arg Pro Arg Ile Asp Leu Ile Val Phe Val Val Asn
 85 90 95

Leu His Ser Lys Tyr Ser Leu Gln Asn Thr Glu Glu Ser Leu Arg His
 100 105 110

Val Asp Ala Ser Phe Phe Leu Gly Lys Val Cys Phe Leu Ala Thr Gly
 115 120 125

Gly Gly Xaa Leu
 130

<210> 964
 <211> 175
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (13)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (72)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 964
 His Glu Arg Ser Cys Cys Asp Ala Arg Ser Glu Ala Xaa Gln Gly Arg
 1 5 10 15
 Gly Arg Val Gly Ala Gly Ala Gly Ala Ala Trp Ser Ser Cys Gly Val
 20 25 30
 Ser Gly Pro Gly Arg Gly Met Gly Val Leu Ala Ala Ala Arg Cys
 35 40 45
 Leu Val Arg Gly Ala Asp Arg Met Ser Lys Trp Thr Ser Lys Arg Gly
 50 55 60
 Pro Arg Ser Phe Arg Gly Arg Xaa Gly Arg Gly Ala Lys Gly Ile Gly
 65 70 75 80
 Phe Leu Thr Ser Gly Trp Arg Phe Val Gln Ile Lys Glu Met Val Pro
 85 90 95
 Glu Phe Val Val Pro Asp Leu Thr Gly Phe Lys Leu Lys Pro Tyr Val
 100 105 110
 Ser Tyr Leu Ala Pro Glu Ser Glu Glu Thr Pro Leu Thr Ala Ala Gln
 115 120 125
 Leu Phe Ser Glu Ala Val Ala Pro Ala Ile Glu Lys Asp Phe Lys Asp
 130 135 140
 Gly Thr Phe Asp Pro Asp Asn Leu Glu Lys Tyr Gly Phe Glu Pro Thr
 145 150 155 160
 Gln Glu Gly Lys Leu Phe Gln Leu Tyr Pro Arg Asn Phe Leu Arg
 165 170 175

<210> 965
 <211> 363
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (356)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 965

Leu Leu Arg Arg Leu Arg Thr Ala Val Pro Gly Ser Leu Glu Ala Gln
 1 5 10 15

Lys Arg Lys Pro Ser Pro Gly Pro Gly Ser Leu Asp Leu Val Ser Leu
 20 25 30

Gly Ser Gly Asn Ser Gly Ser Gln Arg Thr Val Leu Ile Met Asp Lys
 35 40 45

Gln Asn Ser Gln Met Asn Ala Ser His Pro Glu Thr Asn Leu Pro Val
 50 55 60

Gly Tyr Pro Pro Gln Tyr Pro Pro Thr Ala Phe Gln Gly Pro Pro Gly
 65 70 75 80

Tyr Ser Gly Tyr Pro Gly Pro Gln Val Ser Tyr Pro Pro Pro Pro Ala
 85 90 95

Gly His Ser Gly Pro Gly Pro Ala Gly Phe Pro Val Pro Asn Gln Pro
 100 105 110

Val Tyr Asn Gln Pro Val Tyr Asn Gln Pro Val Gly Ala Ala Gly Val
 115 120 125

Pro Trp Met Pro Ala Pro Gln Pro Pro Leu Asn Cys Pro Pro Gly Leu
 130 135 140

Glu Tyr Leu Ser Gln Ile Asp Gln Ile Leu Ile His Gln Gln Ile Glu
 145 150 155 160

Leu Leu Glu Val Leu Thr Gly Phe Glu Thr Asn Asn Lys Tyr Glu Ile
 165 170 175

Lys Asn Ser Phe Gly Gln Arg Val Tyr Phe Ala Ala Glu Asp Thr Asp
 180 185 190

Cys Cys Thr Arg Asn Cys Cys Gly Pro Ser Arg Pro Phe Thr Leu Arg

926

195	200	205
Ile Ile Asp Asn Met Gly Gln Glu Val Ile Thr Leu Glu Arg Pro Leu		
210	215	220
Arg Cys Ser Ser Cys Cys Cys Pro Cys Cys Leu Gln Glu Ile Glu Ile		
225	230	235 240
Gln Ala Pro Pro Gly Val Pro Ile Gly Tyr Val Ile Gln Thr Trp His		
	245	250 255
Pro Cys Leu Pro Lys Phe Thr Ile Gln Asn Glu Lys Arg Glu Asp Val		
	260	265 270
Leu Lys Ile Ser Gly Pro Cys Val Val Cys Ser Cys Cys Gly Asp Val		
	275	280 285
Asp Phe Glu Ile Lys Ser Leu Asp Glu Gln Cys Val Val Gly Lys Ile		
	290	295 300
Ser Lys His Trp Thr Gly Ile Leu Arg Glu Ala Phe Thr Asp Ala Asp		
305	310	315 320
Asn Phe Gly Ile Gln Phe Pro Leu Asp Leu Asp Val Lys Met Lys Ala		
	325	330 335
Val Met Ile Gly Ala Cys Phe Leu Ile Asp Phe Met Phe Phe Glu Ser		
	340	345 350
Thr Gly Ser Xaa Glu Gln Lys Ser Gly Val Trp		
	355	360

<210> 966

<211> 131

<212> PRT

<213> Homo sapiens

<400> 966

Ala Glu Val His Thr Arg Lys Gln Gly Pro Glu Ala Glu Pro Ala Ala
1 5 10 15

Met Ser Gly Glu Pro Gly Gln Thr Ser Val Ala Pro Pro Pro Glu Glu
20 25 30

Val Glu Pro Gly Ser Gly Val Arg Ile Val Val Glu Tyr Cys Glu Pro
35 40 45

Cys Gly Phe Glu Ala Thr Tyr Leu Glu Leu Ala Ser Ala Val Lys Glu
50 55 60

927

Gln Tyr Pro Gly Ile Glu Ile Glu Ser Arg Leu Gly Gly Thr Gly Ala
 65 70 75 80

Phe Glu Ile Glu Ile Asn Gly Gln Leu Val Phe Ser Lys Leu Glu Asn
 85 90 95

Gly Gly Phe Pro Tyr Glu Lys Asp Leu Ile Glu Ala Ile Arg Arg Ala
 100 105 110

Ser Asn Gly Glu Thr Leu Glu Lys Ile Thr Asn Ser Arg Pro Pro Cys
 115 120 125

Val Ile Leu
 130

<210> 967

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (68)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (306)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 967

Pro Thr Pro Ala Ser His Ser Pro Ser Pro Ser Leu Pro Ala Leu Pro
 1 5 10 15

Pro Ser Pro Pro His Arg Pro Asp Ser Pro Leu Phe Asn Ser Arg Cys
 20 25 30

Ser Ser Pro Leu Gln Leu Asn Leu Leu Gln Leu Glu Glu Leu Pro Arg
 35 40 45

Ala Glu Gly Ala Ala Val Ala Gly Gly Pro Gly Ser Ser Ala Gly Pro
 50 55 60

Pro Pro Pro Xaa Ala Glu Ala Ala Glu Pro Glu Ala Arg Leu Ala Glu
 65 70 75 80

Val Thr Glu Ser Ser Asn Gln Asp Ala Leu Ser Gly Ser Ser Asp Leu
 85 90 95

Leu Glu Leu Leu Leu Gln Glu Asp Ser Arg Ser Gly Thr Gly Ser Ala
100 105 110

Ala Ser Gly Ser Leu Gly Ser Gly Leu Gly Ser Gly Ser Gly Ser Gly
115 120 125

Ser His Glu Gly Gly Ser Thr Ser Ala Ser Ile Thr Arg Ser Ser Gln
130 135 140

Ser Ser His Thr Ser Lys Tyr Phe Gly Ser Ile Asp Ser Ser Glu Ala
145 150 155 160

Glu Ala Gly Ala Ala Arg Gly Gly Ala Glu Pro Gly Asp Gln Val Ile
165 170 175

Lys Tyr Val Leu Gln Asp Pro Ile Trp Leu Leu Met Ala Asn Ala Asp
180 185 190

Gln Arg Val Met Met Thr Tyr Gln Val Pro Ser Arg Asp Met Thr Ser
195 200 205

Val Leu Lys Gln Asp Arg Glu Arg Leu Arg Ala Met Gln Lys Gln Gln
210 215 220

Pro Arg Phe Ser Glu Asp Gln Arg Arg Glu Leu Gly Ala Val His Ser
225 230 235 240

Trp Val Arg Lys Gly Gln Leu Pro Arg Ala Leu Asp Val Met Ala Cys
245 250 255

Val Asp Cys Gly Ser Ser Thr Gln Asp Pro Gly His Pro Asp Asp Pro
260 265 270

Leu Phe Ser Glu Leu Asp Gly Leu Gly Leu Glu Pro Met Glu Glu Gly
275 280 285

Gly Gly Glu Gln Gly Ser Ser Gly Gly Gly Ser Gly Glu Gly Glu Gly
290 295 300

Cys Xaa Glu Ala Gln Gly Gly Ala Lys Ala Ser Ser Ser Gln Asp Leu
305 310 315 320

Ala Met Glu Glu Glu Glu Gly Arg Ser Ser Ser Ser Pro Ala Leu
325 330 335

Pro Thr Ala Gly Asn Cys Thr Ser
340

929

<210> 968

<211> 67

<212> PRT

<213> Homo sapiens

<400> 968

Arg Cys Ser Ser Phe Phe Leu Ser Leu Leu Val Lys Ile Thr Asn Ile
1 5 10 15

Trp Glu Gly Phe Lys Asp Ala Cys Tyr Gly Ala Asn Val Leu Ser Leu
20 25 30

Leu Asn Ser Arg Ser Glu Leu Leu Thr Cys Ile Gln Asn Ile Asn Ala
35 40 45

Gln Asn Leu Tyr Met Ser Pro Ile Arg Lys Ile His Trp His Ala Thr
50 55 60

Gly Asp Ser
65

<210> 969

<211> 325

<212> PRT

<213> Homo sapiens

<400> 969

Leu Asn Leu Arg Ser Pro His Ile Cys Phe Arg Ser Ser Lys Pro Ser
1 5 10 15

Trp Ala Asp Gln Val Glu Glu Glu Gly Glu Asp Asp Lys Cys Val Thr
20 25 30

Ser Glu Leu Leu Lys Gly Ile Pro Leu Ala Thr Gly Asp Thr Ser Pro
35 40 45

Glu Pro Glu Leu Leu Pro Gly Ala Pro Leu Pro Pro Pro Lys Glu Val
50 55 60

Ile Asn Gly Asn Ile Lys Thr Val Thr Glu Tyr Lys Ile Asp Glu Asp
65 70 75 80

Gly Lys Lys Phe Lys Ile Val Arg Thr Phe Arg Ile Glu Thr Arg Lys
85 90 95

Ala Ser Lys Ala Val Ala Arg Arg Lys Asn Trp Lys Lys Phe Gly Asn
100 105 110

Ser Glu Phe Asp Pro Pro Gly Pro Asn Val Ala Thr Thr Thr Val Ser

930

115	120	125
Asp Asp Val Ser Met Thr Phe Ile Thr Ser Lys Glu Asp Leu Asn Cys		
130	135	140
Gln Glu Glu Glu Asp Pro Met Asn Lys Leu Lys Gly Gln Lys Ile Val		
145	150	155 160
Ser Cys Arg Ile Cys Lys Gly Asp His Trp Thr Thr Arg Cys Pro Tyr		
	165 170	175
Lys Asp Thr Leu Gly Pro Met Gln Lys Glu Leu Ala Glu Gln Leu Gly		
	180 185	190
Leu Ser Thr Gly Glu Lys Glu Lys Leu Pro Gly Glu Leu Glu Pro Val		
	195 200	205
Gln Ala Thr Gln Asn Lys Thr Gly Lys Tyr Val Pro Pro Ser Leu Arg		
	210 215	220
Asp Gly Ala Ser Arg Arg Gly Glu Ser Met Gln Pro Asn Arg Arg Ala		
225	230 235	240
Asp Asp Asn Ala Thr Ile Arg Val Thr Asn Leu Ser Glu Asp Thr Arg		
	245 250	255
Glu Thr Asp Leu Gln Glu Leu Phe Arg Pro Phe Gly Ser Ile Ser Arg		
	260 265	270
Ile Tyr Leu Ala Lys Asp Lys Thr Thr Gly Gln Ser Lys Gly Phe Ala		
	275 280	285
Phe Ile Ser Phe His Arg Arg Glu Asp Ala Ala Arg Ala Ile Ala Gly		
	290 295	300
Val Ser Gly Phe Gly Tyr Asp His Leu Ile Leu Asn Val Glu Trp Ala		
305	310 315	320
Lys Pro Ser Thr Asn		
	325	

<210> 970

<211> 357

<212> PRT

<213> Homo sapiens

<400> 970

Val Arg Val Lys Met Ala Ala Ala Glu Ala Ala Asn Cys Ile Met Glu
1 5 10 15

Val Ser Cys Gly Gln Ala Glu Ser Ser Glu Lys Pro Asn Ala Glu Asp
 20 25 30
 Met Thr Ser Lys Asp Tyr Tyr Phe Asp Ser Tyr Ala His Phe Gly Ile
 35 40 45
 His Glu Glu Met Leu Lys Asp Glu Val Arg Thr Leu Thr Tyr Arg Asn
 50 55 60
 Ser Met Phe His Asn Arg His Leu Phe Lys Asp Lys Val Val Leu Asp
 65 70 75 80
 Val Gly Ser Gly Thr Gly Ile Leu Cys Met Phe Ala Ala Lys Ala Gly
 85 90 95
 Ala Arg Lys Val Ile Gly Ile Glu Cys Ser Ser Ile Ser Asp Tyr Ala
 100 105 110
 Val Lys Ile Val Lys Ala Asn Lys Leu Asp His Val Val Thr Ile Ile
 115 120 125
 Lys Gly Lys Val Glu Glu Val Glu Leu Pro Val Glu Lys Val Asp Ile
 130 135 140
 Ile Ile Ser Glu Trp Met Gly Tyr Cys Leu Phe Tyr Glu Ser Met Leu
 145 150 155 160
 Asn Thr Val Leu Tyr Ala Arg Asp Lys Trp Leu Ala Pro Asp Gly Leu
 165 170 175
 Ile Phe Pro Asp Arg Ala Thr Leu Tyr Val Thr Ala Ile Glu Asp Arg
 180 185 190
 Gln Tyr Lys Asp Tyr Lys Ile His Trp Trp Glu Asn Val Tyr Gly Phe
 195 200 205
 Asp Met Ser Cys Ile Lys Asp Val Ala Ile Lys Glu Pro Leu Val Asp
 210 215 220
 Val Val Asp Pro Lys Gln Leu Val Thr Asn Ala Cys Leu Ile Lys Glu
 225 230 235 240
 Val Asp Ile Tyr Thr Val Lys Val Glu Asp Leu Thr Phe Thr Ser Pro
 245 250 255
 Phe Cys Leu Gln Val Lys Arg Asn Asp Tyr Val His Ala Leu Val Ala
 260 265 270
 Tyr Phe Asn Ile Glu Phe Thr Arg Cys His Lys Arg Thr Gly Phe Ser
 275 280 285

932

Thr Ser Pro Glu Ser Pro Tyr Thr His Trp Lys Gln Thr Val Phe Tyr
290 295 300

Met Glu Asp Tyr Leu Thr Val Lys Thr Gly Glu Glu Ile Phe Gly Thr
305 310 315 320

Ile Gly Met Arg Pro Asn Ala Lys Asn Asn Arg Asp Leu Asp Phe Thr
325 330 335

Ile Asp Leu Asp Phe Lys Gly Gln Leu Cys Glu Leu Ser Cys Ser Thr
340 345 350

Asp Tyr Arg Met Arg
355

<210> 971

<211> 176

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (11)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (176)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 971

Gly Val Pro Arg Arg Ala Tyr Gln Ala Xaa Xaa Leu Arg Arg Val Asp
1 5 10 15

Asp Phe Lys Lys Ala Phe Ser Lys Glu Lys Met Glu Lys Thr Lys Val
20 25 30

Arg Thr Arg Glu Asn Leu Glu Lys Thr Arg Leu Lys Thr Lys Glu Asn
35 40 45

Leu Glu Lys Thr Arg His Thr Leu Glu Lys Arg Met Asn Lys Leu Gly
50 55 60

Thr Arg Leu Val Pro Ala Glu Arg Arg Glu Lys Leu Lys Thr Ser Arg
 65 70 75 80
 Asp Lys Leu Arg Lys Ser Phe Thr Pro Asp His Val Val Tyr Ala Arg
 85 90 95
 Ser Lys Thr Ala Val Tyr Lys Val Pro Pro Phe Thr Phe His Val Lys
 100 105 110
 Lys Ile Arg Glu Gly Gln Val Glu Val Leu Lys Ala Thr Glu Met Val
 115 120 125
 Glu Val Gly Ala Asp Asp Asp Glu Gly Gly Ala Glu Arg Gly Glu Ala
 130 135 140
 Gly Asp Leu Arg Arg Gly Ser Ser Pro Asp Val His Ala Leu Leu Glu
 145 150 155 160
 Ile Thr Glu Glu Ser Asp Ala Val Leu Val Asp Lys Ser Asp Ser Xaa
 165 170 175

<210> 972
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 972
 Gly Lys Ala Arg Arg Ala Ala Lys Leu Gln Ser Ser Gln Glu Pro
 1 5 10 15
 Glu Ala Pro Pro Pro Arg Asp Val Ala Leu Leu Gln Gly Arg Ala Asn
 20 25 30
 Asp Leu Val Lys Tyr Leu Leu Ala Lys Asp Gln Thr Lys Ile Pro Ile
 35 40 45
 Lys Arg Ser Asp Met Leu Lys Asp Ile Ile Lys Glu Tyr Thr Asp Val
 50 55 60
 Tyr Pro Glu Ile Ile Glu Arg Ala Gly Tyr Ser Leu Glu Lys Val Phe
 65 70 75 80
 Gly Ile Gln Leu Lys Glu Ile Asp Lys Asn Asp His Leu Tyr Ile Leu
 85 90 95
 Leu Ser Thr Leu Glu Pro Thr Asp Ala Gly Ile Leu Gly Thr Thr Lys

934

100	105	110
Asp Ser Pro Lys Leu Gly Leu Leu Met Val Leu Leu Ser Ile Ile Phe		
115	120	125
Met Asn Gly Asn Arg Ser Ser Glu Ala Val Ile Trp Glu Val Leu Arg		
130	135	140
Lys Leu Gly Leu Arg Leu Gly Tyr Ile Ile His Ser Leu Gly Thr		
145	150	155

<210> 973

<211> 233

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 973

Arg Ala Xaa Lys Ala Ala Pro Arg Arg Ala Leu Ala Arg Leu Val Leu
1 5 10 15

Ala Trp Cys Arg Trp Leu Val Ser Ala Thr Cys Val Gly Thr Ala Asp
20 25 30

Arg Lys Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn
35 40 45

Phe Lys Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser
50 55 60

Leu Ser Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu
65 70 75 80

Asp Phe Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg
85 90 95

Ala Glu Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val
100 105 110

Asp Ser His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln
115 120 125

Gly Gly Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg
130 135 140

935

Thr Ile Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser
145 150 155 160

Phe Arg Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile
165 170 175

Thr Val Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg
180 185 190

Leu Val Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro
195 200 205

Ala Gly Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys
210 215 220

Ser Lys Glu Tyr Phe Ser Lys Gln Lys
225 230

<210> 974

<211> 174

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (37)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 974

Ser Trp Asp Arg Arg Leu Met Gln Asp Asp Asn Arg Gly Leu Gly Gln
1 5 10 15

Gly Leu Lys Asp Asn Lys Arg Thr Cys Asn Arg Phe Arg Leu Leu Leu
20 25 30

Glu Arg Arg Thr Xaa Gly Ser Glu Val Gln Asp Ser His Ser Thr Ser
35 40 45

Tyr Pro Ser Leu Leu Ser His Leu Thr Ser Met Tyr Leu Asn Ala Pro
50 55 60

Ala Leu Ala Leu Pro Val Ala Arg Met Gln Leu Pro Gly Pro Gly Leu
65 70 75 80

Arg Ser Phe His Pro Leu Ala Ser Ser Leu Pro Cys Asp Phe His Leu
85 90 95

Leu Asn Leu Arg Thr Leu Gln Ala Glu Glu Asp Thr Leu Pro Ser Ala
100 105 110

936

Glu Thr Ala Leu Ile Leu His Arg Lys Val Leu Thr Ala Ala Trp Arg
 115 120 125

Gln Glu Leu Gly Leu Gln Leu His His Lys Pro Arg Gln Gly Ser Pro
 130 135 140

Gly Gln Pro Phe Pro Trp Pro Gly Cys Gly Ile Pro Ser Ala Asn Leu
 145 150 155 160

Leu Asp Val Thr Val Pro Ser Gly Leu Pro Val Gln Gln His
 165 170

<210> 975

<211> 380

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (134)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 975

Arg Pro Glu Val Arg His Ser Arg Glu Ala Pro Glu Ser Arg Arg Trp
 1 5 10 15

Ala Val Trp Arg Ser Leu Glu Ser Leu Pro Arg His Gln Leu Leu Cys
 20 25 30

Leu Pro Val Gly Ala Pro Pro Ala Pro Ala Met Leu Ser Ala Leu Ala
 35 40 45

Arg Pro Ala Ser Ala Ala Leu Arg Arg Ser Phe Ser Thr Ser Ala Gln
 50 55 60

Asn Asn Ala Lys Val Ala Val Leu Gly Ala Ser Gly Gly Ile Gly Gln
 65 70 75 80

Pro Leu Ser Leu Leu Leu Lys Asn Ser Pro Leu Val Ser Arg Leu Thr
 85 90 95

Leu Tyr Asp Ile Ala His Thr Pro Gly Val Ala Ala Asp Leu Ser His
 100 105 110

Ile Glu Thr Lys Ala Ala Val Lys Gly Tyr Leu Gly Pro Glu Gln Leu
 115 120 125

Pro Asp Cys Leu Lys Xaa Cys Asp Val Val Val Ile Pro Ala Gly Val

130 135 140
Pro Arg Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Asn Thr Asn Ala
145 150 155 160
Thr Ile Val Ala Thr Leu Thr Ala Ala Cys Ala Gln His Cys Pro Glu
165 170 175
Ala Met Ile Cys Val Ile Ala Asn Pro Val Asn Ser Thr Ile Pro Ile
180 185 190
Thr Ala Glu Val Phe Lys Lys His Gly Val Tyr Asn Pro Asn Lys Ile
195 200 205
Phe Gly Val Thr Thr Leu Asp Ile Val Arg Ala Asn Thr Phe Val Ala
210 215 220
Glu Leu Lys Gly Leu Asp Pro Ala Arg Val Asn Val Pro Val Ile Gly
225 230 235 240
Gly His Ala Gly Lys Thr Ile Ile Pro Leu Ile Ser Gln Cys Thr Pro
245 250 255
Lys Val Asp Phe Pro Gln Asp Gln Leu Thr Ala Leu Thr Gly Arg Ile
260 265 270
Gln Glu Ala Gly Thr Glu Val Val Lys Ala Lys Ala Gly Ala Gly Ser
275 280 285
Ala Thr Leu Ser Met Ala Tyr Ala Gly Ala Arg Phe Val Phe Ser Leu
290 295 300
Val Asp Ala Met Asn Gly Lys Glu Gly Val Val Glu Cys Ser Phe Val
305 310 315 320
Lys Ser Gln Glu Thr Glu Cys Thr Tyr Phe Ser Thr Pro Leu Leu Leu
325 330 335
Gly Lys Lys Gly Ile Glu Lys Asn Leu Gly Ile Gly Lys Val Ser Ser
340 345 350
Phe Glu Glu Lys Met Ile Ser Asp Ala Ile Pro Glu Leu Lys Ala Ser
355 360 365
Ile Lys Lys Gly Glu Asp Phe Val Lys Thr Leu Lys
370 375 380

<210> 976

<211> 269

<212> PRT

<213> Homo sapiens

<400> 976

Ala Ala Leu Ser Gln Ile Thr Ile Ala Thr Pro Pro Ala Val Lys Gln
1 5 10 15

Thr Ile Ser Asn Ile Ser Gly Phe Asn Glu Thr Cys Leu Arg Trp Arg
20 25 30

Ser Ile Lys Thr Ala Asp Met Glu Glu Met Tyr Leu Phe His Ile Trp
35 40 45

Gly Gln Arg Trp Tyr Gln Lys Glu Phe Ala Gln Glu Met Thr Phe Asn
50 55 60

Ile Ser Ser Ser Ser Arg Asp Pro Glu Val Cys Leu Asp Leu Arg Pro
65 70 75 80

Gly Thr Asn Tyr Asn Val Ser Leu Arg Ala Leu Ser Ser Glu Leu Pro
85 90 95

Val Val Ile Ser Leu Thr Thr Gln Ile Thr Glu Pro Pro Leu Pro Glu
100 105 110

Val Glu Phe Phe Thr Val His Arg Gly Pro Leu Pro Arg Leu Arg Leu
115 120 125

Arg Lys Ala Lys Glu Lys Asn Gly Pro Ile Ser Ser Tyr Gln Val Leu
130 135 140

Val Leu Pro Leu Ala Leu Gln Ser Thr Phe Ser Cys Asp Ser Glu Gly
145 150 155 160

Ala Ser Ser Phe Phe Ser Asn Ala Ser Asp Ala Asp Gly Tyr Val Ala
165 170 175

Ala Glu Leu Leu Ala Lys Asp Val Pro Asp Asp Ala Met Glu Ile Pro
180 185 190

Ile Gly Asp Arg Leu Tyr Tyr Gly Glu Tyr Tyr Asn Ala Pro Leu Lys
195 200 205

Arg Gly Ser Asp Tyr Cys Ile Ile Leu Arg Ile Thr Ser Glu Trp Asn
210 215 220

Lys Val Arg Arg His Ser Cys Ala Val Trp Ala Gln Val Lys Asp Ser
225 230 235 240

Ser Leu Met Leu Leu Gln Met Ala Gly Val Gly Leu Gly Ser Leu Ala
245 250 255

Val Val Ile Ile Leu Thr Phe Leu Ser Phe Ser Ala Val
 260 265

<210> 977

<211> 477

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (471)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (473)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 977

Leu Phe Ser Pro Gln Val Glu Leu Thr Lys Ala Met Val Met Glu Lys
 1 5 10 15

Pro Ser Pro Leu Leu Val Gly Arg Glu Phe Val Arg Gln Tyr Tyr Thr
 20 25 30

Leu Leu Asn Gln Ala Pro Asp Met Leu His Arg Phe Tyr Gly Lys Asn
 35 40 45

Ser Ser Tyr Val His Gly Gly Leu Asp Ser Asn Gly Lys Pro Ala Asp
 50 55 60

Ala Val Tyr Gly Gln Lys Glu Ile His Arg Lys Val Met Ser Gln Asn
 65 70 75 80

Phe Thr Asn Cys His Thr Lys Ile Arg His Val Asp Ala His Ala Thr
 85 90 95

Leu Asn Asp Gly Val Val Val Gln Val Met Gly Leu Leu Ser Asn Asn
 100 105 110

Asn Gln Ala Leu Arg Arg Phe Met Gln Thr Phe Val Leu Ala Pro Glu
 115 120 125

Gly Ser Val Ala Asn Lys Phe Tyr Val His Asn Asp Ile Phe Arg Tyr
 130 135 140

Gln Asp Glu Val Phe Gly Gly Phe Val Thr Glu Pro Gln Glu Glu Ser
 145 150 155 160

940

Glu Glu Glu Val Glu Glu Pro Glu Glu Arg Gln Gln Thr Pro Glu Val
 165 170 175

Val Pro Asp Asp Ser Gly Thr Phe Tyr Asp Gln Ala Val Val Ser Asn
 180 185 190

Asp Met Glu Glu His Leu Glu Glu Pro Val Ala Glu Pro Glu Pro Asp
 195 200 205

Pro Glu Pro Glu Pro Glu Gln Glu Pro Val Ser Glu Ile Gln Glu Glu
 210 215 220

Lys Pro Glu Pro Val Leu Glu Glu Thr Ala Pro Glu Asp Ala Gln Lys
 225 230 235 240

Ser Ser Ser Pro Ala Pro Ala Asp Ile Ala Gln Thr Val Gln Glu Asp
 245 250 255

Leu Arg Thr Phe Ser Trp Ala Ser Val Thr Ser Lys Asn Leu Pro Pro
 260 265 270

Ser Gly Ala Val Pro Val Thr Gly Ile Pro Pro His Val Val Lys Val
 275 280 285

Pro Ala Ser Gln Pro Arg Pro Glu Ser Lys Pro Glu Ser Gln Ile Pro
 290 295 300

Pro Gln Arg Pro Gln Arg Asp Gln Arg Val Arg Glu Gln Arg Ile Asn
 305 310 315 320

Ile Pro Pro Gln Arg Gly Pro Arg Pro Ile Arg Glu Ala Gly Glu Gln
 325 330 335

Gly Asp Ile Glu Pro Arg Arg Met Val Arg His Pro Asp Ser His Gln
 340 345 350

Leu Phe Ile Gly Asn Leu Pro His Glu Val Asp Lys Ser Glu Leu Lys
 355 360 365

Asp Phe Phe Gln Ser Tyr Gly Asn Val Val Glu Leu Arg Ile Asn Ser
 370 375 380

Gly Gly Lys Leu Pro Asn Phe Gly Phe Val Val Phe Asp Asp Ser Glu
 385 390 395 400

Pro Val Gln Lys Val Leu Ser Asn Arg Pro Ile Met Phe Arg Gly Glu
 405 410 415

Val Arg Leu Asn Val Glu Glu Lys Lys Thr Arg Ala Ala Arg Glu Gly
 420 425 430

941

Asp Arg Arg Asp Asn Arg Leu Arg Gly Pro Gly Gly Pro Arg Gly Gly
 435 440 445

Leu Gly Gly Gly Met Arg Gly Pro Pro Arg Gly Gly Met Val Gln Lys
 450 455 460

Pro Gly Phe Gly Val Gly Xaa Gly Xaa Ala Pro Arg Gln
 465 470 475

<210> 978

<211> 339

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (128)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (326)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (336)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (339)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 978

Pro Val Ala Ala Val Ser Gly Arg Ala Val Gly Gly Ser Arg Gly Gly
 1 5 10 15

Gly Arg Gly Gly Met Ala Ala Ala Ala Gly Ala Gly Ser Gly Pro
 20 25 30

Trp Ala Ala Gln Glu Lys Gln Phe Pro Pro Ala Leu Leu Ser Phe Phe
 35 40 45

Ile Tyr Asn Pro Arg Phe Gly Pro Arg Glu Gly Gln Glu Glu Asn Lys
 50 55 60

Ile Leu Phe Tyr His Pro Asn Glu Val Glu Lys Asn Glu Lys Ile Arg

942

65		70		75		80
Asn Val Gly Leu Cys Glu Ala Ile Val Gln Phe Thr Arg Thr Phe Ser						
	85		90		95	
Pro Ser Lys Pro Ala Lys Ser Leu His Thr Gln Lys Asn Arg Gln Phe						
	100		105		110	
Phe Asn Glu Pro Glu Glu Asn Phe Trp Met Val Met Val Val Arg Xaa						
	115		120		125	
Pro Ile Ile Glu Lys Gln Ser Lys Asp Gly Lys Pro Val Ile Glu Tyr						
	130		135		140	
Gln Glu Glu Glu Leu Leu Asp Lys Val Tyr Ser Ser Val Leu Arg Gln						
	145		150		155	160
Cys Tyr Ser Met Tyr Lys Leu Phe Asn Gly Thr Phe Leu Lys Ala Met						
	165		170		175	
Glu Asp Gly Gly Val Lys Leu Leu Lys Glu Arg Leu Glu Lys Phe Phe						
	180		185		190	
His Arg Tyr Leu Gln Thr Leu His Leu Gln Ser Cys Asp Leu Leu Asp						
	195		200		205	
Ile Phe Gly Gly Ile Ser Phe Phe Pro Leu Asp Lys Met Thr Tyr Leu						
	210		215		220	
Lys Ile Gln Ser Phe Ile Asn Arg Met Glu Glu Ser Leu Asn Ile Val						
	225		230		235	240
Lys Tyr Thr Ala Phe Leu Tyr Asn Asp Gln Leu Ile Trp Ser Gly Leu						
	245		250		255	
Glu Gln Asp Asp Met Arg Ile Leu Tyr Lys Tyr Leu Thr Thr Ser Leu						
	260		265		270	
Phe Pro Arg His Ile Glu Pro Glu Leu Ala Gly Arg Asp Ser Pro Ile						
	275		280		285	
Arg Ala Glu Met Pro Gly Asn Leu Gln His Tyr Gly Arg Phe Leu Thr						
	290		295		300	
Gly Pro Leu Asn Leu Asn Asp Pro Asp Ala Lys Cys Arg Phe Pro Lys						
	305		310		315	320
Ile Phe Val Asn Thr Xaa Asp Thr Tyr Glu Glu Leu His Leu Ile Xaa						
	325		330		335	
Tyr Lys Xaa						

943

<210> 979

<211> 283

<212> PRT

<213> Homo sapiens

<400> 979

His Arg Glu Arg Arg Val Gly Leu Arg Cys Ala Arg Arg Thr Ser Glu
1 5 10 15

Ala Ala Gly Ser Gly Ala Gly Pro Pro Gly Pro Leu Gln Gly Arg Ser
20 25 30

Gly Ser Ser Trp Ala Pro Arg Pro Gly Arg Arg Thr Glu Glu Arg Arg
35 40 45

Lys Gly Ala Gly Gly Thr Arg Pro Arg Pro Ala Ala Ala Met Asn Ser
50 55 60

Asn Val Glu Asn Leu Pro Pro His Ile Ile Arg Leu Val Tyr Lys Glu
65 70 75 80

Val Thr Thr Leu Thr Ala Asp Pro Pro Asp Gly Ile Lys Val Phe Pro
85 90 95

Asn Glu Glu Asp Leu Thr Asp Leu Gln Val Thr Ile Glu Gly Pro Glu
100 105 110

Gly Thr Pro Tyr Ala Gly Gly Leu Phe Arg Met Lys Leu Leu Leu Gly
115 120 125

Lys Asp Phe Pro Ala Ser Pro Pro Lys Gly Tyr Phe Leu Thr Lys Ile
130 135 140

Phe His Pro Asn Val Gly Ala Asn Gly Glu Ile Cys Val Asn Val Leu
145 150 155 160

Lys Arg Asp Trp Thr Ala Glu Leu Gly Ile Arg His Val Leu Leu Thr
165 170 175

Ile Lys Cys Leu Leu Ile His Pro Asn Pro Glu Ser Ala Leu Asn Glu
180 185 190

Glu Ala Gly Arg Leu Leu Leu Glu Asn Tyr Glu Glu Tyr Ala Ala Arg
195 200 205

Ala Arg Leu Leu Thr Glu Ile His Gly Gly Ala Gly Gly Pro Ser Gly
210 215 220

944

Arg Ala Glu Ala Gly Arg Ala Leu Ala Ser Gly Thr Glu Ala Ser Ser
225 230 235 240

Thr Asp Pro Gly Ala Pro Gly Gly Pro Gly Gly Ala Glu Gly Pro Met
245 250 255

Ala Lys Lys His Ala Gly Glu Arg Asp Lys Lys Leu Ala Ala Lys Lys
260 265 270

Lys Thr Asp Lys Lys Arg Ala Leu Arg Arg Leu
275 280

<210> 980

<211> 353

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (333)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (346)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 980

Arg Lys Gln Cys Gln Asp Ser Lys Asp Ser Asn His Leu Pro Lys Met
1 5 10 15

Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr Ser
20 25 30

Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln Ser
35 40 45

Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro Ser
50 55 60

Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val Pro
65 70 75 80

Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His Ile
85 90 95

Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile Leu
100 105 110

945

Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe Ser
 115 120 125
 Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu Thr
 130 135 140
 Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu Thr
 145 150 155 160
 His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn Leu
 165 170 175
 Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val Ser
 180 185 190
 Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser Phe
 195 200 205
 Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu Thr
 210 215 220
 Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr Phe
 225 230 235 240
 Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu Leu
 245 250 255
 Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu Val
 260 265 270
 Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val Asn
 275 280 285
 Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys Phe
 290 295 300
 Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser Lys
 305 310 315 320
 Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Xaa Thr Ser Leu
 325 330 335
 Pro Pro Asp Met Tyr Glu Cys Leu Arg Xaa Ala Asn Glu Val Thr Leu
 340 345 350
 Asn

946

<210> 981
 <211> 343
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (343)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 981

Asn	Leu	Thr	Lys	Asn	Met	Thr	Ala	Leu	Ser	Ser	Glu	Asn	Cys	Ser	Phe
1				5					10					15	
Gln	Tyr	Gln	Leu	Arg	Gln	Thr	Asn	Gln	Pro	Leu	Asp	Val	Asn	Tyr	Leu
			20					25					30		
Leu	Phe	Leu	Ile	Ile	Leu	Gly	Lys	Ile	Leu	Leu	Asn	Ile	Leu	Thr	Leu
		35					40					45			
Gly	Met	Arg	Arg	Lys	Asn	Thr	Cys	Gln	Asn	Phe	Met	Glu	Tyr	Phe	Cys
	50					55					60				
Ile	Ser	Leu	Ala	Phe	Val	Asp	Leu	Leu	Leu	Val	Asn	Ile	Ser	Ile	
65					70					75				80	
Ile	Leu	Tyr	Phe	Arg	Asp	Phe	Val	Leu	Leu	Ser	Ile	Arg	Phe	Thr	Lys
				85						90				95	
Tyr	His	Ile	Cys	Leu	Phe	Thr	Gln	Ile	Ile	Ser	Phe	Thr	Tyr	Gly	Phe
			100					105						110	
Leu	His	Tyr	Pro	Val	Phe	Leu	Thr	Ala	Cys	Ile	Asp	Tyr	Cys	Leu	Asn
			115					120				125			
Phe	Ser	Lys	Thr	Thr	Lys	Leu	Ser	Phe	Lys	Cys	Gln	Lys	Leu	Phe	Tyr
		130				135					140				
Phe	Phe	Thr	Val	Ile	Leu	Ile	Trp	Ile	Ser	Val	Leu	Ala	Tyr	Val	Leu
145					150					155					160
Gly	Asp	Pro	Ala	Ile	Tyr	Gln	Ser	Leu	Lys	Ala	Gln	Asn	Ala	Tyr	Ser
			165						170					175	
Arg	His	Cys	Pro	Phe	Tyr	Val	Ser	Ile	Gln	Ser	Tyr	Trp	Leu	Ser	Phe
			180						185				190		
Phe	Met	Val	Met	Ile	Leu	Phe	Val	Ala	Phe	Ile	Thr	Cys	Trp	Glu	Glu
		195					200					205			
Val	Thr	Thr	Leu	Val	Gln	Ala	Ile	Arg	Ile	Thr	Ser	Tyr	Met	Asn	Glu

947

210	215	220
Thr Ile Leu Tyr Phe Pro Phe Ser Ser His Ser Ser Tyr Thr Val Arg		
225	230	235 240
Ser Lys Lys Ile Phe Leu Ser Lys Leu Ile Val Cys Phe Leu Ser Thr		
	245	250 255
Trp Leu Pro Phe Val Leu Leu Gln Val Ile Ile Val Leu Leu Lys Val		
	260	265 270
Gln Ile Pro Ala Tyr Ile Glu Met Asn Ile Pro Trp Leu Tyr Phe Val		
	275	280 285
Asn Ser Phe Leu Ile Ala Thr Val Tyr Trp Phe Asn Cys His Lys Leu		
	290	295 300
Asn Leu Lys Asp Ile Gly Leu Pro Leu Asp Pro Phe Val Asn Trp Lys		
	305	310 315 320
Cys Cys Phe Ile Pro Leu Thr Ile Pro Asn Leu Glu Gln Ile Glu Lys		
	325	330 335
Pro Ile Ser Ile Met Ile Xaa		
	340	

<210> 982

<211> 142

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (108)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (111)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (114)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (121)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (122)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (126)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (127)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (132)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 982

Gly	Leu	Pro	Pro	Ser	Thr	Phe	Leu	His	Ser	Ala	Val	Ser	Thr	Leu	Pro
1				5					10					15	

His	Arg	Pro	Ser	Pro	Pro	Ser	Leu	Leu	Pro	Ala	Pro	Cys	Lys	Pro	Leu
			20				25						30		

Arg	Leu	Gly	Leu	Ala	Thr	Val	Pro	Ala	Gly	Ser	Pro	Gly	Leu	Gly	Val
	35						40					45			

Gly	Asp	Ser	Leu	Gln	Ala	Arg	Ser	Pro	Glu	Thr	Ser	Glu	Gly	His	Pro
	50					55						60			

Leu	Arg	Val	Ala	Arg	Pro	Pro	Val	Ala	Asn	Leu	Ser	Ala	Ala	Ser	Ala
	65				70				75					80	

Thr	Ser	Pro	Ala	Gly	Pro	Trp	Phe	Arg	Trp	Pro	Pro	Arg	Cys	Leu	Ala
				85					90					95	

Glu	Thr	Arg	His	Gly	Pro	Ser	Ala	Gly	Pro	His	Xaa	Phe	Pro	Xaa	Pro
			100					105						110	

Gly	Xaa	Trp	His	Cys	Ser	Arg	Gln	Xaa	Xaa	Gly	His	Gln	Xaa	Xaa	Asn
	115						120					125			

Arg	Thr	Gln	Xaa	Pro	Ala	Gln	Thr	Ala	Ala	Gly	Met	Gly	Ala
	130					135					140		

<210> 983
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (72)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (135)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (139)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 983

Val Asn Phe Lys Ala Phe Glu Met Gly Lys Asp Tyr Tyr Cys Ile Leu
 1 5 10 15

Gly Ile Glu Lys Gly Ala Ser Asp Glu Asp Ile Lys Lys Ala Tyr Arg
 20 25 30

Lys Gln Ala Leu Lys Phe His Pro Asp Lys Asn Lys Ser Pro Gln Ala
 35 40 45

Glu Glu Lys Phe Lys Glu Val Ala Glu Ala Tyr Glu Val Leu Ser Asp
 50 55 60

Pro Lys Lys Arg Glu Ile Tyr Xaa Gln Phe Gly Glu Glu Gly Leu Lys
 65 70 75 80

Gly Gly Ala Gly Gly Thr Asp Gly Gln Gly Gly Thr Phe Arg Tyr Thr
 85 90 95

Phe His Gly Asp Pro His Ala Thr Phe Ala Ala Phe Phe Gly Gly Ser
 100 105 110

Asn Pro Phe Glu Ile Phe Phe Gly Arg Arg Met Gly Gly Gly Arg Asp
 115 120 125

Ser Glu Glu Met Glu Ile Xaa Gly Asp Pro Xaa Ser Ala Phe Gly Phe
 130 135 140

Ser Met Asn Gly Tyr Pro Arg Asp Arg Asn Ser Val Gly Pro Ser Arg
 145 150 155 160

950

Leu Lys Gln Asp Pro Pro Val Ile His Glu Leu Arg Val Ser Leu Glu
 165 170 175

Glu Ile Tyr Ser Gly Cys Thr Lys Arg Asp Glu Arg Phe Leu Glu Lys
 180 185 190

Gly

<210> 984

<211> 402

<212> PRT

<213> Homo sapiens

<400> 984

Lys Ser Tyr Glu Met Glu Leu Glu Glu Gly Lys Ala Gly Ser Gly Leu
 1 5 10 15

Arg Gln Tyr Tyr Leu Ser Lys Ile Glu Glu Leu Gln Leu Ile Val Asn
 20 25 30

Asp Lys Ser Gln Asn Leu Arg Arg Leu Gln Ala Gln Arg Asn Glu Leu
 35 40 45

Asn Ala Lys Val Arg Leu Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu
 50 55 60

Gln Gly Ser Tyr Val Gly Glu Val Val Arg Ala Met Asp Lys Lys Lys
 65 70 75 80

Val Leu Val Lys Val His Pro Glu Gly Lys Phe Val Val Asp Val Asp
 85 90 95

Lys Asn Ile Asp Ile Asn Asp Val Thr Pro Asn Cys Arg Val Ala Leu
 100 105 110

Arg Asn Asp Ser Tyr Thr Leu His Lys Ile Leu Pro Asn Lys Val Asp
 115 120 125

Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro Asp Ser Thr Tyr
 130 135 140

Glu Met Ile Gly Gly Leu Asp Lys Gln Ile Lys Glu Ile Lys Glu Val
 145 150 155 160

Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu Ala Leu Gly Ile
 165 170 175

Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys
 180 185 190
 Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr Phe Ile
 195 200 205
 Arg Val Ser Gly Ser Glu Leu Val Gln Lys Phe Ile Gly Glu Gly Ala
 210 215 220
 Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala Pro Ser
 225 230 235 240
 Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ser Arg Leu Glu
 245 250 255
 Gly Gly Ser Gly Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu
 260 265 270
 Leu Asn Gln Leu Asp Gly Phe Glu Ala Thr Lys Asn Ile Lys Val Ile
 275 280 285
 Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Ser Ala Leu Leu Arg Pro
 290 295 300
 Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro Asn Glu Glu Ala
 305 310 315 320
 Arg Leu Asp Ile Leu Lys Ile His Ser Arg Lys Met Asn Leu Thr Arg
 325 330 335
 Gly Ile Asn Leu Arg Lys Ile Ala Glu Leu Met Pro Gly Ala Ser Gly
 340 345 350
 Ala Glu Val Lys Gly Val Cys Thr Glu Ala Gly Met Tyr Ala Leu Arg
 355 360 365
 Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala
 370 375 380
 Lys Val Met Gln Lys Asp Ser Glu Lys Asn Met Ser Ile Lys Lys Leu
 385 390 395 400
 Trp Lys

<210> 985

<211> 347

<212> PRT

<213> Homo sapiens

952

<400> 985

Arg Arg Arg Arg Trp His Pro Gly Pro Gly Gly Pro Arg Arg Thr Ala
 1 5 10 15

Gly Lys Gly Pro Arg Lys Val Ala Ser Ala Ser Ala Ala Ser Thr
 20 25 30

Leu Ser Glu Pro Pro Arg Arg Thr Gln Glu Ser Arg Thr Arg Thr Arg
 35 40 45

Ala Leu Gly Leu Pro Thr Leu Pro Met Glu Lys Leu Ala Ala Ser Thr
 50 55 60

Glu Pro Gln Gly Pro Arg Pro Val Leu Gly Arg Glu Ser Val Gln Val
 65 70 75 80

Pro Asp Asp Gln Asp Phe Arg Ser Phe Arg Ser Glu Cys Glu Ala Glu
 85 90 95

Val Gly Trp Asn Leu Thr Tyr Ser Arg Ala Gly Val Ser Val Trp Val
 100 105 110

Gln Ala Val Glu Met Asp Arg Thr Leu His Lys Ile Lys Cys Arg Met
 115 120 125

Glu Cys Cys Asp Val Pro Ala Glu Thr Leu Tyr Asp Val Leu His Asp
 130 135 140

Ile Glu Tyr Arg Lys Lys Trp Asp Ser Asn Val Ile Glu Thr Phe Asp
 145 150 155 160

Ile Ala Arg Leu Thr Val Asn Ala Asp Val Gly Tyr Tyr Ser Trp Arg
 165 170 175

Cys Pro Lys Pro Leu Lys Asn Arg Asp Val Ile Thr Leu Arg Ser Trp
 180 185 190

Leu Pro Met Gly Ala Asp Tyr Ile Ile Met Asn Tyr Ser Val Lys His
 195 200 205

Pro Lys Tyr Pro Pro Arg Lys Asp Leu Val Arg Ala Val Ser Ile Gln
 210 215 220

Thr Gly Tyr Leu Ile Gln Ser Thr Gly Pro Lys Ser Cys Val Ile Thr
 225 230 235 240

Tyr Leu Ala Gln Val Asp Pro Lys Gly Ser Leu Pro Lys Trp Val Val
 245 250 255

Asn Lys Ser Ser Gln Phe Leu Ala Pro Lys Ala Met Lys Lys Met Tyr

953

260 265 270
 Lys Ala Cys Leu Lys Tyr Pro Glu Trp Lys Gln Lys His Leu Pro His
 275 280 285
 Phe Lys Pro Trp Leu His Pro Glu Gln Ser Pro Leu Pro Ser Leu Ala
 290 295 300
 Leu Ser Glu Leu Ser Val Gln His Ala Asp Ser Leu Glu Asn Ile Asp
 305 310 315 320
 Glu Ser Ala Val Ala Glu Ser Arg Glu Glu Arg Met Gly Gly Ala Gly
 325 330 335
 Gly Glu Gly Ser Asp Asp Thr Ser Leu Thr
 340 345

<210> 986

<211> 106

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (36)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 986

Ala Ser Ile Cys Ala Asp Ala Lys Leu Trp Thr Met Tyr Ala Arg Pro
 1 5 10 15
 Ser Asn Arg Gln Arg Cys Leu Gly Ser Lys His Thr Glu Arg Thr Trp
 20 25 30
 Thr Ala Trp Xaa Arg Ser Leu Ile Arg Pro Phe Ser Met His Ile Leu
 35 40 45
 Pro Lys Gln Ser Gln Ile Pro Leu Lys Gly Ala Asp Ser Ile Ser Ser
 50 55 60
 Ser Val Gln Thr Leu Arg Ala Glu Arg Ser Gly Ser Gly Ser His Val
 65 70 75 80
 Thr Ala Gln Asn Asn Leu Arg Asn Pro Leu Cys Pro Glu Gly Ser Leu
 85 90 95
 Thr Ser Pro Ser Gly Ser Glu Gln Ser Leu
 100 105

954

<210> 987

<211> 172

<212> PRT

<213> Homo sapiens

<400> 987

Thr Pro Arg Gly Ala Val Lys Pro Ser Ala Asn Lys Tyr Pro Ile Phe
1 5 10 15

Phe Phe Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe
20 25 30

Pro Tyr Lys Glu Tyr Lys Asp Lys Phe Gly Lys Ser Asn Lys Arg Lys
35 40 45

Gly Phe Asn Glu Gly Leu Trp Glu Ile Glu Asn Asn Pro Gly Val Lys
50 55 60

Phe Thr Gly Tyr Gln Ala Ile Gln Gln Gln Ser Ser Ser Glu Thr Glu
65 70 75 80

Gly Glu Gly Gly Asn Thr Ala Asp Ala Ser Ser Glu Glu Glu Gly Asp
85 90 95

Arg Val Glu Glu Asp Gly Lys Gly Lys Arg Lys Asn Glu Lys Ala Gly
100 105 110

Ser Lys Arg Lys Lys Ser Tyr Thr Ser Lys Lys Ser Ser Lys Gln Ser
115 120 125

Arg Lys Ser Pro Gly Asp Glu Asp Asp Lys Asp Cys Lys Glu Glu Glu
130 135 140

Asn Lys Ser Ser Ser Glu Gly Gly Asp Ala Gly Asn Asp Thr Arg Asn
145 150 155 160

Thr Thr Ser Asp Leu Gln Lys Thr Ser Glu Gly Thr
165 170

<210> 988

<211> 238

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (101)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (146)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 988

Ala Lys Gln Asp Pro Val Pro Glu Gln Glu Met Ser Pro Ser Ile Ser
1 5 10 15

Asp Pro Cys Leu Gly Gln Ala Leu Met Gly Gly Pro Ser Phe Lys Ala
20 25 30

Val Val Gly Thr Ala Pro Pro Asn Ala Ser Leu Ser Phe Leu Pro Ile
35 40 45

His Gln Tyr Thr Ala Gly Pro Phe Leu Val Phe Val Gln Gln Glu Thr
50 55 60

His Phe Trp Trp Asp Met Pro Ser Ser Ala Thr Gly Pro Leu Thr Pro
65 70 75 80

Cys Ile Ser Val Leu Pro Val Ser Ala Gly Thr Asp Ser Lys Gly Lys
85 90 95

Pro Ser Val Trp Xaa Ile Gly Gly Trp Glu Gln Arg Gly Glu Asn Ala
100 105 110

Val Leu Ser Phe Cys Leu Gly Ile Pro His Thr Thr Trp Val Leu Pro
115 120 125

Gly Lys Pro Val Leu Ser Lys Thr Met Asp Leu Ala Ser Pro Thr Gly
130 135 140

Leu Xaa Ser Gln His Leu Arg Glu Gly Gly Trp Lys Arg Leu Cys Pro
145 150 155 160

His Phe Glu Leu Gln Ala Gly Ser Ala Ala Leu Lys Pro Ser Ser Asp
165 170 175

Phe Leu Thr Gln Asp Pro Ala Pro Gly Arg Arg Arg Val Gly Ala Gly
180 185 190

Leu Val Gly Gln Lys Glu Ala Ser Ala Gly Leu Glu Asp Pro Ser Ser
195 200 205

Thr Ser His Ser Val Ser Ser Ser Trp Glu Asn Leu Cys Gln Ala Arg
210 215 220

Ala Val Ile Gly Pro His Glu Val Ser Glu Ala Pro Ser Trp

956

225

230

235

<210> 989

<211> 74

<212> PRT

<213> Homo sapiens

<400> 989

Ser Leu Ile Lys Ala Leu Tyr Ile Leu Tyr Gly Phe Arg His His His
1 5 10 15

Thr Lys Lys Leu Thr Pro Ser Ile Pro Val Phe Val Gly Gln Ala Ser
20 25 30

Phe Phe Ser Pro Cys Ser Val Ser His Thr Val Cys Leu Gln Lys Leu
35 40 45

Leu Ile Gly Ala Lys Tyr Asn Cys Gln Tyr Asn Leu Lys Thr Thr Met
50 55 60

Cys Pro Arg Arg Pro Thr Cys Leu Phe Pro
65 70

<210> 990

<211> 295

<212> PRT

<213> Homo sapiens

<400> 990

Ala Pro Ala Arg Pro Gly Ser Leu Pro Ser Thr Arg Ser Ala Pro Leu
1 5 10 15

Val Pro Ser Ser Arg Arg Arg Pro Ala Glu Ser Pro Leu Arg Ser Arg
20 25 30

Arg Cys Arg Gly Asp Met Val Leu Cys Val Gln Gly Pro Arg Pro Leu
35 40 45

Leu Ala Val Glu Arg Thr Gly Gln Arg Pro Leu Trp Ala Pro Ser Leu
50 55 60

Glu Leu Pro Lys Pro Val Met Gln Pro Leu Pro Ala Gly Ala Phe Leu
65 70 75 80

Glu Glu Val Ala Glu Gly Thr Pro Ala Gln Thr Glu Ser Glu Pro Lys
85 90 95

957

Val Leu Asp Pro Glu Glu Asp Leu Leu Cys Ile Ala Lys Thr Phe Ser
 100 105 110
 Tyr Leu Arg Glu Ser Gly Trp Tyr Trp Gly Ser Ile Thr Ala Ser Glu
 115 120 125
 Ala Arg Gln His Leu Gln Lys Met Pro Glu Gly Thr Phe Leu Val Arg
 130 135 140
 Asp Ser Thr His Pro Ser Tyr Leu Phe Thr Leu Ser Val Lys Thr Thr
 145 150 155 160
 Arg Gly Pro Thr Asn Val Arg Ile Glu Tyr Ala Asp Ser Ser Phe Arg
 165 170 175
 Leu Asp Ser Asn Cys Leu Ser Arg Pro Arg Ile Leu Ala Phe Pro Asp
 180 185 190
 Val Val Ser Leu Val Gln His Tyr Val Ala Ser Cys Thr Ala Asp Thr
 195 200 205
 Arg Ser Asp Ser Pro Asp Pro Ala Pro Thr Pro Ala Leu Pro Met Pro
 210 215 220
 Lys Glu Asp Ala Pro Ser Asp Pro Ala Leu Pro Ala Pro Pro Pro Ala
 225 230 235 240
 Thr Ala Val His Leu Lys Leu Val Gln Pro Phe Val Arg Arg Ser Ser
 245 250 255
 Ala Arg Ser Leu Gln His Leu Cys Arg Leu Val Ile Asn Arg Leu Val
 260 265 270
 Ala Asp Val Asp Cys Leu Pro Leu Pro Arg Arg Met Ala Asp Tyr Leu
 275 280 285
 Arg Gln Tyr Pro Phe Gln Leu
 290 295

<210> 991

<211> 58

<212> PRT

<213> Homo sapiens

<400> 991

Leu His Lys Val Ser Ile Leu Leu Tyr Ser Ala Val Leu Val Ser Phe
 1 5 10 15

Ser Cys Ile Gly Phe His Cys Ile Tyr Ser Leu Phe Met Leu Asn Leu

958

	20		25		30
Ala	Lys	Asp	Glu	His	Cys
	35		40		45
Pro	Pro	Leu	Lys	Cys	Leu
Cys	His	Phe	Glu		
Phe	Cys	Ala	Asn	Phe	Val
	50		55		
Ala	Arg	Met	Arg		

<210> 992
 <211> 203
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (8)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 992
 Ala His Ala Ser Pro Thr Arg Xaa Glu Ala Arg Val Val Val Val Arg
 1 5 10 15
 Cys Leu Pro Ala Cys Val Arg Asp Leu Pro Asp Ser Val Ala Ala Met
 20 25 30
 Ala Ser Asp Glu Gly Lys Leu Phe Val Gly Gly Leu Ser Phe Asp Thr
 35 40 45
 Asn Glu Gln Ser Leu Glu Gln Val Phe Ser Lys Tyr Gly Gln Ile Ser
 50 55 60
 Glu Val Val Val Val Lys Asp Arg Glu Thr Gln Arg Ser Arg Gly Phe
 65 70 75 80
 Gly Phe Val Thr Phe Glu Asn Ile Asp Asp Ala Lys Asp Ala Met Met
 85 90 95
 Ala Met Asn Gly Lys Ser Val Asp Gly Arg Gln Ile Arg Val Asp Gln
 100 105 110
 Ala Gly Lys Ser Ser Asp Asn Arg Ser Arg Gly Tyr Arg Gly Gly Ser
 115 120 125
 Ala Gly Gly Arg Gly Phe Phe Arg Gly Gly Arg Gly Arg Gly Gly
 130 135 140
 Phe Ser Arg Gly Gly Gly Asp Arg Gly Tyr Gly Gly Asn Arg Phe Glu
 145 150 155 160

959

Ser Arg Ser Gly Gly Tyr Gly Gly Ser Arg Asp Tyr Tyr Ser Ser Arg
165 170 175

Ser Gln Ser Gly Gly Tyr Ser Asp Arg Ser Ser Gly Gly Ser Tyr Arg
180 185 190

Asp Ser Tyr Asp Ser Tyr Ala Thr His Asn Glu
195 200

<210> 993

<211> 252

<212> PRT

<213> Homo sapiens

<400> 993

Gly Gly Leu Ala Trp Arg Ala Leu Arg Thr Ser Gly Thr Leu Leu Arg
1 5 10 15

Val Glu Arg Leu Leu Leu Glu Asp Tyr Cys Pro Glu Glu Lys Met Phe
20 25 30

Gly Phe His Lys Pro Lys Met Tyr Arg Ser Ile Glu Gly Cys Cys Ile
35 40 45

Cys Arg Ala Lys Ser Ser Ser Ser Arg Phe Thr Asp Ser Lys Arg Tyr
50 55 60

Glu Lys Asp Phe Gln Ser Cys Phe Gly Leu His Glu Thr Arg Ser Gly
65 70 75 80

Asp Ile Cys Asn Ala Cys Val Leu Leu Val Lys Arg Trp Lys Lys Leu
85 90 95

Pro Ala Gly Ser Lys Lys Asn Trp Asn His Val Val Asp Ala Arg Ala
100 105 110

Gly Pro Ser Leu Lys Thr Thr Leu Lys Pro Lys Lys Val Lys Thr Leu
115 120 125

Ser Gly Asn Arg Ile Lys Ser Asn Gln Ile Ser Lys Leu Gln Lys Glu
130 135 140

Phe Lys Arg His Asn Ser Asp Ala His Ser Thr Thr Ser Ser Ala Ser
145 150 155 160

Pro Ala Gln Ser Pro Cys Tyr Ser Asn Gln Ser Asp Asp Gly Ser Asp
165 170 175

Thr Glu Met Ala Ser Gly Ser Asn Arg Thr Pro Val Phe Ser Phe Leu

960

180	185	190
Asp Leu Thr Tyr Trp Lys Arg Gln Lys Ile Cys Cys Gly Ile Ile Tyr		
195	200	205
Lys Gly Arg Phe Gly Glu Val Leu Ile Asp Thr His Leu Phe Lys Pro		
210	215	220
Cys Cys Ser Asn Lys Lys Ala Ala Ala Glu Lys Pro Glu Glu Gln Gly		
225	230	235 240
Gln Ser Leu Cys Pro Ser Pro Leu Arg Ser Gly Asp		
245	250	

<210> 994

<211> 170

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 994

Arg Thr Arg Gly Xaa Asp Thr Gln Pro Thr Val Cys Thr Asp Ala Pro
1 5 10 15

Ser Leu Leu Pro Leu Ser Arg Leu His Leu Arg Gly Ser Trp Asp Arg
20 25 30

Arg Ser Val Ala Asn Met Gln Leu Phe Val Arg Ala Gln Glu Leu His
35 40 45

Thr Phe Glu Val Thr Gly Gln Glu Thr Val Ala Gln Ile Lys Ala His
50 55 60

Val Ala Ser Leu Glu Gly Ile Ala Pro Glu Asp Gln Val Val Leu Leu
65 70 75 80

Ala Gly Ala Pro Leu Glu Asp Glu Ala Thr Leu Gly Gln Cys Gly Val
85 90 95

Glu Ala Leu Thr Thr Leu Glu Val Ala Gly Arg Met Leu Gly Gly Lys
100 105 110

Val His Gly Ser Leu Ala Arg Ala Gly Lys Val Arg Gly Gln Thr Pro
115 120 125

Lys Val Ala Lys Gln Glu Lys Lys Lys Lys Lys Thr Gly Arg Ala Lys
 130 135 140

Arg Arg Met Gln Tyr Asn Arg Arg Phe Val Asn Val Val Pro Thr Phe
 145 150 155 160

Gly Lys Lys Lys Gly Pro Asn Ala Asn Ser
 165 170

<210> 995

<211> 156

<212> PRT

<213> Homo sapiens

<400> 995

Gly Ser Gly Thr His Pro Ala Arg Ala Ala Pro Ala Pro His Ala Arg
 1 5 10 15

Ala Ser Phe Ser Arg Pro Leu Ala Pro Arg Arg Ser His Leu Ser Ser
 20 25 30

Leu Ala His Ala Arg Pro Ala Arg Glu Pro Arg Arg Arg Leu Gly Pro
 35 40 45

Ala Glu Ala Pro Pro Arg His Val Phe Ala Ser Arg Arg Lys Leu Glu
 50 55 60

Thr Lys Ala Gly His Pro Pro Ala Val Lys Ala Gly Gly Met Arg Ile
 65 70 75 80

Val Gln Lys His Pro His Thr Gly Asp Thr Lys Glu Glu Lys Asp Lys
 85 90 95

Asp Asp Gln Glu Trp Glu Ser Pro Ser Pro Pro Lys Pro Thr Val Phe
 100 105 110

Ile Ser Gly Val Ile Ala Arg Gly Asp Lys Asp Phe Pro Pro Ala Ala
 115 120 125

Ala Gln Val Ala His Gln Lys Pro His Ala Ser Met Asp Lys His Pro
 130 135 140

Ser Pro Arg Thr Gln His Ile Gln Gln Pro Arg Lys
 145 150 155

<210> 996

<211> 217

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (27)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 996

Asn Ser Ala Glu Gln Glu Gly Ser Gln Trp Ser Leu Pro Val Leu His
 1 5 10 15

Ser Val Pro Asp Pro Ala Cys Leu Thr Leu Xaa Arg Val Ser Lys Gly
 20 25 30

Leu Ala Ala Val Arg Ser Ser Val Pro Arg Ala Gly Gly Val Ser Arg
 35 40 45

Arg Leu Ala Ala Val Arg Ser Thr Val Leu Cys Arg Ala Val Gly Cys
 50 55 60

Ile Leu Ala Glu Leu Leu Ala His Arg Pro Leu Leu Pro Gly Thr Ser
 65 70 75 80

Glu Ile His Gln Ile Asp Leu Ile Val Gln Leu Leu Gly Thr Pro Ser
 85 90 95

Glu Asn Ile Trp Pro Gly Phe Ser Lys Leu Pro Leu Val Gly Gln Tyr
 100 105 110

Ser Leu Arg Lys Gln Pro Tyr Asn Asn Leu Lys His Lys Phe Pro Trp
 115 120 125

Leu Ser Glu Ala Gly Leu Arg Cys Cys Thr Ser Cys Ser Cys Thr Thr
 130 135 140

Leu Arg Lys Gly Arg Arg Pro Gly Thr Ala Trp Arg Ala Pro Ile Ser
 145 150 155 160

Arg Arg Ser Pro Tyr Pro Val Ser Arg Ser Ser Cys Arg Pro Phe Pro
 165 170 175

Thr Thr Ala Thr Ser Gly Pro Pro Gln Pro Pro Pro Arg Ala Arg Ala
 180 185 190

Ser Ala Val Asn Pro Asp Gly Gly Pro Gly Thr Arg Leu Tyr Ser His
 195 200 205

Thr Arg Ser Ser Asp Gln Trp Cys Leu
 210 215

963

<210> 997

<211> 466

<212> PRT

<213> Homo sapiens

<400> 997

Val Ser Pro Arg Ala Gly Gly Ala Gly Asn Asn Arg Gly Arg Ala His
 1 5 10 15
 Arg Ala Ser Ser Cys Ser Leu Pro Ala Pro Pro Ala Thr Leu Asp Pro
 20 25 30
 Arg Ile Pro Pro Ala Arg Leu Pro Ala Met Ala Asp Lys Glu Ala Ala
 35 40 45
 Phe Asp Asp Ala Val Glu Glu Arg Val Ile Asn Glu Glu Tyr Lys Ile
 50 55 60
 Trp Lys Lys Asn Thr Pro Phe Leu Tyr Asp Leu Val Met Thr His Ala
 65 70 75 80
 Leu Glu Trp Pro Ser Leu Thr Ala Gln Trp Leu Pro Asp Val Thr Arg
 85 90 95
 Pro Glu Gly Lys Asp Phe Ser Ile His Arg Leu Val Leu Gly Thr His
 100 105 110
 Thr Ser Asp Glu Gln Asn His Leu Val Ile Ala Ser Val Gln Leu Pro
 115 120 125
 Asn Asp Asp Ala Gln Phe Asp Ala Ser His Tyr Asp Ser Glu Lys Gly
 130 135 140
 Glu Phe Gly Gly Phe Gly Ser Val Ser Gly Lys Ile Glu Ile Glu Ile
 145 150 155 160
 Lys Ile Asn His Glu Gly Glu Val Asn Arg Ala Arg Tyr Met Pro Gln
 165 170 175
 Asn Pro Cys Ile Ile Ala Thr Lys Thr Pro Ser Ser Asp Val Leu Val
 180 185 190
 Phe Asp Tyr Thr Lys His Pro Ser Lys Pro Asp Pro Ser Gly Glu Cys
 195 200 205
 Asn Pro Asp Leu Arg Leu Arg Gly His Gln Lys Glu Gly Tyr Gly Leu
 210 215 220
 Ser Trp Asn Pro Asn Leu Ser Gly His Leu Leu Ser Ala Ser Asp Asp

964

225 230 235 240
 His Thr Ile Cys Leu Trp Asp Ile Ser Ala Val Pro Lys Glu Gly Lys
 245 250 255
 Val Val Asp Ala Lys Thr Ile Phe Thr Gly His Thr Ala Val Val Glu
 260 265 270
 Asp Val Ser Trp His Leu Leu His Glu Ser Leu Phe Gly Ser Val Ala
 275 280 285
 Asp Asp Gln Lys Leu Met Ile Trp Asp Thr Arg Ser Asn Asn Thr Ser
 290 295 300
 Lys Pro Ser His Ser Val Asp Ala His Thr Ala Glu Val Asn Cys Leu
 305 310 315 320
 Ser Phe Asn Pro Tyr Ser Glu Phe Ile Leu Ala Thr Gly Ser Ala Asp
 325 330 335
 Lys Thr Val Ala Leu Trp Asp Leu Arg Asn Leu Lys Leu Lys Leu His
 340 345 350
 Ser Phe Glu Ser His Lys Asp Glu Ile Phe Gln Val Gln Trp Ser Pro
 355 360 365
 His Asn Glu Thr Ile Leu Ala Ser Ser Gly Thr Asp Arg Arg Leu Asn
 370 375 380
 Val Trp Asp Leu Ser Lys Ile Gly Glu Glu Gln Ser Pro Glu Asp Ala
 385 390 395 400
 Glu Asp Gly Pro Pro Glu Leu Leu Phe Ile His Gly Gly His Thr Ala
 405 410 415
 Lys Ile Ser Asp Phe Ser Trp Asn Pro Asn Glu Pro Trp Val Ile Cys
 420 425 430
 Ser Val Ser Glu Asp Asn Ile Met Gln Val Trp Gln Met Ala Glu Asn
 435 440 445
 Ile Tyr Asn Asp Glu Asp Pro Glu Gly Ser Val Asp Pro Glu Gly Gln
 450 455 460
 Gly Ser
 465

<210> 998

<211> 165

965

<212> PRT

<213> Homo sapiens

<400> 998

Thr Arg Pro Pro Thr Arg Arg Pro Thr Arg Pro Pro Lys Ala Lys Lys
 1 5 10 15

Glu Ala Pro Ala Pro Pro Lys Ala Glu Ala Lys Ala Lys Ala Leu Lys
 20 25 30

Ala Lys Lys Ala Val Leu Lys Gly Val His Ser His Lys Lys Lys Lys
 35 40 45

Ile Arg Thr Ser Pro Thr Phe Arg Arg Pro Lys Thr Leu Arg Leu Arg
 50 55 60

Arg Gln Pro Lys Tyr Pro Arg Lys Ser Ala Pro Arg Arg Asn Lys Leu
 65 70 75 80

Asp His Tyr Ala Ile Ile Lys Phe Pro Leu Thr Thr Glu Ser Ala Met
 85 90 95

Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val Asp Val Lys
 100 105 110

Ala Asn Lys His Gln Ile Lys Gln Ala Val Lys Lys Leu Tyr Asp Ile
 115 120 125

Asp Val Ala Lys Val Asn Thr Leu Ile Arg Pro Asp Gly Glu Lys Lys
 130 135 140

Ala Tyr Val Arg Leu Ala Pro Asp Tyr Asp Ala Leu Asp Val Ala Asn
 145 150 155 160

Lys Ile Gly Ile Ile
 165

<210> 999

<211> 194

<212> PRT

<213> Homo sapiens

<400> 999

Pro Glu Asn Ser Thr Ser Ser Phe Leu Leu Trp Gly Cys Pro Pro Ser
 1 5 10 15

Val Val Cys Phe Thr Val Gly Ser Pro Ala Arg Arg Pro Gln Cys Phe
 20 25 30

966

Leu Arg Ala Glu Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser
 35 40 45

Met Ala Leu Leu Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro
 50 55 60

Gln Trp Gln Met Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln
 65 70 75 80

Ala Met Tyr Lys Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly
 85 90 95

Met Met Ser Cys Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala
 100 105 110

Leu Gln Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe
 115 120 125

Leu Ala Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly
 130 135 140

Gly Asp Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile
 145 150 155 160

Ile Phe Ile Val Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr
 165 170 175

Gly His Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn
 180 185 190

Ile Lys

<210> 1000

<211> 362

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (25)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1000

Arg Gln Gln Arg Thr Arg Lys Lys Lys Pro Ala Gly Ala Ala Leu Gly
 1 5 10 15

Ala Leu Gly Pro Arg Ala Gln Leu Xaa Ala Ala Ala Gln Thr Asn Ser
 20 25 30

Asn Ala Ala Gly Lys Gln Leu Arg Lys Glu Ser Gln Lys Asp Arg Lys
 35 40 45
 Asn Pro Leu Pro Pro Ser Val Gly Val Val Asp Lys Lys Glu Glu Thr
 50 55 60
 Gln Pro Pro Val Ala Leu Lys Lys Glu Gly Ile Arg Arg Val Gly Arg
 65 70 75 80
 Arg Pro Asp Gln Gln Leu Gln Gly Glu Gly Lys Ile Ile Asp Arg Arg
 85 90 95
 Pro Glu Arg Arg Pro Pro Arg Glu Arg Arg Phe Glu Lys Pro Leu Glu
 100 105 110
 Glu Lys Gly Glu Gly Gly Glu Phe Ser Val Asp Arg Pro Ile Ile Asp
 115 120 125
 Arg Pro Ile Arg Gly Arg Gly Gly Leu Gly Arg Gly Arg Gly Gly Arg
 130 135 140
 Gly Arg Gly Met Gly Arg Gly Asp Gly Phe Asp Ser Arg Gly Lys Arg
 145 150 155 160
 Glu Phe Asp Arg His Ser Gly Ser Asp Arg Ser Ser Phe Ser His Tyr
 165 170 175
 Ser Gly Leu Lys His Glu Asp Lys Arg Gly Gly Ser Gly Ser His Asn
 180 185 190
 Trp Gly Thr Val Lys Asp Glu Leu Thr Asp Leu Asp Gln Ser Asn Val
 195 200 205
 Thr Glu Glu Thr Pro Glu Gly Glu Glu His His Pro Val Ala Asp Thr
 210 215 220
 Glu Asn Lys Glu Asn Glu Val Glu Glu Val Lys Glu Glu Gly Pro Lys
 225 230 235 240
 Glu Met Thr Leu Asp Glu Trp Lys Ala Ile Gln Asn Lys Asp Arg Ala
 245 250 255
 Lys Val Glu Phe Asn Ile Arg Lys Pro Asn Glu Gly Ala Asp Gly Gln
 260 265 270
 Trp Lys Lys Gly Phe Val Leu His Lys Ser Lys Ser Glu Glu Ala His
 275 280 285
 Ala Glu Asp Ser Val Met Asp His His Phe Arg Lys Pro Ala Asn Asp
 290 295 300

968

Ile Thr Ser Gln Leu Glu Ile Asn Phe Gly Asp Leu Gly Arg Pro Gly
 305 310 315 320

Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg Gly Arg Gly Arg Pro
 325 330 335

Asn Arg Gly Ser Arg Thr Asp Lys Ser Ser Ala Ser Ala Pro Asp Val
 340 345 350

Asp Asp Pro Glu Ala Phe Pro Ala Leu Ala
 355 360

<210> 1001

<211> 207

<212> PRT

<213> Homo sapiens

<400> 1001

Leu Met Ser Val Val Arg Gly Phe Ser Glu Ala Ala Ala Gln Tyr Asn
 1 5 10 15

Pro Glu Pro Pro Pro Arg Thr His Tyr Ser Asn Ile Glu Ala Asn
 20 25 30

Glu Ser Glu Glu Val Arg Gln Phe Arg Arg Leu Phe Ala Gln Leu Ala
 35 40 45

Gly Asp Asp Met Glu Val Ser Ala Thr Glu Leu Met Asn Ile Leu Asn
 50 55 60

Lys Val Val Thr Arg His Pro Asp Leu Lys Thr Asp Gly Phe Gly Ile
 65 70 75 80

Asp Thr Cys Arg Ser Met Val Ala Val Met Asp Ser Asp Thr Thr Gly
 85 90 95

Lys Leu Gly Phe Glu Glu Phe Lys Tyr Leu Trp Asn Asn Ile Lys Arg
 100 105 110

Trp Gln Ala Ile Tyr Lys Gln Phe Asp Thr Asp Arg Ser Gly Thr Ile
 115 120 125

Cys Ser Ser Glu Leu Pro Gly Ala Phe Glu Ala Ala Gly Phe His Leu
 130 135 140

Asn Glu His Leu Tyr Asn Met Ile Ile Arg Arg Tyr Ser Asp Glu Ser
 145 150 155 160

Gly Asn Met Asp Phe Asp Asn Phe Ile Ser Cys Leu Val Arg Leu Asp
165 170 175
Ala Met Phe Arg Ala Phe Lys Ser Leu Asp Lys Asp Gly Thr Gly Gln
180 185 190
Ile Gln Val Asn Ile Gln Glu Trp Leu Gln Leu Thr Met Tyr Ser
195 200 205

<210> 1002

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (12)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1002

Ile Phe Cys Asp Thr Arg Ser His Gln Val Ala Xaa Gly Trp Phe Arg
1 5 10 15

Ile Pro Gly Leu Lys
20

<210> 1003

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (15)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (103)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1003

970

Met Pro Gln Leu Gly Leu Ser Cys Ile Pro Val Glu Gly Pro Xaa Pro
1 5 10 15
Cys Leu Xaa Glu Val Arg Leu Cys Cys Val Asn Gly Gln Ala Leu Pro
20 25 30
Gln Pro Thr Pro Gly Lys Val His Leu Phe Ser Gly Leu Tyr Lys Val
35 40 45
Ser Trp Gly Pro Val Ala Ser Leu Pro Val Arg Ser Asp Phe Ser Leu
50 55 60
Ser Ser Ser Pro Val Gly Glu Thr Lys Pro Asp Trp Gly Ala Gln Gly
65 70 75 80
Glu His Gly Lys Gly Arg Leu Pro Cys Leu Ser Leu Ala Val Arg Val
85 90 95
Arg Val Thr His Thr Lys Xaa Glu Cys Gly Gln Gln Val
100 105

<210> 1004

<211> 542

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (252)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (519)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1004

Lys Asp Pro Glu Glu Tyr Cys Cys Thr Pro Ala Ala Arg Gly Arg Gly
1 5 10 15
Lys Ser Ala Ala Leu Gly Leu Ala Ile Ala Gly Ala Val Ala Phe Gly
20 25 30
Tyr Ser Asn Ile Phe Val Thr Ser Pro Ser Pro Asp Asn Leu His Thr
35 40 45
Leu Phe Glu Phe Val Phe Lys Gly Phe Asp Ala Leu Gln Tyr Gln Glu
50 55 60

971

His Leu Asp Tyr Glu Ile Ile Gln Ser Leu Asn Pro Glu Phe Asn Lys
65 70 75 80

Ala Val Ile Arg Val Asn Val Phe Arg Glu His Arg Gln Thr Ile Gln
85 90 95

Tyr Ile His Pro Ala Asp Ala Val Lys Leu Gly Gln Ala Glu Leu Val
100 105 110

Val Ile Asp Glu Ala Ala Ala Ile Pro Leu Pro Leu Val Lys Ser Leu
115 120 125

Leu Gly Pro Tyr Leu Val Phe Met Ala Ser Thr Ile Asn Gly Tyr Glu
130 135 140

Gly Thr Gly Arg Ser Leu Ser Leu Lys Leu Ile Gln Gln Leu Arg Gln
145 150 155 160

Gln Ser Ala Gln Ser Gln Val Ser Thr Thr Ala Glu Asn Lys Thr Thr
165 170 175

Thr Thr Ala Arg Leu Ala Ser Ala Arg Thr Leu His Glu Val Ser Leu
180 185 190

Gln Glu Ser Ile Arg Tyr Ala Pro Gly Asp Ala Val Glu Lys Trp Leu
195 200 205

Asn Asp Leu Leu Cys Leu Asp Cys Leu Asn Ile Thr Arg Ile Val Ser
210 215 220

Gly Cys Pro Leu Pro Glu Ala Cys Glu Leu Tyr Tyr Val Asn Arg Asp
225 230 235 240

Thr Leu Phe Cys Tyr His Lys Ala Ser Glu Val Xaa Leu Gln Arg Leu
245 250 255

Met Ala Leu Tyr Val Ala Ser His Tyr Lys Asn Ser Pro Asn Asp Leu
260 265 270

Gln Met Leu Ser Asp Ala Pro Ala His His Leu Phe Cys Leu Leu Pro
275 280 285

Pro Val Pro Pro Thr Gln Asn Ala Leu Pro Glu Val Leu Ala Val Ile
290 295 300

Gln Val Cys Leu Glu Gly Glu Ile Ser Arg Gln Ser Ile Leu Asn Ser
305 310 315 320

Leu Ser Arg Gly Lys Lys Ala Ser Gly Asp Leu Ile Pro Trp Thr Val
325 330 335

972

Ser Glu Gln Phe Gln Asp Pro Asp Phe Gly Gly Leu Ser Gly Gly Arg
340 345 350

Val Val Arg Ile Ala Val His Pro Asp Tyr Gln Gly Met Gly Tyr Gly
355 360 365

Ser Arg Ala Leu Gln Leu Leu Gln Met Tyr Tyr Glu Gly Arg Phe Pro
370 375 380

Cys Leu Glu Glu Lys Val Leu Glu Thr Pro Gln Glu Ile His Thr Val
385 390 395 400

Ser Ser Glu Ala Val Ser Leu Leu Glu Glu Val Ile Thr Pro Arg Lys
405 410 415

Asp Leu Pro Pro Leu Leu Leu Lys Leu Asn Glu Arg Pro Ala Glu Arg
420 425 430

Leu Asp Tyr Leu Gly Val Ser Tyr Gly Leu Thr Pro Arg Leu Leu Lys
435 440 445

Phe Trp Lys Arg Ala Gly Phe Val Pro Val Tyr Leu Arg Gln Thr Pro
450 455 460

Asn Asp Leu Thr Gly Glu His Ser Cys Ile Met Leu Lys Thr Leu Thr
465 470 475 480

Asp Glu Asp Glu Ala Asp Gln Gly Gly Trp Leu Ala Ala Phe Trp Lys
485 490 495

Asp Phe Arg Arg Arg Phe Leu Ala Leu Leu Ser Tyr Gln Phe Ser Thr
500 505 510

Phe Ser Pro Ser Leu Ala Xaa Asn Ile Ile Gln Asn Arg Asn Met Gly
515 520 525

Lys Pro Ala Gln Pro Ala Leu Ser Arg Glu Glu Leu Glu Ala
530 535 540

<210> 1005

<211> 202

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (77)

<223> Xaa equals any of the naturally occurring L-amino acids

973

<400> 1005

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Asp Ala Ala Asp Thr Ile Glu Thr Asp Thr Ala Thr Ala Asp Thr Thr
 1             5             10             15

Val Ala Asn Asn Val Pro Pro Ala Ala Thr Ser Leu Ile Asp Leu Trp
          20             25             30

Pro Gly Asn Gly Glu Gly Ala Ser Thr Leu Gln Gly Glu Pro Arg Ala
          35             40             45

Pro Thr Pro Pro Ser Gly Thr Glu Val Thr Leu Ala Glu Val Pro Leu
          50             55             60

Leu Asp Glu Val Ala Pro Glu Pro Leu Leu Pro Ala Xaa Glu Gly Cys
 65             70             75             80

Ala Thr Leu Leu Asn Phe Asp Glu Leu Pro Glu Pro Pro Ala Thr Phe
          85             90             95

Cys Asp Pro Glu Glu Val Glu Gly Glu Pro Leu Ala Ala Pro Gln Thr
          100             105             110

Pro Thr Leu Pro Ser Ala Leu Glu Glu Leu Glu Gln Glu Gln Glu Pro
          115             120             125

Glu Pro His Leu Leu Thr Asn Gly Glu Thr Thr Gln Lys Glu Gly Thr
          130             135             140

Gln Ala Ser Glu Gly Tyr Phe Ser Gln Ser Gln Glu Glu Glu Phe Ala
          145             150             155             160

Gln Ser Glu Glu Leu Cys Ala Lys Ala Pro Pro Pro Val Phe Tyr Asn
          165             170             175

Lys Pro Pro Glu Ile Asp Ile Thr Cys Trp Asp Ala Asp Pro Val Pro
          180             185             190

Glu Glu Glu Glu Gly Phe Glu Gly Gly Asp
          195             200

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<210> 1006

<211> 561

<212> PRT

<213> Homo sapiens

<400> 1006

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Ser Ala Met Arg Lys Phe Ala Tyr Cys Lys Val Val Leu Ala Thr Ser
 1             5             10             15

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974

Leu Ile Trp Val Leu Leu Asp Met Phe Leu Leu Leu Tyr Phe Ser Glu
 20 25 30
 Cys Asn Lys Cys Asp Glu Lys Lys Glu Arg Gly Leu Pro Ala Gly Asp
 35 40 45
 Val Leu Glu Pro Val Gln Lys Pro His Glu Gly Pro Gly Glu Met Gly
 50 55 60
 Lys Pro Val Val Ile Pro Lys Glu Asp Gln Glu Lys Met Lys Glu Met
 65 70 75 80
 Phe Lys Ile Asn Gln Phe Asn Leu Met Ala Ser Glu Met Ile Ala Leu
 85 90 95
 Asn Arg Ser Leu Pro Asp Val Arg Leu Glu Gly Cys Lys Thr Lys Val
 100 105 110
 Tyr Pro Asp Asn Leu Pro Thr Thr Ser Val Val Ile Val Phe His Asn
 115 120 125
 Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val Ile Asn Arg
 130 135 140
 Ser Pro Arg His Met Ile Glu Glu Ile Val Leu Val Asp Asp Ala Ser
 145 150 155 160
 Glu Arg Asp Phe Leu Lys Arg Pro Leu Glu Ser Tyr Val Lys Lys Leu
 165 170 175
 Lys Val Pro Val His Val Ile Arg Met Glu Gln Arg Ser Gly Leu Ile
 180 185 190
 Arg Ala Arg Leu Lys Gly Ala Ala Val Ser Lys Gly Gln Val Ile Thr
 195 200 205
 Phe Leu Asp Ala His Cys Glu Cys Thr Val Gly Trp Leu Glu Pro Leu
 210 215 220
 Leu Ala Arg Ile Lys His Asp Arg Arg Thr Val Val Cys Pro Ile Ile
 225 230 235 240
 Asp Val Ile Ser Asp Asp Thr Phe Glu Tyr Met Ala Gly Ser Asp Met
 245 250 255
 Thr Tyr Gly Gly Phe Asn Trp Lys Leu Asn Phe Arg Trp Tyr Pro Val
 260 265 270
 Pro Gln Arg Glu Met Asp Arg Arg Lys Gly Asp Arg Thr Leu Pro Val
 275 280 285

975

Arg Thr Pro Thr Met Ala Gly Gly Leu Phe Ser Ile Asp Arg Asp Tyr
 290 295 300

Phe Gln Glu Ile Gly Thr Tyr Asp Ala Gly Met Asp Ile Trp Gly Gly
 305 310 315 320

Glu Asn Leu Glu Ile Ser Phe Arg Ile Trp Gln Cys Gly Gly Thr Leu
 325 330 335

Glu Ile Val Thr Cys Ser His Val Gly His Val Phe Arg Lys Ala Thr
 340 345 350

Pro Tyr Thr Phe Pro Gly Gly Thr Gly Gln Ile Ile Asn Lys Asn Asn
 355 360 365

Arg Arg Leu Ala Glu Val Trp Met Asp Glu Phe Lys Asn Phe Phe Tyr
 370 375 380

Ile Ile Ser Pro Gly Val Thr Lys Val Asp Tyr Gly Asp Ile Ser Ser
 385 390 395 400

Arg Val Gly Leu Arg His Lys Leu Gln Cys Lys Pro Phe Ser Trp Tyr
 405 410 415

Leu Glu Asn Ile Tyr Pro Asp Ser Gln Ile Pro Arg His Tyr Phe Ser
 420 425 430

Leu Gly Glu Ile Arg Asn Val Glu Thr Asn Gln Cys Leu Asp Asn Met
 435 440 445

Ala Arg Lys Glu Asn Glu Lys Val Gly Ile Phe Asn Cys His Gly Met
 450 455 460

Gly Gly Asn Gln Val Phe Ser Tyr Thr Ala Asn Lys Glu Ile Arg Thr
 465 470 475 480

Asp Asp Leu Cys Leu Asp Val Ser Lys Leu Asn Gly Pro Val Thr Met
 485 490 495

Leu Lys Cys His His Leu Lys Gly Asn Gln Leu Trp Glu Tyr Asp Pro
 500 505 510

Val Lys Leu Thr Leu Gln His Val Asn Ser Asn Gln Cys Leu Asp Lys
 515 520 525

Ala Thr Glu Glu Asp Ser Gln Val Pro Ser Ile Arg Asp Cys Asn Gly
 530 535 540

Ser Arg Ser Gln Gln Trp Leu Leu Arg Asn Val Thr Leu Pro Glu Ile
 545 550 555 560

976

Phe

<210> 1007

<211> 189

<212> PRT

<213> Homo sapiens

<400> 1007

Phe Ile Pro Ile Gly Glu Asn Ser Ala Thr Gly Glu Asn Arg Leu Ala
 1 5 10 15

Ser Ala Leu Trp Ile Gly Asp Arg Ser Tyr Pro Gly Leu Ser Glu Gly
 20 25 30

Asn Ser Arg Pro Pro Ile Pro Gly Pro Pro Tyr Val Ala Ser Pro Asp
 35 40 45

Leu Trp Ser His Trp Glu Asp Ser Ala Leu Pro Pro Pro Ser Leu Arg
 50 55 60

Pro Val Gln Pro Thr Trp Glu Gly Ser Ser Glu Ala Gly Leu Asp Trp
 65 70 75 80

Ala Gly Ala Ser Phe Ser Pro Gly Thr Pro Met Trp Ala Ala Leu Asp
 85 90 95

Glu Gln Met Leu Gln Glu Gly Ile Gln Ala Ser Leu Leu Asp Gly Pro
 100 105 110

Ala Gln Glu Pro Gln Ser Ala Pro Trp Leu Ser Lys Ser Ser Val Ser
 115 120 125

Ser Leu Arg Leu Gln Gln Leu Glu Arg Met Gly Phe Pro Thr Glu Gln
 130 135 140

Ala Val Val Ala Leu Ala Ala Thr Gly Arg Val Glu Gly Ala Val Ser
 145 150 155 160

Leu Leu Val Gly Gly Gln Val Gly Thr Glu Thr Leu Val Thr His Gly
 165 170 175

Lys Gly Gly Pro Ala His Ser Glu Gly Pro Gly Pro Pro
 180 185

<210> 1008

<211> 300

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (13)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (39)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1008

Arg	Gln	Lys	Ser	Ser	Xaa	Leu	Trp	Pro	His	Pro	Leu	Xaa	Arg	His	Arg
1				5				10					15		

Ala	Gly	Pro	Gly	Leu	Ala	Gly	Asn	Gly	Gly	Ile	Leu	Pro	Asn	Leu	Gly
			20				25						30		

Asp	Gly	Gly	Gly	Gly	Trp	Xaa	Trp	Trp	Glu	Gly	Asn	His	Val	Leu	Leu
	35						40					45			

Asn	Leu	Phe	Leu	Val	Pro	Pro	Ile	Pro	Arg	Pro	Thr	Arg	His	His	Thr
	50					55					60				

Ala	Asp	Asn	Thr	His	Pro	Leu	Ala	Gln	Ala	Ser	Ile	His	Met	Cys	Cys
65					70					75				80	

Thr	Phe	Ser	Ser	Arg	His	Ala	Asp	Asn	Pro	Thr	Arg	Pro	His	His	His
				85					90					95	

Met	Pro	Lys	Cys	Thr	His	Thr	Glu	Pro	His	Arg	Pro	Ser	Gly	Pro	Ala
		100						105					110		

Gly	Ser	Ser	Leu	Gly	Phe	Pro	Leu	Ala	His	Phe	Gln	Gly	Pro	Gly	Ala
	115						120					125			

Ala	Thr	Lys	Cys	Glu	Ser	Ser	Val	Ala	Ala	Pro	Ser	Phe	Ser	Pro	Ser
	130						135					140			

Thr	Ser	Ile	Gly	Pro	Ile	Gly	Lys	His	Arg	Gly	Leu	Thr	Leu	Phe	His
145					150					155				160	

Ile	Pro	Cys	Pro	Ala	Leu	Lys	Trp	Thr	Ile	Thr	Phe	Trp	Asp	Arg	Leu
				165					170					175	

978

Lys Phe Leu Lys Ser Leu His His Ser Val Pro Ser Lys Gly Ser Pro
 180 185 190
 Cys Gln Trp Gly Phe Glu Arg Glu Phe Leu Glu Pro Thr Phe Lys Phe
 195 200 205
 Cys Leu Ile Trp Arg Glu Thr Lys Ile Gly Arg Gly Lys Arg Thr Pro
 210 215 220
 Asp Val Leu Leu Leu Pro Glu Ile Leu Glu Thr Asp Ser Leu Asp Trp
 225 230 235 240
 Lys Met Asp Lys Ser Ala Leu Thr Trp Arg Val Gly Thr Arg Trp Gly
 245 250 255
 Pro Ala Leu Pro Thr Ala Ala Val Ala Ser Ser Leu Ala Gly Phe Ala
 260 265 270
 Gly Arg Gln Gln Glu Gly Glu Gly Gly Ser Thr Ala Arg Gly Thr Gly
 275 280 285
 Gly Ala Ala Gly Leu Gln Glu Leu Phe Phe His Cys
 290 295 300

<210> 1009

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (38)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1009

Arg Pro Pro Cys Pro His Ser Arg Ser Xaa Trp Arg Ile Leu Ser Leu
 1 5 10 15

Thr Pro Asn Pro Asp Pro Leu Pro Asn Met Ser Val Phe Phe Phe Ile
 20 25 30

Phe Leu Asn Ile Phe Xaa Leu Ala Phe Ser Ser Pro Gly Ser Gln Pro
 35 40 45

979

Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg Gly Phe Met
50 55 60

Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys Arg Phe Cys
65 70 75 80

Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe Pro Glu Glu
85 90 95

Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe Ser Ser Trp Pro
100 105 110

Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu Gln Val Gln Arg
115 120 125

Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp Val Ser Glu Leu
130 135 140

Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln Val Arg Trp Leu
145 150 155 160

Arg Pro Val His Arg Gln Leu Gly Glu Ala Asn Glu Glu Phe Ala Leu
165 170 175

Arg Val Gln Gln Leu Val Ala Lys Glu Leu Gly Gln Thr Gly Thr Arg
180 185 190

Leu Thr Pro Ala Asp Lys Ala Glu His Met Lys Arg Gln Arg His Pro
195 200 205

Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser Phe Pro Pro Ser Pro Gly
210 215 220

Pro Ser Pro Asp Val Gln Leu Ala Thr Leu Ala Gln Arg Val Lys Glu
225 230 235 240

Val Leu Pro His Val Pro Leu Gly Val Ile Gln Arg Asp Leu Ala Lys
245 250 255

Thr Gly Cys Val Asp Leu Thr Ile Thr Asn Leu Leu Glu Gly Ala Val
260 265 270

Ala Phe Met Pro Glu Asp Ile Thr Lys Gly Thr Gln Ser Leu Pro Thr
275 280 285

Ala Ser Ala Ser Lys Phe Pro Ser Ser Gly Pro Val Thr Pro Gln Pro
290 295 300

Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp Ala Arg Gln Glu Ser Leu
305 310 315 320

980

Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr Ala Arg Arg Arg Phe Thr
 325 330 335

Glu Arg Arg Ala Gln Glu Ala Asp
 340

<210> 1010

<211> 233

<212> PRT

<213> Homo sapiens

<400> 1010

Pro His Cys Glu Pro Asn Pro Gly Ala Gly Ala Met Val Leu Leu His
 1 5 10 15

Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu Leu Ala Leu Lys Glu
 20 25 30

Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val Glu Glu Ser Val Leu
 35 40 45

Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu Val Ala Phe Cys Pro
 50 55 60

Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala Asn Ala Val Ser Glu
 65 70 75 80

Gly Val Val His Glu Asp Leu Arg Leu Leu Leu Glu Thr His Leu Pro
 85 90 95

Ser Lys Lys Lys Lys Val Leu Leu Gly Val Gly Asp Pro Lys Ile Gly
 100 105 110

Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys Gln Thr Gly Gly Val
 115 120 125

Ile Ala Glu Ile Leu Arg Gly Val Arg Leu His Phe His Asn Leu Val
 130 135 140

Lys Gly Leu Thr Asp Leu Ser Ala Cys Lys Ala Gln Leu Gly Leu Gly
 145 150 155 160

His Ser Tyr Ser Arg Ala Lys Val Lys Phe Asn Val Asn Arg Val Asp
 165 170 175

Asn Met Ile Ile Gln Ser Ile Ser Leu Leu Asp Gln Leu Asp Lys Asp
 180 185 190

Ile Asn Thr Phe Ser Met Arg Val Arg Glu Trp Tyr Gly Tyr His Phe
195 200 205

Pro Glu Leu Val Lys Ile Ile Asn Asp Asn Ala Thr Tyr Cys Arg Leu
210 215 220

Ala Gln Phe Ile Gly Asn Arg Arg Asn
225 230

<210> 1011

<211> 187

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1011

Gly Thr Ser Xaa Phe Ser Phe Pro Leu Gly Arg Glu Glu Ala Met Ala
1 5 10 15

Ala Met Ala Ser Leu Gly Ala Leu Ala Leu Leu Leu Ser Ser Leu
20 25 30

Ser Arg Cys Ser Ala Glu Ala Cys Leu Glu Pro Gln Ile Thr Pro Ser
35 40 45

Tyr Tyr Thr Thr Ser Asp Ala Val Ile Ser Thr Glu Thr Val Phe Ile
50 55 60

Val Glu Ile Ser Leu Thr Cys Lys Asn Arg Val Gln Asn Met Ala Leu
65 70 75 80

Tyr Ala Asp Val Gly Gly Lys Gln Phe Pro Val Thr Arg Gly Gln Asp
85 90 95

Val Gly Arg Tyr Gln Val Ser Trp Ser Leu Asp His Lys Ser Ala His
100 105 110

Ala Gly Thr Tyr Glu Val Arg Phe Phe Asp Glu Glu Ser Tyr Ser Leu
115 120 125

Leu Arg Lys Ala Gln Arg Asn Asn Glu Asp Ile Ser Ile Ile Pro Pro
130 135 140

Leu Phe Thr Val Ser Val Asp His Arg Gly Thr Trp Asn Gly Pro Trp
145 150 155 160

Val Ser Thr Glu Val Leu Ala Ala Ala Ile Gly Leu Val Ile Tyr Tyr
 165 170 175

Leu Ala Phe Ser Ala Lys Ser His Ile Gln Ala
 180 185

<210> 1012

<211> 708

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (18)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (153)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (229)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (433)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1012

Ala Leu Arg Pro Ile Ser Ser Val Arg Ala Gly Asp Arg Cys Gln Arg
 1 5 10 15

Ser Xaa Ala Ala Asp Met Ala Ala Ser Thr Ala Ala Gly Lys Gln Arg
 20 25 30

Ile Pro Lys Val Ala Lys Val Lys Asn Lys Ala Pro Ala Glu Val Gln
 35 40 45

Ile Thr Ala Glu Gln Leu Leu Arg Glu Ala Lys Glu Arg Glu Leu Glu
 50 55 60

Leu Leu Pro Pro Pro Pro Gln Gln Lys Ile Thr Asp Glu Glu Glu Leu
 65 70 75 80

Asn Asp Tyr Lys Leu Arg Lys Arg Lys Thr Phe Glu Asp Asn Ile Arg

983

85	90	95
Lys Asn Arg Thr Val Ile Ser Asn Trp Ile Lys Tyr Ala Gln Trp Glu		
100	105	110
Glu Ser Leu Lys Glu Ile Gln Arg Ala Arg Ser Ile Tyr Glu Arg Ala		
115	120	125
Leu Asp Val Asp Tyr Arg Asn Ile Thr Leu Trp Leu Lys Tyr Ala Glu		
130	135	140
Met Glu Met Lys Asn Arg Gln Val Xaa His Ala Arg Asn Ile Trp Asp		
145	150	155
Arg Ala Ile Thr Thr Leu Pro Arg Val Asn Gln Phe Trp Tyr Lys Tyr		
165	170	175
Thr Tyr Met Glu Glu Met Leu Gly Asn Val Ala Gly Ala Arg Gln Val		
180	185	190
Phe Glu Arg Trp Met Glu Trp Gln Pro Glu Glu Gln Ala Trp His Ser		
195	200	205
Tyr Ile Asn Phe Glu Leu Arg Tyr Lys Glu Val Asp Arg Ala Arg Thr		
210	215	220
Ile Tyr Glu Arg Xaa Val Leu Val His Pro Asp Val Lys Asn Trp Ile		
225	230	235
Lys Tyr Ala Arg Phe Glu Glu Lys His Ala Tyr Phe Ala His Ala Arg		
245	250	255
Lys Val Tyr Glu Arg Ala Val Glu Phe Phe Gly Asp Glu His Met Asp		
260	265	270
Glu His Leu Tyr Val Ala Phe Ala Lys Phe Glu Glu Asn Gln Lys Glu		
275	280	285
Phe Glu Arg Val Arg Val Ile Tyr Lys Tyr Ala Leu Asp Arg Ile Ser		
290	295	300
Lys Gln Asp Ala Gln Glu Leu Phe Lys Asn Tyr Thr Ile Phe Glu Lys		
305	310	315
Lys Phe Gly Asp Arg Arg Gly Ile Glu Asp Ile Ile Val Ser Lys Arg		
325	330	335
Arg Phe Gln Tyr Glu Glu Glu Val Lys Ala Asn Pro His Asn Tyr Asp		
340	345	350
Ala Trp Phe Asp Tyr Leu Arg Leu Val Glu Ser Asp Ala Glu Ala Glu		

984

355 360 365
 Ala Val Arg Glu Val Tyr Glu Arg Ala Ile Ala Asn Val Pro Pro Ile
 370 375 380
 Gln Glu Lys Arg His Trp Lys Arg Tyr Ile Tyr Leu Trp Ile Asn Tyr
 385 390 395 400
 Ala Leu Tyr Glu Glu Leu Glu Ala Lys Asp Pro Glu Arg Thr Arg Gln
 405 410 415
 Val Tyr Gln Ala Ser Leu Glu Leu Ile Pro His Lys Lys Phe Thr Phe
 420 425 430
 Xaa Lys Met Trp Ile Leu Tyr Ala Gln Phe Glu Ile Arg Gln Lys Asn
 435 440 445
 Leu Ser Leu Ala Arg Arg Ala Leu Gly Thr Ser Ile Gly Lys Cys Pro
 450 455 460
 Lys Asn Lys Leu Phe Lys Val Tyr Ile Glu Leu Glu Leu Gln Leu Arg
 465 470 475 480
 Glu Phe Asp Arg Cys Arg Lys Leu Tyr Glu Lys Phe Leu Glu Phe Gly
 485 490 495
 Pro Glu Asn Cys Thr Ser Trp Ile Lys Phe Ala Glu Leu Glu Thr Ile
 500 505 510
 Leu Gly Asp Ile Asp Arg Ala Arg Ala Ile Tyr Glu Leu Ala Ile Ser
 515 520 525
 Gln Pro Arg Leu Asp Met Pro Glu Val Leu Trp Lys Ser Tyr Ile Asp
 530 535 540
 Phe Glu Ile Glu Gln Glu Glu Thr Glu Arg Thr Arg Asn Leu Tyr Arg
 545 550 555 560
 Arg Leu Leu Gln Arg Thr Gln His Val Lys Val Trp Ile Ser Phe Ala
 565 570 575
 Gln Phe Glu Leu Ser Ser Gly Lys Glu Gly Ser Leu Thr Lys Cys Arg
 580 585 590
 Gln Ile Tyr Glu Glu Ala Asn Lys Thr Met Arg Asn Cys Glu Glu Lys
 595 600 605
 Glu Glu Arg Leu Met Leu Leu Glu Ser Trp Arg Ser Phe Glu Glu Glu
 610 615 620
 Phe Gly Thr Ala Ser Asp Lys Glu Arg Val Asp Lys Leu Met Pro Glu

985

625 630 635 640
 Lys Val Lys Lys Arg Arg Lys Val Gln Thr Asp Asp Gly Ser Asp Ala
 645 650 655
 Gly Trp Glu Glu Tyr Phe Asp Tyr Ile Phe Pro Glu Asp Ala Ala Asn
 660 665 670
 Gln Pro Asn Leu Lys Leu Leu Ala Met Ala Lys Leu Trp Lys Lys Gln
 675 680 685
 Gln Gln Glu Lys Glu Asp Ala Glu His His Pro Asp Glu Asp Val Asp
 690 695 700
 Glu Ser Glu Ser
 705

<210> 1013
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 1013
 Leu Pro Pro Gln Val Ala Asp Thr Met Leu Pro Pro Met Ala Leu Pro
 1 5 10 15
 Ser Val Ser Trp Met Leu Leu Ser Cys Leu Met Leu Leu Ser Gln Val
 20 25 30
 Gln Gly Glu Glu Pro Gln Arg Glu Leu Pro Ser Ala Arg Ile Arg Cys
 35 40 45
 Pro Lys Gly Ser Lys Ala Tyr Gly Ser His Cys Tyr Ala Leu Phe Leu
 50 55 60
 Ser Pro Lys Ser Trp Thr Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro
 65 70 75 80
 Ser Gly Asn Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val
 85 90 95
 Ser Ser Leu Val Lys Ser Ile Gly Asn Ser Tyr Ser Tyr Val Trp Ile
 100 105 110
 Gly Leu His Asp Pro Thr Gln Gly Thr Glu Pro Asn Gly Glu Gly Trp
 115 120 125
 Glu Trp Ser Ser Ser Asp Val Met Asn Tyr Phe Ala Trp Glu Arg Asn
 130 135 140

986

Pro Ser Thr Ile Ser Ser Pro Gly His Cys Ala Ser Leu Ser Arg Ser
145 150 155 160

Thr Ala Phe Leu Arg Trp Lys Asp Tyr Asn Cys Asn Val Arg Leu Pro
165 170 175

Tyr Val Cys Lys Phe Thr Asp
180

<210> 1014

<211> 213

<212> PRT

<213> Homo sapiens

<400> 1014

Val Thr Asp Gly Gly Ser Ala Arg Lys Pro Lys Met Ala Val Pro Ala
1 5 10 15

Ala Leu Ile Leu Arg Glu Ser Pro Ser Met Lys Lys Ala Val Ser Leu
20 25 30

Ile Asn Ala Ile Asp Thr Gly Arg Phe Pro Arg Leu Leu Thr Arg Ile
35 40 45

Leu Gln Lys Leu His Leu Lys Ala Glu Ser Ser Phe Ser Glu Glu Glu
50 55 60

Glu Glu Lys Leu Gln Ala Ala Phe Ser Leu Glu Lys Gln Asp Leu His
65 70 75 80

Leu Val Leu Glu Thr Ile Ser Phe Ile Leu Glu Gln Ala Val Tyr His
85 90 95

Asn Val Lys Pro Ala Ala Leu Gln Gln Gln Leu Glu Asn Ile His Leu
100 105 110

Arg Gln Asp Lys Ala Glu Ala Phe Val Asn Thr Trp Ser Ser Met Gly
115 120 125

Gln Glu Thr Val Glu Lys Phe Arg Gln Arg Ile Leu Ala Pro Cys Lys
130 135 140

Leu Glu Thr Val Gly Trp Gln Leu Asn Leu Gln Met Ala His Ser Ala
145 150 155 160

Gln Ala Lys Leu Lys Ser Pro Gln Ala Val Leu Gln Leu Gly Val Asn
165 170 175

987

Asn Glu Asp Ser Lys Ser Leu Glu Lys Val Leu Val Glu Phe Ser His
 180 185 190

Lys Glu Leu Phe Asp Phe Tyr Asn Lys Leu Glu Thr Ile Gln Ala Gln
 195 200 205

Leu Asp Ser Leu Thr
 210

<210> 1015

<211> 544

<212> PRT

<213> Homo sapiens

<400> 1015

Ala Pro Gly Thr Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr
 1 5 10 15

Ile Pro Tyr His Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala
 20 25 30

Ser Gly Thr Val Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val
 35 40 45

Ala Val Lys His Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg
 50 55 60

Lys Asp Val Leu Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser
 65 70 75 80

Tyr Ile Leu Pro Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly
 85 90 95

Ile Val Thr Glu Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His
 100 105 110

Arg Lys Thr Glu Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile
 115 120 125

Leu His Glu Ile Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro
 130 135 140

Pro Leu Leu His His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn
 145 150 155 160

Glu Phe His Val Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met
 165 170 175

Met Ser Leu Ser Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly

988

180	185	190
Thr Ile Ile Tyr Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser		
195	200	205
Arg Ala Ser Ile Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp		
210	215	220
Glu Val Leu Ser Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu		
225	230	235 240
Gln Ile Met Tyr Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu		
	245	250 255
Glu Ser Leu Pro Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu		
	260	265 270
Ile Glu Ser Gly Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu		
	275	280 285
Lys Cys Leu Ile Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile		
	290	295 300
Thr Phe Leu Glu Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser		
305	310	315 320
Val Ser Ser Ala Ile His Leu Cys Asp Lys Lys Lys Met Glu Leu Ser		
	325	330 335
Leu Asn Ile Pro Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser		
	340	345 350
Ser Gln Leu His Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu		
	355	360 365
Pro Ala Pro Gln Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys		
	370	375 380
Tyr Phe Met Lys Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser		
385	390	395 400
Thr Ile Ser Gly Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr		
	405	410 415
Pro Cys Ser Ser Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser		
	420	425 430
Glu Arg Leu Gln Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg		
	435	440 445
Glu Asp Ile Val Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu		

989

450 455 460
Asp Ala Leu Leu Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu
465 470 475 480
Val Ser Thr Lys Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp
485 490 495
Thr Thr Asp Ile Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys
500 505 510
Leu Lys Asp Asn Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu
515 520 525
Val Val Ser Arg Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met
530 535 540

<210> 1016
<211> 257
<212> PRT
<213> Homo sapiens

<400> 1016
His Pro Ser Ala Pro Arg Ala Gly Lys Ala His Leu Lys Arg Ala Ile
1 5 10 15
Leu Gly Gln Glu Glu Ala Leu Arg Leu His Ala Leu Cys Arg Val Leu
20 25 30
Arg Glu Val Asp Leu Leu Arg Ala Val Ile Ser Gln Thr Leu Gln Arg
35 40 45
Ser Leu Ala Lys Tyr Ala Glu Leu Asp Arg Glu Asp Asp Phe Cys Glu
50 55 60
Ala Ala Glu Ala Pro Asp Ile Gln Pro Lys Thr His Gln Lys Pro Glu
65 70 75 80
Ala Arg Met Pro Arg Leu Ser Gln Gly Lys Gly Pro Asp Ile Phe His
85 90 95
Arg Leu Gly Pro Leu Ser Val Phe Ser Ala Lys Asn Arg Trp Arg Leu
100 105 110
Val Gly Pro Val His Leu Thr Arg Gly Glu Gly Gly Phe Gly Leu Thr
115 120 125

990

Leu Arg Gly Asp Ser Pro Val Leu Ile Ala Ala Val Ile Pro Gly Ser
130 135 140

Gln Ala Ala Ala Ala Gly Leu Lys Glu Gly Asp Tyr Ile Val Ser Val
145 150 155 160

Asn Gly Gln Pro Cys Arg Trp Trp Arg His Ala Glu Val Val Thr Glu
165 170 175

Leu Lys Ala Ala Gly Glu Ala Gly Ala Ser Leu Gln Val Val Ser Leu
180 185 190

Leu Pro Ser Ser Arg Leu Pro Ser Leu Gly Asp Arg Arg Pro Val Leu
195 200 205

Leu Gly Pro Arg Gly Leu Leu Arg Ser Gln Arg Glu His Gly Cys Lys
210 215 220

Thr Pro Ala Ser Thr Trp Ala Ser Pro Arg Ala Leu Leu Asn Trp Ser
225 230 235 240

Arg Lys Ala Gln Gln Gly Lys Thr Gly Gly Cys Pro Ser Pro Val Pro
245 250 255

Gln

<210> 1017

<211> 248

<212> PRT

<213> Homo sapiens

<400> 1017

Ala Ser Asp Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met
1 5 10 15

Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly
20 25 30

Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr
35 40 45

Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile
50 55 60

Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu
65 70 75 80

991

Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly
85 90 95

Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu
100 105 110

Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp
115 120 125

Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Ala
130 135 140

Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser
145 150 155 160

Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro
165 170 175

Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln
180 185 190

Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys
195 200 205

Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys
210 215 220

Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu
225 230 235 240

Gln Met Glu Arg Asp Leu Lys Thr
245

<210> 1018

<211> 224

<212> PRT

<213> Homo sapiens

<400> 1018

Gly Arg Val Ser Ala Pro Val Pro Gly Lys Met Val Leu Gly Gly Cys
1 5 10 15

Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln Ala Ala Leu Leu Gly
20 25 30

Asn Leu Leu Leu Leu His Cys Val Ser Arg Ser His Ser Gln Asn Ala
35 40 45

Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly Ala Ala Gln Pro Glu Gly

992

50	55	60
Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly Asp Pro His Ser Pro Val		
65	70	75 80
Ile Leu Cys Ser Tyr Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro		
	85	90 95
Val Asp His Val Gly Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly		
	100	105 110
Cys Leu Lys Phe Gly Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser		
	115	120 125
Val Gln Cys His Ala Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr		
	130	135 140
Phe Leu Arg Glu Asn Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe		
145	150	155 160
Ile Thr Thr Leu Leu Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val Asp		
	165	170 175
Arg Phe Cys Leu Gly His Thr Gly Thr Ala Val Gly Lys Leu Leu Thr		
	180	185 190
Leu Gly Gly Leu Gly Ile Trp Trp Phe Val Asp Leu Ile Leu Leu Ile		
	195	200 205
Thr Gly Gly Leu Met Pro Ser Asp Gly Ser Asn Trp Cys Thr Val Tyr		
210	215	220

<210> 1019

<211> 53

<212> PRT

<213> Homo sapiens

<400> 1019

Asn Val Pro Val Cys His Leu Ser Thr Trp Lys Ile Leu Tyr Ile Trp
1 5 10 15

Lys Val Tyr Ala Ser Leu Asn Lys Tyr Met Leu Leu Asn Lys Pro Tyr
20 25 30

His Ser Leu Arg Asn Cys Ile Tyr Phe Ile Ile Cys Pro Phe Arg Asn
35 40 45

Gln Val Phe Cys Ile
50

<210> 1020

<211> 70

<212> PRT

<213> Homo sapiens

<400> 1020

Phe Tyr Thr Asn Leu Ile Trp Leu Pro Phe Val Pro Leu Ile Ser Gln
1 5 10 15

Met Phe Lys Cys Ile Gly Phe Gly Phe Ser Met Tyr Lys Leu Pro Tyr
20 25 30

Leu Leu Met Ser Ile Phe Cys Leu Phe Asn Phe Val Tyr Leu Leu Phe
35 40 45

Cys Phe Trp Ile His Phe Leu Ile Arg Ser His Met Ile Asn Ile Ile
50 55 60

Ser Ile Val Ile Ile Pro
65 70

<210> 1021

<211> 337

<212> PRT

<213> Homo sapiens

<400> 1021

Arg Lys Arg Lys Gln Ala Ala Arg Ala Ala Glu Glu Pro Gly Ala Ala
1 5 10 15

Met Asp Val Arg Ala Leu Pro Trp Leu Pro Trp Leu Leu Trp Leu Leu
20 25 30

Cys Arg Gly Gly Gly Asp Ala Asp Ser Arg Ala Pro Phe Thr Pro Thr
35 40 45

Trp Pro Arg Ser Arg Glu Arg Glu Ala Ala Ala Phe Arg Glu Ser Leu
50 55 60

Asn Arg His Arg Tyr Leu Asn Ser Leu Phe Pro Ser Glu Asn Ser Thr
65 70 75 80

Ala Phe Tyr Gly Ile Asn Gln Phe Ser Tyr Leu Phe Pro Glu Glu Phe

994

85	90	95
Lys Ala Ile Tyr Leu Arg Ser Lys Pro Ser Lys Phe Pro Arg Tyr Ser 100 105 110		
Ala Glu Val His Met Ser Ile Pro Asn Val Ser Leu Pro Leu Arg Phe 115 120 125		
Asp Trp Arg Asp Lys Gln Val Val Thr Gln Val Arg Asn Gln Gln Met 130 135 140		
Cys Gly Gly Cys Trp Ala Phe Ser Val Val Gly Ala Val Glu Ser Ala 145 150 155 160		
Tyr Ala Ile Lys Gly Lys Pro Leu Glu Asp Leu Ser Val Gln Gln Val 165 170 175		
Ile Asp Cys Ser Tyr Asn Asn Tyr Gly Cys Asn Gly Gly Ser Thr Leu 180 185 190		
Asn Ala Leu Asn Trp Leu Asn Lys Met Gln Val Lys Leu Val Lys Asp 195 200 205		
Ser Glu Tyr Pro Phe Lys Ala Gln Asn Gly Leu Cys His Tyr Phe Ser 210 215 220		
Gly Ser His Ser Gly Phe Ser Ile Lys Gly Tyr Ser Ala Tyr Asp Phe 225 230 235 240		
Ser Asp Gln Glu Asp Glu Met Ala Lys Ala Leu Leu Thr Phe Gly Pro 245 250 255		
Leu Val Val Ile Val Asp Ala Val Ser Trp Gln Asp Tyr Leu Gly Gly 260 265 270		
Ile Ile Gln His His Cys Ser Ser Gly Glu Ala Asn His Ala Val Leu 275 280 285		
Ile Thr Gly Phe Asp Lys Thr Gly Ser Thr Pro Tyr Trp Ile Val Arg 290 295 300		
Asn Ser Trp Gly Ser Ser Trp Gly Val Asp Gly Tyr Ala His Val Lys 305 310 315 320		
Met Gly Ser Asn Val Cys Gly Ile Ala Asp Ser Val Ser Ser Ile Phe 325 330 335		
Val		

995

<210> 1022

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1022

Ala Ser Ala Glu Phe Glu Met Ala Gly Gly Lys Ala Gly Lys Asp Ser
 1 5 10 15

Gly Lys Ala Lys Thr Lys Ala Val Ser Arg Ser Gln Arg Ala Gly Leu
 20 25 30

Gln Phe Pro Val Gly Arg Ile His Arg His Leu Lys Ser Arg Thr Thr
 35 40 45

Ser His Gly Arg Val Gly Ala Thr Ala Ala Val Tyr Ser Ala Ala Ile
 50 55 60

Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu Ala Gly Asn Ala Ser
 65 70 75 80

Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg His Leu Gln Leu Ala
 85 90 95

Ile Arg Gly Asp Glu Glu Leu Asp Ser Leu Ile Lys Ala Thr Ile Ala
 100 105 110

Gly Gly Gly Val Ile Pro His Ile His Lys Ser Leu Ile Gly Lys Lys
 115 120 125

Gly Gln Gln Lys Thr Val
 130

<210> 1023

<211> 226

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (33)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (42)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (67)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1023

Gly Leu Phe Gln Thr Cys Ile His Leu Leu Thr Leu Pro Val Leu Val
 1 5 10 15

His Gly Glu Leu Phe Ala Pro Pro Arg Trp Leu Arg Arg Ala Ala Gly
 20 25 30

Xaa Pro Trp Thr Leu Val Thr Ser Cys Xaa Ser Leu Arg Pro Ser Gly
 35 40 45

Pro Cys Pro Arg Pro Gly Arg Ala Leu Leu Pro Ser Cys Ala Pro Ala
 50 55 60

Ala Arg Xaa Pro Trp Gly Gly Val Val Trp Cys Trp Glu Gly Val Leu
 65 70 75 80

Gln Gly Glu Glu Asp Leu Glu Gly Leu Gly Ala Ala Val Leu Asn Arg
 85 90 95

Leu Thr Leu Arg Arg Pro Leu Ser Ala Ala Leu Leu Phe Ile Thr Val
 100 105 110

Pro His Ser Gly Arg Arg Ser Pro Val Ala Gly Gln Val Pro Met Ala
 115 120 125

Cys Ser Leu Glu Pro Asp Phe Arg Cys Phe Gly Ile Arg Ser Pro Gln
 130 135 140

His Arg Gln Val His Pro Ile Ile Thr Leu Pro Val Pro Gly Trp Ala
 145 150 155 160

Gly Asp Ser Gly Thr Val Met Pro Gly Ala Arg Thr Ala Ala Leu Pro
 165 170 175

Leu His Thr Asp Gly Leu Gly Val Ala Leu Arg Pro His Pro Thr Leu
 180 185 190

Ile Ser Gly Arg Gly Ser Pro Glu Trp Ser Leu Val Arg Ala Val Ala
 195 200 205

Lys Pro Ala Val Ser Phe Leu His Lys Val Pro Pro Pro Leu Ser Val
 210 215 220

Ser Gly
 225

<210> 1024
<211> 760
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (330)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1024

Gln Gly Lys Lys Arg Ala Gly Asn Phe Ala Ile Met Glu Ile Gln Cys
1 5 10 15

Pro Ala Leu Arg Lys Thr Leu Pro Ile Leu Phe Gly Ser Leu Arg Arg
20 25 30

Cys Leu Cys Leu Ser Asp Lys Tyr Ser Gln Ala Cys His Pro Leu Gly
35 40 45

Ser Lys Val Arg Arg Cys Arg Lys Pro Gly Pro Arg Asp Arg Gln Leu
50 55 60

Thr Arg Val Asp Lys Ser Pro Glu Met Trp Cys Ile Val Leu Phe Ser
65 70 75 80

Leu Leu Ala Trp Val Tyr Ala Glu Pro Thr Met Tyr Gly Glu Ile Leu
85 90 95

Ser Pro Asn Tyr Pro Gln Ala Tyr Pro Ser Glu Val Glu Lys Ser Trp
100 105 110

Asp Ile Glu Val Pro Glu Gly Tyr Gly Ile His Leu Tyr Phe Thr His
115 120 125

Leu Asp Ile Glu Leu Ser Glu Asn Cys Ala Tyr Asp Ser Val Gln Ile
130 135 140

Ile Ser Gly Asp Thr Glu Glu Gly Arg Leu Cys Gly Gln Arg Ser Ser
145 150 155 160

Asn Asn Pro His Ser Pro Ile Val Glu Glu Phe Gln Val Pro Tyr Asn
165 170 175

Lys Leu Gln Val Ile Phe Lys Ser Asp Phe Ser Asn Glu Glu Arg Phe
180 185 190

Thr Gly Phe Ala Ala Tyr Tyr Val Ala Thr Asp Ile Asn Glu Cys Thr
195 200 205

Asp Phe Val Asp Val Pro Cys Ser His Phe Cys Asn Asn Phe Ile Gly
210 215 220

Gly Tyr Phe Cys Ser Cys Pro Pro Glu Tyr Phe Leu His Asp Asp Met
225 230 235 240

Lys Asn Cys Gly Val Asn Cys Ser Gly Asp Val Phe Thr Ala Leu Ile
245 250 255

Gly Glu Ile Ala Ser Pro Asn Tyr Pro Lys Pro Tyr Pro Glu Asn Ser
260 265 270

Arg Cys Glu Tyr Gln Ile Arg Leu Glu Lys Gly Phe Gln Val Val Val
275 280 285

Thr Leu Arg Arg Glu Asp Phe Asp Val Glu Ala Ala Asp Ser Ala Gly
290 295 300

Asn Cys Leu Asp Ser Leu Val Phe Val Ala Gly Asp Arg Gln Phe Gly
305 310 315 320

Pro Tyr Cys Gly His Gly Phe Pro Gly Xaa Leu Asn Ile Glu Thr Lys
325 330 335

Ser Asn Ala Leu Asp Ile Ile Phe Gln Thr Asp Leu Thr Gly Gln Lys
340 345 350

Lys Gly Trp Lys Leu Arg Tyr His Gly Asp Pro Met Pro Cys Pro Lys
355 360 365

Glu Asp Thr Pro Asn Ser Val Trp Glu Pro Ala Lys Ala Lys Tyr Val
370 375 380

Phe Arg Asp Val Val Gln Ile Thr Cys Leu Asp Gly Phe Glu Val Val
385 390 395 400

Glu Gly Arg Val Gly Ala Thr Ser Phe Tyr Ser Thr Cys Gln Ser Asn
405 410 415

Gly Lys Trp Ser Asn Ser Lys Leu Lys Cys Gln Pro Val Asp Cys Gly
420 425 430

Ile Pro Glu Ser Ile Glu Asn Gly Lys Val Glu Asp Pro Glu Ser Thr
435 440 445

Leu Phe Gly Ser Val Ile Arg Tyr Thr Cys Glu Glu Pro Tyr Tyr Tyr
450 455 460

Met Glu Asn Gly Gly Gly Glu Tyr His Cys Ala Gly Asn Gly Ser
465 470 475 480

Trp Val Asn Glu Val Leu Gly Pro Glu Leu Pro Lys Cys Val Pro Val
 485 490 495
 Cys Gly Val Pro Arg Glu Pro Phe Glu Glu Lys Gln Arg Ile Ile Gly
 500 505 510
 Gly Ser Asp Ala Asp Ile Lys Asn Phe Pro Trp Gln Val Phe Phe Asp
 515 520 525
 Asn Pro Trp Ala Gly Gly Ala Leu Ile Asn Glu Tyr Trp Val Leu Thr
 530 535 540
 Ala Ala His Val Val Glu Gly Asn Arg Glu Pro Thr Met Tyr Val Gly
 545 550 555 560
 Ser Thr Ser Val Gln Thr Ser Arg Leu Ala Lys Ser Lys Met Leu Thr
 565 570 575
 Pro Glu His Val Phe Ile His Pro Gly Trp Lys Leu Leu Glu Val Pro
 580 585 590
 Glu Gly Arg Thr Asn Phe Asp Asn Asp Ile Ala Leu Val Arg Leu Lys
 595 600 605
 Asp Pro Val Lys Met Gly Pro Thr Val Ser Pro Ile Cys Leu Pro Gly
 610 615 620
 Thr Ser Ser Asp Tyr Asn Leu Met Asp Gly Asp Leu Gly Leu Ile Ser
 625 630 635 640
 Gly Trp Gly Arg Thr Glu Lys Arg Asp Arg Ala Val Arg Leu Lys Ala
 645 650 655
 Ala Arg Leu Pro Val Ala Pro Leu Arg Lys Cys Lys Glu Val Lys Val
 660 665 670
 Glu Lys Pro Thr Ala Asp Ala Glu Ala Tyr Val Phe Thr Pro Asn Met
 675 680 685
 Ile Cys Ala Gly Gly Glu Lys Gly Met Asp Ser Cys Lys Gly Asp Ser
 690 695 700
 Gly Gly Ala Phe Ala Val Gln Asp Pro Asn Asp Lys Thr Lys Phe Tyr
 705 710 715 720
 Ala Ala Gly Leu Val Ser Trp Gly Pro Gln Cys Gly Thr Tyr Gly Leu
 725 730 735
 Tyr Thr Arg Val Lys Asn Tyr Val Asp Trp Ile Met Lys Thr Met Gln
 740 745 750

1000

Glu Asn Ser Thr Pro Arg Glu Asp
755 760

<210> 1025
<211> 216
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (115)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (139)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1025
Gly Gly Gly Arg Leu Arg Arg Arg Arg Ser Gly Ser Pro Gly Trp Arg
1 5 10 15
Ala Pro Arg Thr Gly Met Leu Leu Gly Leu Ala Ala Met Glu Leu Lys
20 25 30
Val Trp Val Asp Gly Ile Gln Arg Val Val Cys Gly Val Ser Glu Gln
35 40 45
Thr Thr Cys Gln Glu Val Val Ile Ala Leu Ala Gln Ala Ile Gly Gln
50 55 60
Thr Gly Arg Phe Val Leu Val Gln Arg Leu Arg Glu Lys Glu Arg Gln
65 70 75 80
Leu Leu Pro Gln Glu Cys Pro Val Gly Ala Gln Ala Thr Cys Gly Gln
85 90 95
Phe Ala Ser Asp Val Gln Phe Val Leu Arg Arg Thr Gly Pro Ser Leu
100 105 110
Ala Gly Xaa Pro Ser Ser Asp Ser Cys Pro Pro Pro Glu Arg Cys Leu
115 120 125
Ile Arg Ala Ser Leu Pro Val Lys Pro Arg Xaa Ala Leu Gly Cys Glu
130 135 140
Pro Arg Lys Thr Leu Thr Pro Glu Pro Ala Pro Ser Leu Ser Arg Pro
145 150 155 160

Gly Pro Ala Ala Cys Glu His Pro His Gln Ala Ala Ala Gln Thr Cys
165 170 175

Gly Ala Trp Ser Ser Gly Cys Arg Gly Met Leu Arg Ser Trp Ala Met
180 185 190

Arg Pro Ser Gly Ser Lys Ser Cys Ala Gly Ser Arg Pro Gly Ser Glu
195 200 205

Arg Asp Arg His Ala Cys Arg His
210 215

<213> Homo sapiens

<223> Xaa equals any of the naturally occurring L-amino acids

<223> Xaa equals any of the naturally occurring L-amino acids

Gly Thr Ser Ser Asp Ile Leu Lys Gly Asn Phe Ser Ile Arg Thr Ala
1 5 10 15

Lys Met Gln Gln His Val Cys Glu Thr Ile Ile Arg Ile Phe Lys Arg
20 25 30

His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu Leu Pro Arg Asn Arg
35 40 45

Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe Met Asp His Ser Gly
50 55 60

Met	Leu	Val	Met	Leu	Pro	Phe	Asp	Leu	Arg	Ile	Pro	Phe	Ala	Arg	Tyr
65					70					75					80

Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg Tyr Cys Ile Glu Arg
85 90 95

Val	Phe	Arg	Pro	Arg	Lys	Leu	Asp	Arg	Phe	His	Pro	Lys	Glu	Leu	Leu
			100					105					110		

1002

Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr Asn Ser Phe Leu Pro
 115 120 125
 Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu Ile Ile Gln Glu Phe Pro
 130 135 140
 Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu Asn His Thr Met Leu
 145 150 155 160
 Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro Glu Asp Lys Leu Ser
 165 170 175
 Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val Thr Glu Lys Leu Thr Arg
 180 185 190
 Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser Leu Ser Ser Asn Ser
 195 200 205
 Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys Gly Asp Leu Gln Asp
 210 215 220
 Leu Met Pro Thr Ile Asn Ser Leu Ile Lys Gln Lys Thr Gly Ile Ala
 225 230 235 240
 Gln Leu Val Lys Tyr Gly Leu Lys Asp Leu Glu Glu Val Val Gly Leu
 245 250 255
 Leu Lys Lys Leu Gly Ile Lys Leu Gln Val Leu Ile Asn Leu Gly Leu
 260 265 270
 Val Tyr Lys Val Gln Gln His Asn Gly Ile Ile Phe Gln Phe Val Ala
 275 280 285
 Phe Ile Lys Arg Arg Gln Arg Ala Val Pro Glu Ile Leu Ala Xaa Gly
 290 295 300
 Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg Gly Pro Gln Ala Leu
 305 310 315 320
 Gly Pro Val Pro Thr Ala Ile Gly Val Ser Ile Ala Ile Asp Lys Ile
 325 330 335
 Ser Ala Ala Val Leu Asn Met Glu Glu Ser Val Thr Ile Ser Ser Cys
 340 345 350
 Asp Leu Leu Val Val Ser Xaa Gly Gln Met Ser Met Ser Arg Ala Ile
 355 360 365
 Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile Thr Ala Glu Ile Met
 370 375 380

1003

Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln Glu Tyr Cys Arg His
385 390 395 400

His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp Lys Glu Gly Ser His
405 410 415

Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln Thr Glu Lys Arg Val
420 425 430

Leu Glu Thr Glu Leu Val Asp His Val Leu Gln Lys Leu Arg Thr Lys
435 440 445

Val Thr Asp Glu Arg Asn Gly Arg Glu Ala Ser Asp Asn Leu Ala Val
450 455 460

Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala Ser Gly Leu Phe Glu Ile
465 470 475 480

His Gly Ala Thr Val Val Pro Ile Val Ser Val Leu Ala Pro Glu Lys
485 490 495

Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu Thr Gln Val Gln Thr Arg
500 505 510

Leu Gln Thr Ser Leu Ala Asn Leu His Gln Lys Ser Ser Glu Ile Glu
515 520 525

Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu Gln Phe Leu Ser
530 535 540

Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr Thr Val Lys Gln
545 550 555 560

Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys Leu Val Cys Asp
565 570 575

Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser Val Leu Phe Leu
580 585 590

Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu Phe
595 600

<210> 1027

<211> 459

<212> PRT

<213> Homo sapiens

<220>

1004

<221> SITE

<222> (27)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1027

Thr Ser Cys Gly Ile Asn Thr Lys Phe Thr Ser Lys Glu Pro Ile Phe
 1 5 10 15

Leu Thr Gln Leu Leu His Phe Ser Asn Leu Xaa Gln Glu Tyr Lys Ile
 20 25 30

Asn Ser Arg Leu Leu Gln Asn Ile Leu Asp Ala Gly Phe Gln Met Pro
 35 40 45

Thr Pro Ile Gln Met Gln Ala Ile Pro Val Met Leu His Gly Arg Glu
 50 55 60

Leu Leu Ala Ser Ala Pro Thr Gly Ser Gly Lys Thr Leu Ala Phe Ser
 65 70 75 80

Ile Pro Ile Leu Met Gln Leu Lys Gln Pro Ala Asn Lys Gly Phe Arg
 85 90 95

Ala Leu Ile Ile Ser Pro Thr Arg Glu Leu Ala Ser Gln Ile His Arg
 100 105 110

Glu Leu Ile Lys Ile Ser Glu Gly Thr Gly Phe Arg Ile His Met Ile
 115 120 125

His Lys Ala Ala Val Ala Ala Lys Lys Phe Gly Pro Lys Ser Ser Lys
 130 135 140

Lys Phe Asp Ile Leu Val Thr Thr Pro Asn Arg Leu Ile Tyr Leu Leu
 145 150 155 160

Lys Gln Asp Pro Pro Gly Ile Asp Leu Ala Ser Val Glu Trp Leu Val
 165 170 175

Val Asp Glu Ser Asp Lys Leu Phe Glu Asp Gly Lys Thr Gly Phe Arg
 180 185 190

Asp Gln Leu Ala Ser Ile Phe Leu Ala Cys Thr Ser His Lys Val Arg
 195 200 205

Arg Ala Met Phe Ser Ala Thr Phe Ala Tyr Asp Val Glu Gln Trp Cys
 210 215 220

Lys Leu Asn Leu Asp Asn Val Ile Ser Val Ser Ile Gly Ala Arg Asn
 225 230 235 240

Ser Ala Val Glu Thr Val Glu Gln Glu Leu Leu Phe Val Gly Ser Glu

1005

	245		250		255
Thr Gly Lys Leu Leu Ala Val Arg Glu Leu Val Lys Lys Gly Phe Asn					
	260		265		270
Pro Pro Val Leu Val Phe Val Gln Ser Ile Glu Arg Ala Lys Glu Leu					
	275		280		285
Phe His Glu Leu Ile Tyr Glu Gly Ile Asn Val Asp Val Ile His Ala					
	290		295		300
Glu Arg Thr Gln Gln Gln Arg Asp Asn Thr Val His Ser Phe Arg Ala					
305		310		315	320
Gly Lys Ile Trp Val Leu Ile Cys Thr Ala Leu Leu Ala Arg Gly Ile					
	325		330		335
Asp Phe Lys Gly Val Asn Leu Val Ile Asn Tyr Asp Phe Pro Thr Ser					
	340		345		350
Ser Val Glu Tyr Ile His Arg Ile Gly Arg Thr Gly Arg Ala Gly Asn					
	355		360		365
Lys Gly Lys Ala Ile Thr Phe Phe Thr Glu Asp Asp Lys Pro Leu Leu					
	370		375		380
Arg Ser Val Ala Asn Val Ile Gln Gln Ala Gly Cys Pro Val Pro Glu					
385		390		395	400
Tyr Ile Lys Gly Phe Gln Lys Leu Leu Ser Lys Gln Lys Lys Lys Met					
	405		410		415
Ile Lys Lys Pro Leu Glu Arg Glu Ser Ile Ser Thr Thr Pro Lys Cys					
	420		425		430
Phe Leu Glu Lys Ala Lys Asp Lys Gln Lys Lys Val Thr Gly Gln Asn					
	435		440		445
Ser Lys Lys Lys Val Ala Leu Glu Asp Lys Ser					
	450		455		

<210> 1028

<211> 68

<212> PRT

<213> Homo sapiens

<400> 1028

Gln	Arg	Gly	Phe	Tyr	Ala	Asn	Ala	Leu	Thr	Ser	Ala	Leu	Gly	Asn	Glu
1															
					5					10					15

1006

Arg Val Thr Ser Ala Ser Ser Leu Ala Ser Phe Leu Val Leu Glu Arg
 20 25 30

Leu Thr Asn Val Cys His Ser His Lys Cys Phe Glu Leu Asp Leu Cys
 35 40 45

Asp Leu Cys Phe Phe Ser Phe Ser Leu Glu Ser Glu Tyr His Cys Leu
 50 55 60

Pro Pro Arg Ser
 65

<210> 1029
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 1029
 Tyr Pro Leu Thr Pro Ala Pro Ala Pro His Asp Pro Ser Pro Arg Ala
 1 5 10 15

His Gly Arg Gly Asp Asp Val Thr Gln Ala Thr Ala Leu Thr Ser His
 20 25 30

Ile Thr Val Val Met Ala Ser Arg Gly His Val Asp Val Thr Lys Arg
 35 40 45

Tyr Ser Asp Gly Val Val Gln Met Gln His Val Ala His Arg His Gly
 50 55 60

Glu Leu Gly Met Thr Ser His Arg Asp Ala Ala Thr Thr Ser Arg Ala
 65 70 75 80

Met Ser Thr Ser His Ile Leu Met Ser His Arg Arg Gly Asp Gly Ile
 85 90 95

Thr Gln Thr Val Met Met Ser His Thr Asp Thr Val Thr Thr His Thr
 100 105 110

Met Thr Thr Thr Pro Ile Asp Met Ala Pro Thr Ser His Ala Arg Met
 115 120 125

Pro Phe His Thr His Phe Leu Pro Asn Ser His Leu Val Ser Arg Ser
 130 135 140

Pro Asp Pro Gly Thr Arg Ala Lys Val Pro Thr Gly Ser His Pro Leu
 145 150 155 160

1007

Pro His Ser Pro Gly Pro Gln His Leu Pro Ser Ser Ser Phe Leu Ala
 165 170 175

Ser Gln Pro Leu Pro His Pro Gln Cys Leu Asp Pro Glu Val Arg Thr
 180 185 190

Gly Ser His Ser Pro Pro Leu Leu Glu Arg Glu Cys Phe Gln Asp Pro
 195 200 205

Leu Gly Ala Leu Ser Arg Gly
 210 215

<210> 1030

<211> 297

<212> PRT

<213> Homo sapiens

<400> 1030

Lys Val Arg Leu Gln Val Pro Val Arg Asn Ser Arg Val Asp Pro Arg
 1 5 10 15

Val Arg Pro Arg Val Arg Pro Arg Val Arg Trp Thr Ala Ala Met Arg
 20 25 30

Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu Ala Leu
 35 40 45

Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp Glu Gln
 50 55 60

Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu Thr Lys
 65 70 75 80

Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys Phe Phe
 85 90 95

Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu Ile Met
 100 105 110

Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser Leu Phe
 115 120 125

Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg Ile Val
 130 135 140

Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu Val Ser
 145 150 155 160

Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe Arg Lys

1008

	165		170		175
Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg Gly Ala					
	180		185		190
His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu Ala His					
	195		200		205
Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe Asp Glu					
	210		215		220
Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe Leu Tyr					
	225		230		235
					240
Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His Ser Ser					
	245		250		255
Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp Pro Gln					
	260		265		270
Asn Phe Lys Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Lys Leu Tyr					
	275		280		285
Gly Lys Arg Ser Asn Ser Arg Lys Lys					
	290		295		

<210> 1031

<211> 571

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (44)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (81)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (484)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1031

Arg Val Arg Ser Lys Val Pro Arg Cys Val Asn Thr Gln Pro Gly Phe					
1		5		10	15

1009

His Cys Leu Pro Cys Pro Pro Arg Tyr Arg Gly Asn Gln Pro Val Gly
20 25 30

Val Gly Leu Glu Ala Ala Lys Thr Glu Lys Gln Xaa Cys Glu Pro Glu
35 40 45

Asn Pro Cys Lys Asp Lys Thr His Asn Cys His Lys His Ala Glu Cys
50 55 60

Ile Tyr Leu Gly His Phe Ser Asp Pro Met Tyr Lys Cys Glu Cys Gln
65 70 75 80

Xaa Gly Tyr Ala Gly Asp Gly Leu Ile Cys Gly Glu Asp Ser Asp Leu
85 90 95

Asp Gly Trp Pro Asn Leu Asn Leu Val Cys Ala Thr Asn Ala Thr Tyr
100 105 110

His Cys Ile Lys Asp Asn Cys Pro His Leu Pro Asn Ser Gly Gln Glu
115 120 125

Asp Phe Asp Lys Asp Gly Ile Gly Asp Ala Cys Asp Asp Asp Asp Asp
130 135 140

Asn Asp Gly Val Thr Asp Glu Lys Asp Asn Cys Gln Leu Leu Phe Asn
145 150 155 160

Pro Arg Gln Ala Asp Tyr Asp Lys Asp Glu Val Gly Asp Arg Cys Asp
165 170 175

Asn Cys Pro Tyr Val His Asn Pro Ala Gln Ile Asp Thr Asp Asn Asn
180 185 190

Gly Glu Gly Asp Ala Cys Ser Val Asp Ile Asp Gly Asp Asp Val Phe
195 200 205

Asn Glu Arg Asp Asn Cys Pro Tyr Val Tyr Asn Thr Asp Gln Arg Asp
210 215 220

Thr Asp Gly Asp Gly Val Gly Asp His Cys Asp Asn Cys Pro Leu Val
225 230 235 240

His Asn Pro Asp Gln Thr Asp Val Asp Asn Asp Leu Val Gly Asp Gln
245 250 255

Cys Asp Asn Asn Glu Asp Ile Asp Asp Asp Gly His Gln Asn Asn Gln
260 265 270

Asp Asn Cys Pro Tyr Ile Ser Asn Ala Asn Gln Ala Asp His Asp Arg
275 280 285

1010

Asp Gly Gln Gly Asp Ala Cys Asp Pro Asp Asp Asp Asn Asp Gly Val
290 295 300

Pro Asp Asp Arg Asp Asn Cys Arg Leu Val Phe Asn Pro Asp Gln Glu
305 310 315 320

Asp Leu Asp Gly Asp Gly Arg Gly Asp Ile Cys Lys Asp Asp Phe Asp
325 330 335

Asn Asp Asn Ile Pro Asp Ile Asp Asp Val Cys Pro Glu Asn Asn Ala
340 345 350

Ile Ser Glu Thr Asp Phe Arg Asn Phe Gln Met Val Pro Leu Asp Pro
355 360 365

Lys Gly Thr Thr Gln Ile Asp Pro Asn Trp Val Ile Arg His Gln Gly
370 375 380

Lys Glu Leu Val Gln Thr Ala Asn Ser Asp Pro Gly Ile Ala Val Gly
385 390 395 400

Phe Asp Glu Phe Gly Ser Val Asp Phe Ser Gly Thr Phe Tyr Val Asn
405 410 415

Thr Asp Arg Asp Asp Asp Tyr Ala Gly Phe Val Phe Gly Tyr Gln Ser
420 425 430

Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln Val Thr Gln Thr Tyr
435 440 445

Trp Glu Asp Gln Pro Thr Arg Ala Tyr Gly Tyr Ser Gly Val Ser Leu
450 455 460

Lys Val Val Asn Ser Thr Thr Gly Thr Gly Glu His Leu Arg Asn Ala
465 470 475 480

Leu Trp His Xaa Gly Asn Thr Pro Gly Gln Val Arg Thr Leu Trp His
485 490 495

Asp Pro Arg Asn Ile Gly Trp Lys Asp Tyr Thr Ala Tyr Arg Trp His
500 505 510

Leu Thr His Arg Pro Lys Thr Gly Tyr Ile Arg Val Leu Val His Glu
515 520 525

Gly Lys Gln Val Met Ala Asp Ser Gly Pro Ile Tyr Asp Gln Thr Tyr
530 535 540

Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser Gln Glu Met Val Tyr
545 550 555 560

1011

Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Ile
 565 570

<210> 1032

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1032

Gly Arg Gly Thr Ala Thr Phe Pro Thr Gly His Glu Phe Val Gly Pro
 1 5 10 15

Cys Leu Gly Arg Ala Glu Ala Phe Trp Arg Ser Lys Met Gly Arg Lys
 20 25 30

Asp Ala Ala Thr Ile Lys Leu Pro Val Asp Gln Tyr Arg Lys Gln Ile
 35 40 45

Gly Lys Gln Asp Tyr Lys Lys Thr Lys Pro Ile Leu Arg Ala Thr Lys
 50 55 60

Leu Lys Ala Glu Ala Lys Lys Thr Ala Ile Gly Ile Lys Glu Val Gly
 65 70 75 80

Leu Val Leu Ala Ala Ile Leu Ala Leu Leu Leu Ala Phe Tyr Ala Phe
 85 90 95

Phe Tyr Leu Arg Leu Thr Thr Asp Val Asp Pro Asp Leu Asp Gln Asp
 100 105 110

Glu Asp

<210> 1033

<211> 243

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (88)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (101)

1012

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1033

His Arg Arg Asp Glu Ala Leu Gln Ser Leu Arg Phe Arg Arg Arg Pro
 1 5 10 15

Gly Ala Gln Ala Ala Asp Ala Cys Gly Pro Arg Ala Asp Leu Gly Gly
 20 25 30

Pro Arg Glu Pro Ala Ala Gly Gly Arg Ala Ala Trp His Arg Pro Ala
 35 40 45

Ala Arg Gly Gln Ser Pro Arg Arg Cys His Ala Gly Val His Arg Ser
 50 55 60

Gln Cys His Leu Cys Arg Leu Gly Ala Ala Glu Arg Phe Arg Gly Ile
 65 70 75 80

Val Ala Leu Leu Ala Ser Arg Xaa Leu Leu Arg Pro Pro Leu His Trp
 85 90 95

Val Leu Leu Ala Xaa Ala Leu Val Asn Leu Leu Leu Ser Val Ala Cys
 100 105 110

Ser Leu Gly Leu Leu Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly
 115 120 125

Arg Arg Leu Ile Ala Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val
 130 135 140

Pro Leu Asp Glu Gly Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr
 145 150 155 160

Arg Ile Tyr Asp Thr Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met
 165 170 175

Ser Ala Gly Glu Ala Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu
 180 185 190

Thr Leu Arg Gly Val Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln
 195 200 205

Leu Glu Glu Met Thr Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln Glu
 210 215 220

Asn Glu Gln Leu Leu Asp Gln Asn Gln Glu Ile Arg Ala Ser Gln Arg
 225 230 235 240

Ser Trp Val

1013

<210> 1034

<211> 173

<212> PRT

<213> Homo sapiens

<400> 1034

Tyr Thr Trp His Ser Glu Lys Met Asp Leu Lys Asp Lys Asn Gly Gly
1 5 10 15

Pro Gly Arg Cys Asn Ser His Arg Leu Lys Val Ser Ser Gly Leu Cys
20 25 30

Lys Thr His Glu Ile Gly Phe Asp Pro Leu Ala Leu Lys Cys Pro Leu
35 40 45

Arg Ser Arg Thr Ala Pro Trp Trp Pro Leu Asp Arg Val Ser Phe Asp
50 55 60

Leu His His Leu Val Ile Gly Asn Phe Phe Val Gly Asn Arg Lys Ile
65 70 75 80

Phe Leu Asp Tyr Leu Val Tyr Gly Phe Ala His Asn Asn Arg Trp Lys
85 90 95

Leu Leu Val Gln Ser Trp Ser Asp Gly Cys Val His Arg Thr Phe Gly
100 105 110

Leu Val Lys Ser Phe Ser Lys Ala Ser Phe Cys Ile Phe Ile Thr Lys
115 120 125

Gln Arg Lys Ser Ser Glu Asp Leu Ala Leu Lys Gln Ile Cys Ala Asn
130 135 140

Thr Ala Arg Val Ile Leu Lys Leu Lys His Phe His Phe Val Ser Tyr
145 150 155 160

Met Cys Thr Phe Leu Phe Thr Cys Glu Asn Gly His Leu
165 170

<210> 1035

<211> 241

<212> PRT

<213> Homo sapiens

<400> 1035

Ser Phe Ser Glu Met Ala Gly Val Ser Ala Cys Ile Lys Tyr Ser Met
1 5 10 15

1014

Phe Thr Phe Asn Phe Leu Phe Trp Leu Cys Gly Ile Leu Ile Leu Ala
 20 25 30
 Leu Ala Ile Trp Val Arg Val Ser Asn Asp Ser Gln Ala Ile Phe Gly
 35 40 45
 Ser Glu Asp Val Gly Ser Ser Ser Tyr Val Ala Val Asp Ile Leu Ile
 50 55 60
 Ala Val Gly Ala Ile Ile Met Ile Leu Gly Phe Leu Gly Cys Cys Gly
 65 70 75 80
 Ala Ile Lys Glu Ser Arg Cys Met Leu Leu Leu Phe Phe Ile Gly Leu
 85 90 95
 Leu Leu Ile Leu Leu Leu Gln Val Ala Thr Gly Ile Leu Gly Ala Val
 100 105 110
 Phe Lys Ser Lys Ser Asp Arg Ile Val Asn Glu Thr Leu Tyr Glu Asn
 115 120 125
 Thr Lys Leu Leu Ser Ala Thr Gly Glu Ser Glu Lys Gln Phe Gln Glu
 130 135 140
 Ala Ile Ile Val Phe Gln Glu Glu Phe Lys Cys Cys Gly Leu Val Asn
 145 150 155 160
 Gly Ala Ala Asp Trp Gly Asn Asn Phe Gln His Tyr Pro Glu Leu Cys
 165 170 175
 Ala Cys Leu Asp Lys Gln Arg Pro Cys Gln Ser Tyr Asn Gly Lys Gln
 180 185 190
 Val Tyr Lys Glu Thr Cys Ile Ser Phe Ile Lys Asp Phe Leu Ala Lys
 195 200 205
 Asn Leu Ile Ile Val Ile Gly Ile Ser Phe Gly Leu Ala Val Ile Glu
 210 215 220
 Ile Leu Gly Leu Val Phe Ser Met Val Leu Tyr Cys Gln Ile Gly Asn
 225 230 235 240
 Lys

<210> 1036

<211> 335

<212> PRT

1015

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1036

Pro Thr Xaa Gly Arg Ala Glu Glu Ala Lys Met Ala Ala Ala Ala Ala
 1 5 10 15

Ser Leu Arg Gly Val Val Leu Gly Pro Arg Gly Ala Gly Leu Pro Gly
 20 25 30

Ala Arg Ala Arg Gly Leu Leu Cys Ser Ala Arg Pro Gly Gln Leu Pro
 35 40 45

Leu Arg Thr Pro Gln Ala Val Ala Leu Ser Ser Lys Ser Gly Leu Ser
 50 55 60

Arg Gly Arg Lys Val Met Leu Ser Ala Leu Gly Met Leu Ala Ala Gly
 65 70 75 80

Gly Ala Gly Leu Ala Val Ala Leu His Ser Ala Val Ser Ala Ser Asp
 85 90 95

Leu Glu Leu His Pro Pro Ser Tyr Pro Trp Ser His Arg Gly Leu Leu
 100 105 110

Ser Ser Leu Asp His Thr Ser Ile Arg Arg Gly Phe Gln Val Tyr Lys
 115 120 125

Gln Val Cys Ala Ser Cys His Ser Met Asp Phe Val Ala Tyr Arg His
 130 135 140

Leu Val Gly Val Cys Tyr Thr Glu Asp Glu Ala Lys Glu Leu Ala Ala
 145 150 155 160

Glu Val Glu Val Gln Asp Gly Pro Asn Glu Asp Gly Glu Met Phe Met
 165 170 175

Arg Pro Gly Lys Leu Phe Asp Tyr Phe Pro Lys Pro Tyr Pro Asn Ser
 180 185 190

Glu Ala Ala Arg Ala Ala Asn Asn Gly Ala Leu Pro Pro Asp Leu Ser
 195 200 205

Tyr Ile Val Arg Ala Arg His Gly Gly Glu Asp Tyr Val Phe Ser Leu
 210 215 220

Leu Thr Gly Tyr Cys Glu Pro Pro Thr Gly Val Ser Leu Arg Glu Gly

1016

225 230 235 240
 Leu Tyr Phe Asn Pro Tyr Phe Pro Gly Gln Ala Ile Ala Met Ala Pro
 245 250 255
 Pro Ile Tyr Thr Asp Val Leu Glu Phe Asp Asp Gly Thr Pro Ala Thr
 260 265 270
 Met Ser Gln Ile Ala Lys Asp Val Cys Thr Phe Leu Arg Trp Ala Ser
 275 280 285
 Glu Pro Glu His Asp His Arg Lys Arg Met Gly Leu Lys Met Leu Met
 290 295 300
 Met Met Ala Leu Leu Val Pro Leu Val Tyr Thr Ile Lys Arg His Lys
 305 310 315 320
 Trp Ser Val Leu Lys Ser Arg Lys Leu Ala Tyr Arg Pro Pro Lys
 325 330 335

<210> 1037

<211> 511

<212> PRT

<213> Homo sapiens

<400> 1037

His Gln Leu Gln Gly Pro Leu Pro Leu Arg Ala Leu Pro Trp His Ser
 1 5 10 15
 Ser Arg Ser Arg Val Thr Cys Thr Arg Cys Phe Ser Trp Met His Pro
 20 25 30
 Ser Pro Met His Pro Leu Arg Ala Gly Ser Lys Ser Gln Gly Ser Arg
 35 40 45
 Ser Pro Ala Pro Ser Pro Met Arg Ala Ala Asn Arg Ser His Ser Ala
 50 55 60
 Gly Arg Thr Pro Gly Arg Thr Pro Gly Lys Ser Ser Ser Lys Val Gln
 65 70 75 80
 Thr Thr Pro Ser Lys Pro Gly Gly Asp Arg Tyr Ile Pro His Arg Ser
 85 90 95
 Ala Ala Gln Met Glu Val Ala Ser Phe Leu Leu Ser Lys Glu Asn Gln
 100 105 110
 Pro Glu Asn Ser Gln Thr Pro Thr Lys Lys Glu His Gln Lys Ala Trp
 115 120 125

1017

Ala Leu Asn Leu Asn Gly Phe Asp Val Glu Glu Ala Lys Ile Leu Arg
130 135 140

Leu Ser Gly Lys Pro Gln Asn Ala Pro Glu Gly Tyr Gln Asn Arg Leu
145 150 155 160

Lys Val Leu Tyr Ser Gln Lys Ala Thr Pro Gly Ser Ser Arg Lys Thr
165 170 175

Cys Arg Tyr Ile Pro Ser Leu Pro Asp Arg Ile Leu Asp Ala Pro Glu
180 185 190

Ile Arg Asn Asp Tyr Tyr Leu Asn Leu Val Asp Trp Ser Ser Gly Asn
195 200 205

Val Leu Ala Val Ala Leu Asp Asn Ser Val Tyr Leu Trp Ser Ala Ser
210 215 220

Ser Gly Asp Ile Leu Gln Leu Leu Gln Met Glu Gln Pro Gly Glu Tyr
225 230 235 240

Ile Ser Ser Val Ala Trp Ile Lys Glu Gly Asn Tyr Leu Ala Val Gly
245 250 255

Thr Ser Ser Ala Glu Val Gln Leu Trp Asp Val Gln Gln Gln Lys Arg
260 265 270

Leu Arg Asn Met Thr Ser His Ser Ala Arg Val Gly Ser Leu Ser Trp
275 280 285

Asn Ser Tyr Ile Leu Ser Ser Gly Ser Arg Ser Gly His Ile His His
290 295 300

His Asp Val Arg Val Ala Glu His His Val Ala Thr Leu Ser Gly His
305 310 315 320

Ser Gln Glu Val Cys Gly Leu Arg Trp Ala Pro Asp Gly Arg His Leu
325 330 335

Ala Ser Gly Gly Asn Asp Asn Leu Val Asn Val Trp Pro Ser Ala Pro
340 345 350

Gly Glu Gly Gly Trp Val Pro Leu Gln Thr Phe Thr Gln His Gln Gly
355 360 365

Ala Val Lys Ala Val Ala Trp Cys Pro Trp Gln Ser Asn Val Leu Ala
370 375 380

Thr Gly Gly Gly Thr Ser Asp Arg His Ile Arg Ile Trp Asn Val Cys
385 390 395 400

1018

Ser Gly Ala Cys Leu Ser Ala Val Asp Ala His Ser Gln Val Cys Ser
 405 410 415

Ile Leu Trp Ser Pro His Tyr Lys Glu Leu Ile Ser Gly His Gly Phe
 420 425 430

Ala Gln Asn Gln Leu Val Ile Trp Lys Tyr Pro Thr Met Ala Lys Val
 435 440 445

Ala Glu Leu Lys Gly His Thr Ser Arg Val Leu Ser Leu Thr Met Ser
 450 455 460

Pro Asp Gly Ala Thr Val Ala Ser Ala Ala Asp Glu Thr Leu Arg
 465 470 475 480

Leu Trp Arg Cys Phe Glu Leu Asp Pro Ala Arg Arg Arg Glu Arg Glu
 485 490 495

Lys Ala Ser Ala Ala Lys Ser Ser Leu Ile His Gln Gly Ile Arg
 500 505 510

<210> 1038

<211> 209

<212> PRT

<213> Homo sapiens

<400> 1038

His Glu Pro Pro Ser Ala Ser Ser Val Ala Gly Asp Leu Gly Arg Gly
 1 5 10 15

Thr Arg Thr Glu Val Glu Ala Arg Ala Ala Arg Pro Gly Ala Glu Ser
 20 25 30

Ala Pro Ala Ala Ala Met Pro Asp Ser Trp Asp Lys Asp Val Tyr Pro
 35 40 45

Glu Pro Pro Arg Arg Thr Pro Val Gln Pro Asn Pro Ile Val Tyr Met
 50 55 60

Met Lys Ala Phe Asp Leu Ile Val Asp Arg Pro Val Thr Leu Val Arg
 65 70 75 80

Glu Phe Ile Glu Arg Gln His Ala Lys Asn Arg Tyr Tyr Tyr Tyr His
 85 90 95

Arg Gln Tyr Arg Arg Val Pro Asp Ile Thr Glu Cys Lys Glu Glu Asp
 100 105 110

1019

Ile Met Cys Met Tyr Glu Ala Glu Met Gln Trp Lys Arg Asp Tyr Lys
 115 120 125
 Val Asp Gln Glu Ile Ile Asn Ile Met Gln Asp Arg Leu Lys Ala Cys
 130 135 140
 Gln Gln Arg Glu Gly Gln Asn Tyr Gln Gln Asn Cys Ile Lys Glu Val
 145 150 155 160
 Glu Gln Phe Thr Gln Val Ala Lys Ala Tyr Gln Asp Arg Tyr Gln Asp
 165 170 175
 Leu Gly Ala Tyr Ser Ser Ala Arg Lys Cys Leu Ala Lys Gln Arg Gln
 180 185 190
 Arg Met Leu Gln Glu Arg Lys Ala Ala Lys Glu Ala Ala Ala Ala Thr
 195 200 205

Ser

<210> 1039

<211> 219

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (153)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1039

Leu Ala Ala Pro Asp Leu Ser Lys Pro Arg Gly Tyr His Trp Asp Thr
 1 5 10 15
 Ser Asp Trp Met Pro Ser Val Pro Leu Pro Asp Ile Gln Glu Phe Pro
 20 25 30
 Asn Tyr Glu Val Ile Asp Glu Gln Thr Pro Leu Tyr Ser Ala Asp Pro
 35 40 45
 Asn Ala Ile Asp Thr Asp Tyr Tyr Pro Gly Gly Tyr Asp Ile Glu Ser
 50 55 60
 Asp Phe Pro Pro Pro Glu Asp Phe Pro Ala Ala Asp Glu Leu Pro
 65 70 75 80
 Pro Leu Pro Pro Glu Phe Ser Asn Gln Phe Glu Ser Ile His Pro Pro
 85 90 95

1020

Arg Asp Met Pro Ala Ala Gly Ser Leu Gly Ser Ser Ser Arg Asn Arg
 100 105 110

Gln Arg Phe Asn Leu Asn Gln Tyr Leu Pro Asn Phe Tyr Pro Leu Asp
 115 120 125

Met Ser Glu Pro Gln Thr Lys Gly Thr Gly Glu Asn Ser Thr Cys Arg
 130 135 140

Glu Pro His Ala Pro Tyr Pro Pro Xaa Tyr Gln Arg His Phe Glu Ala
 145 150 155 160

Pro Ala Val Glu Ser Met Pro Met Ser Val Tyr Ala Ser Thr Ala Ser
 165 170 175

Cys Ser Asp Val Ser Ala Cys Cys Glu Val Glu Ser Glu Val Met Met
 180 185 190

Ser Asp Tyr Glu Ser Gly Asp Asp Gly His Phe Glu Glu Val Thr Ile
 195 200 205

Pro Pro Leu Asp Ser Gln Gln His Thr Glu Val
 210 215

<210> 1040

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (11)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1040

Phe Asp Leu Pro Tyr Arg Ala Glu Phe Gly Xaa Pro Gly Pro Pro Leu
 1 5 10 15

Ser Ala Ala Cys Ser Trp Lys Phe Arg Leu Gly Cys Leu Leu Gly Ala
 20 25 30

Met Glu Ser Asp Phe Tyr Leu Arg Tyr Tyr Val Gly His Lys Gly Lys
 35 40 45

Phe Gly His Glu Phe Leu Glu Phe Glu Phe Arg Pro Asp Gly Lys Leu
 50 55 60

Arg Tyr Ala Asn Asn Ser Asn Tyr Lys Asn Asp Val Met Ile Arg Lys

1021

65 70 75 80
 Glu Ala Tyr Val His Lys Ser Val Met Glu Glu Leu Lys Arg Ile Ile
 85 90 95
 Asp Asp Ser Glu Ile Thr Lys Glu Asp Asp Ala Leu Trp Pro Pro Pro
 100 105 110
 Asp Arg Val Gly Arg Gln Glu Leu Glu Ile Val Ile Gly Asp Glu His
 115 120 125
 Ile Ser Phe Thr Thr Ser Lys Ile Gly Ser Leu Ile Asp Val Asn Gln
 130 135 140
 Ser Lys Asp Pro Glu Gly Leu Arg Val Phe Tyr Tyr Leu Val Gln Asp
 145 150 155 160
 Leu Lys Cys Leu Val Phe Ser Leu Ile Gly Leu His Phe Lys Ile Lys
 165 170 175
 Pro Ile

<210> 1041
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1041
 Leu Val Pro Asn Ser Ala Arg Ala Gly Ala Ser Tyr Ala Ala Ala Ala
 1 5 10 15
 Val Thr Met Ala His Tyr Lys Ala Ala Asp Ser Lys Arg Glu Gln Phe
 20 25 30
 Arg Arg Tyr Leu Glu Lys Ser Gly Val Leu Asp Thr Leu Thr Lys Val
 35 40 45
 Leu Val Ala Leu Tyr Glu Glu Pro Glu Lys Pro Asn Ser Ala Leu Asp
 50 55 60
 Phe Leu Lys His His Leu Gly Ala Ala Thr Pro Glu Asn Pro Glu Ile
 65 70 75 80
 Glu Leu Leu Arg Leu Glu Leu Ala Glu Met Lys Glu Lys Tyr Glu Ala
 85 90 95
 Ile Val Glu Glu Asn Lys Lys Leu Lys Ala Lys Leu Ala Gln Tyr Glu
 100 105 110

1022

Pro Pro Gln Glu Glu Lys Arg Ala Glu
 115 120

<210> 1042

<211> 253

<212> PRT

<213> Homo sapiens

<400> 1042

Val Asp Pro Arg Val Arg Pro Arg Ser Val Asn Gly Glu Leu Gln Lys
 1 5 10 15

Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn Pro Arg Leu Ala
 20 25 30

Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys Leu Gln Lys Pro
 35 40 45

Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu Ile Asn Pro Asp
 50 55 60

Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His Arg Leu Leu Gly
 65 70 75 80

His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala Cys Lys Leu Asp
 85 90 95

Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val Gln Pro Arg Ala
 100 105 110

Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg Lys Arg Glu Glu
 115 120 125

Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys Ala Arg Glu Glu
 130 135 140

His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg Gln Ser Gly Ala
 145 150 155 160

Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly Met Pro Gly Asn
 165 170 175

Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met Pro Gly Met Ala
 180 185 190

Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro Glu Val Leu Ala
 195 200 205

1023

Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln Asp Val Ala Gln
210 215 220

Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro Lys Val Met Asn
225 230 235 240

Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln Ala
245 250

<210> 1043

<211> 343

<212> PRT

<213> Homo sapiens

<400> 1043

Met Lys Thr Cys Gln Glu Glu Lys Leu Met Gly His Leu Gly Val Val
1 5 10 15

Leu Tyr Glu Tyr Leu Gly Glu Glu Tyr Pro Glu Val Leu Gly Ser Ile
20 25 30

Leu Gly Ala Leu Lys Ala Ile Val Asn Val Ile Gly Met His Lys Met
35 40 45

Thr Pro Pro Ile Lys Asp Leu Leu Pro Arg Leu Thr Pro Ile Leu Lys
50 55 60

Asn Arg His Glu Lys Val Gln Glu Asn Cys Ile Asp Leu Val Gly Arg
65 70 75 80

Ile Ala Asp Arg Gly Ala Glu Tyr Val Ser Ala Arg Glu Trp Met Arg
85 90 95

Ile Cys Phe Glu Leu Leu Glu Leu Leu Lys Ala His Lys Lys Ala Ile
100 105 110

Arg Arg Ala Thr Val Asn Thr Phe Gly Tyr Ile Ala Lys Ala Ile Gly
115 120 125

Pro His Asp Val Leu Ala Thr Leu Leu Asn Asn Leu Lys Val Gln Glu
130 135 140

Arg Gln Asn Arg Val Cys Thr Thr Val Ala Ile Ala Ile Val Ala Glu
145 150 155 160

Thr Cys Ser Pro Phe Thr Val Leu Pro Ala Leu Met Asn Glu Tyr Arg
165 170 175

Val Pro Glu Leu Asn Val Gln Asn Gly Val Leu Lys Ser Leu Ser Phe

1024

180	185	190
Leu Phe Glu Tyr Ile Gly Glu Met Gly Lys Asp Tyr Ile Tyr Ala Val		
195	200	205
Thr Pro Leu Leu Glu Asp Ala Leu Met Asp Arg Asp Leu Val His Arg		
210	215	220
Gln Thr Ala Ser Ala Val Val Gln His Met Ser Leu Gly Val Tyr Gly		
225	230	235 240
Phe Gly Cys Glu Asp Ser Leu Asn His Leu Leu Asn Tyr Val Trp Pro		
245	250	255
Asn Val Phe Glu Thr Ser Pro His Val Ile Gln Ala Val Met Gly Ala		
260	265	270
Leu Glu Gly Leu Arg Val Ala Ile Gly Pro Cys Arg Met Leu Gln Tyr		
275	280	285
Cys Leu Gln Gly Leu Phe His Pro Ala Arg Lys Val Arg Asp Val Tyr		
290	295	300
Trp Lys Ile Tyr Asn Ser Ile Tyr Ile Gly Ser Gln Asp Ala Leu Ile		
305	310	315 320
Ala His Tyr Pro Arg Ile Tyr Asn Asp Asp Lys Asn Thr Tyr Ile Arg		
325	330	335
Tyr Glu Leu Asp Tyr Ile Leu		
340		

<210> 1044

<211> 268

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (20)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1044

Leu Arg Arg Pro Tyr Ala Arg Tyr Asn Gly Leu Tyr Arg Ser Gly Ile
1 5 10 15

Arg Gly Arg Xaa Asn Leu Glu Ser Thr Arg Val Arg Glu Leu Pro Gly
20 25 30

1025

Gly Ala Met Ser Cys Ile Asn Leu Pro Thr Val Leu Pro Gly Ser Pro
 35 40 45
 Ser Lys Thr Arg Gly Gln Ile Gln Val Ile Leu Gly Pro Met Phe Ser
 50 55 60
 Gly Lys Ser Thr Glu Leu Met Arg Arg Val Arg Arg Phe Gln Ile Ala
 65 70 75 80
 Gln Tyr Lys Cys Leu Val Ile Lys Tyr Ala Lys Asp Thr Arg Tyr Ser
 85 90 95
 Ser Ser Phe Cys Thr His Asp Arg Asn Thr Met Glu Ala Leu Pro Ala
 100 105 110
 Cys Leu Leu Arg Asp Val Ala Gln Glu Ala Leu Gly Val Ala Val Ile
 115 120 125
 Gly Ile Asp Glu Gly Gln Phe Phe Pro Asp Ile Val Glu Phe Cys Glu
 130 135 140
 Ala Met Ala Asn Ala Gly Lys Thr Val Ile Val Ala Ala Leu Asp Gly
 145 150 155 160
 Thr Phe Gln Arg Lys Pro Phe Gly Ala Ile Leu Asn Leu Val Pro Leu
 165 170 175
 Ala Glu Ser Val Val Lys Leu Thr Ala Val Cys Met Glu Cys Phe Arg
 180 185 190
 Glu Ala Ala Tyr Thr Lys Arg Leu Gly Thr Glu Lys Glu Val Glu Val
 195 200 205
 Ile Gly Gly Ala Asp Lys Tyr His Ser Val Cys Arg Leu Cys Tyr Phe
 210 215 220
 Lys Lys Ala Ser Gly Gln Pro Ala Gly Pro Asp Asn Lys Glu Asn Cys
 225 230 235 240
 Pro Val Pro Gly Lys Pro Gly Glu Ala Val Ala Ala Arg Lys Leu Phe
 245 250 255
 Ala Pro Gln Gln Ile Leu Gln Cys Ser Pro Ala Asn
 260 265

<210> 1045

<211> 139

<212> PRT

<213> Homo sapiens

1026

<220>

<221> SITE

<222> (128)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1045

Pro Gly Gln Ser Arg Trp Gln Gly Pro Pro Leu Pro Leu Cys Gln Ala
 1 5 10 15

Gly Ser Ala Lys Ser Gly Glu Pro Gly Ala Gly Gly Lys Ala Gly Asp
 20 25 30

Ser Pro Ala Leu Pro Pro Pro Pro Leu Gly Ala Gln Gln Leu Leu Arg
 35 40 45

Lys Val Trp His Pro Trp Arg Gly Gly Ala Pro Gly Trp Ala Gly Ser
 50 55 60

Arg Trp Pro Gly Ala Trp Arg Cys Ala Ala Gly Ala Cys Met Ala Pro
 65 70 75 80

Arg Gly Thr Gln Ala Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn
 85 90 95

Ile Thr Gly Ala Arg Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln
 100 105 110

Val Gln Gly Glu Pro Pro Glu Val His Trp Leu Arg Asp Gly Gln Xaa
 115 120 125

Leu Glu Leu Ala Asp Ser Thr Gln Thr Gln Val
 130 135

<210> 1046

<211> 416

<212> PRT

<213> Homo sapiens

<400> 1046

Ser Pro Ser Glu Arg Leu Gln Arg Gly Arg Glu Glu Gln Pro Ala Gly
 1 5 10 15

Gly Gly Gly Glu Ser Val Ser Ser Trp Glu Glu Gln Asn Arg Gly Gly
 20 25 30

Ala Pro Ala Gly Ala Gly Gly Gly Pro Thr Met Ala Ile Arg Lys Lys
 35 40 45

1027

Ser Thr Lys Ser Pro Pro Val Leu Ser His Glu Phe Val Leu Gln Asn
 50 55 60

His Ala Asp Ile Val Ser Cys Val Ala Met Val Phe Leu Leu Gly Leu
 65 70 75 80

Met Phe Glu Ile Thr Ala Lys Ala Ser Ile Ile Phe Val Thr Leu Gln
 85 90 95

Tyr Asn Val Thr Leu Pro Ala Thr Glu Glu Gln Ala Thr Glu Ser Val
 100 105 110

Ser Leu Tyr Tyr Tyr Gly Ile Lys Asp Leu Ala Thr Val Phe Phe Tyr
 115 120 125

Met Leu Val Ala Ile Ile Ile His Ala Val Ile Gln Glu Tyr Met Leu
 130 135 140

Asp Lys Ile Asn Arg Arg Met His Phe Ser Lys Thr Lys His Ser Lys
 145 150 155 160

Phe Asn Glu Ser Gly Gln Leu Ser Ala Phe Tyr Leu Phe Ala Cys Val
 165 170 175

Trp Gly Thr Phe Ile Leu Ile Ser Glu Asn Tyr Ile Ser Asp Pro Thr
 180 185 190

Ile Leu Trp Arg Ala Tyr Pro His Asn Leu Met Thr Phe Gln Met Lys
 195 200 205

Phe Phe Tyr Ile Ser Gln Leu Ala Tyr Trp Leu His Ala Phe Pro Glu
 210 215 220

Leu Tyr Phe Gln Lys Thr Lys Lys Glu Asp Ile Pro Arg Gln Leu Val
 225 230 235 240

Tyr Ile Gly Leu Tyr Leu Phe His Ile Ala Gly Ala Tyr Leu Leu Asn
 245 250 255

Leu Asn His Leu Gly Leu Val Leu Leu Val Leu His Tyr Phe Val Glu
 260 265 270

Phe Leu Phe His Ile Ser Arg Leu Phe Tyr Phe Ser Asn Glu Lys Tyr
 275 280 285

Gln Lys Gly Phe Ser Leu Trp Ala Val Leu Phe Val Leu Gly Arg Leu
 290 295 300

Leu Thr Leu Ile Leu Ser Val Leu Thr Val Gly Phe Gly Leu Ala Arg
 305 310 315 320

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<210> 1047
<211> 466
<212> PRT
<213> Homo sapiens
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BNSDOCID: <WO__0055350A1_1_>

1029

115	120	125
Gln Asp Leu Val Asp Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu		
130	135	140
Ala Ser Leu Arg Gln Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu		
145	150	155 160
Glu Arg Lys Asp His Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly		
	165	170 175
Lys Ala Gly Thr Leu Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His		
	180	185 190
Val Val Ser Val Glu Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser		
	195	200 205
Ile Thr Leu Phe Val Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys		
	210	215 220
Glu Lys Met Glu Asn Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe		
	225	230 235 240
Thr Arg Asp Leu Ala Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly		
	245	250 255
Val Asn Asp Asn Phe Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe		
	260	265 270
Gly Thr Thr Pro Glu Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser		
	275	280 285
Thr Ser Val Leu Leu Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser		
	290	295 300
Pro Ala Ile Arg Thr Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln		
	305	310 315 320
Ala Ile Cys Gly Ile Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu		
	325	330 335
Leu Arg Gly Leu Arg Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg		
	340	345 350
Lys Val Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro		
	355	360 365
Pro Leu Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp		
	370	375 380
Thr Val Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile		

1030

385 390 395 400
 Cys Lys Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val
 405 410 415
 Pro Asp Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp
 420 425 430
 Asp Gly Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys
 435 440 445
 Gly Asn Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Ala Gln Gln
 450 455 460
 Pro Met
 465

<210> 1048
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (122)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (186)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (200)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1048
 Asp Pro Arg Val Arg Gln Ser His Ile Ser Asp Thr Ser Val Val Val
 1 5 10 15
 Lys Leu Asp Asn Ser Arg Asp Leu Asn Met Asp Cys Ile Ile Ala Glu
 20 25 30
 Ile Lys Ala Gln Tyr Asp Asp Ile Val Thr Arg Ser Arg Ala Glu Ala
 35 40 45
 Glu Ser Trp Tyr Arg Ser Lys Cys Glu Glu Met Lys Ala Thr Val Ile
 50 55 60

1031

Arg His Gly Glu Thr Leu Arg Arg Thr Lys Glu Glu Ile Asn Glu Leu
65 70 75 80

Asn Arg Met Ile Gln Arg Leu Thr Ala Glu Val Glu Asn Ala Lys Cys
85 90 95

Gln Asn Ser Lys Leu Glu Ala Ala Val Ala Gln Ser Glu Gln Gln Gly
100 105 110

Glu Ala Ala Leu Ser Asp Ala Arg Cys Xaa Leu Ala Glu Leu Glu Gly
115 120 125

Ala Leu Gln Lys Ala Lys Gln Asp Met Ala Cys Leu Ile Arg Glu Tyr
130 135 140

Gln Glu Val Met Asn Ser Lys Leu Gly Leu Asp Ile Glu Ile Ala Thr
145 150 155 160

Tyr Arg Arg Leu Leu Glu Gly Glu Glu Gln Arg Leu Cys Glu Gly Ile
165 170 175

Gly Ala Val Asn Val Cys Val Ser Ser Xaa Arg Gly Gly Val Val Cys
180 185 190

Gly Asp Leu Cys Val Ser Gly Xaa Arg Pro Val Thr Ala Val Ser Ala
195 200 205

Ala Leu Arg Ala Thr Gly Thr Trp Arg
210 215

<210> 1049

<211> 406

<212> PRT

<213> Homo sapiens

<400> 1049

Gly Ser Ala Ala Ala Arg Tyr Leu Ser Ala Thr Trp Arg Asn Trp Ile
1 5 10 15

Ser Leu Pro Pro Ala Gly Leu Pro Ala Thr Ala Gly Leu Arg His Ser
20 25 30

Gly Ser Leu Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn
35 40 45

Tyr Phe Ser Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val
50 55 60

1032

Pro Pro Ala Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser
 65 70 75 80
 Asn Pro Gln Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly
 85 90 95
 Glu Gln Pro Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser
 100 105 110
 Tyr Gln Val Glu Lys Asn Lys Tyr Asp Ala Ser Ala Ile Asp Phe Ser
 115 120 125
 Arg Cys Asp Met Asp Gly Ala Thr Leu Cys Asn Cys Ala Leu Glu Glu
 130 135 140
 Leu Arg Leu Val Phe Gly Pro Leu Gly Asp Gln Leu His Ala Gln Leu
 145 150 155 160
 Arg Asp Leu Thr Ser Ser Ser Ser Asp Glu Leu Ser Trp Ile Ile Glu
 165 170 175
 Leu Leu Glu Lys Asp Gly Met Ala Phe Gln Glu Ala Leu Asp Pro Gly
 180 185 190
 Pro Phe Asp Gln Gly Ser Pro Phe Ala Gln Glu Leu Leu Asp Asp Gly
 195 200 205
 Gln Gln Ala Ser Pro Tyr His Pro Gly Ser Cys Gly Ala Gly Ala Pro
 210 215 220
 Ser Pro Gly Ser Ser Asp Val Ser Thr Ala Gly Thr Gly Ala Ser Arg
 225 230 235 240
 Ser Ser His Ser Ser Asp Ser Gly Gly Ser Asp Val Asp Leu Asp Pro
 245 250 255
 Thr Asp Gly Lys Leu Phe Pro Ser Asp Gly Phe Arg Asp Cys Lys Lys
 260 265 270
 Gly Asp Pro Lys His Gly Lys Arg Lys Arg Gly Arg Pro Arg Lys Leu
 275 280 285
 Ser Lys Glu Tyr Trp Asp Cys Leu Glu Gly Lys Lys Ser Lys His Ala
 290 295 300
 Pro Arg Gly Thr His Leu Trp Glu Phe Ile Arg Asp Ile Leu Ile His
 305 310 315 320
 Pro Glu Leu Asn Glu Gly Leu Met Lys Trp Glu Asn Arg His Glu Gly
 325 330 335

1033

Val Phe Lys Phe Leu Arg Ser Glu Ala Val Ala Gln Leu Trp Gly Gln
 340 345 350

Lys Lys Lys Asn Ser Asn Met Thr Tyr Glu Lys Leu Ser Arg Ala Met
 355 360 365

Arg Tyr Tyr Tyr Lys Arg Glu Ile Leu Glu Arg Val Asp Gly Arg Arg
 370 375 380

Leu Val Tyr Lys Phe Gly Lys Asn Ser Ser Gly Trp Lys Glu Glu Glu
 385 390 395 400

Val Leu Gln Ser Arg Asn
 405

<210> 1050

<211> 251

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (53)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (86)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1050

Arg Pro Ala Leu Asp Thr Cys Cys Pro Phe Pro Ala Arg Ile Leu Gly
 1 5 10 15

Ser Phe Pro Leu Ser Gln His Leu Gly Pro Ala Phe Asp Thr Thr Pro
 20 25 30

Arg Leu Pro Thr Leu Arg Ala Trp Ser Leu Pro Gln Gly Pro Leu Ser
 35 40 45

Trp Ala Met Ala Xaa Lys Gly Val Leu Gly Pro Gly Gln Leu Gly Ala
 50 55 60

Val Ala Ile Leu Leu Tyr Leu Gly Leu Leu Arg Ser Gly Thr Gly Ala
 65 70 75 80

Glu Gly Ala Glu Ala Xaa Cys Gly Val Ala Pro Gln Ala Arg Ile Thr
 85 90 95

1034

Gly Gly Ser Ser Ala Val Ala Gly Gln Trp Pro Trp Gln Val Ser Ile
 100 105 110
 Thr Tyr Glu Gly Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln
 115 120 125
 Trp Val Leu Ser Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu
 130 135 140
 Ala Tyr Glu Val Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu
 145 150 155 160
 Asp Ala Lys Val Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr
 165 170 175
 Leu Gln Glu Gly Ser Gln Gly Asp Ile Ala Leu Leu Gln Leu Ser Arg
 180 185 190
 Pro Ile Thr Phe Ser Arg Tyr Ile Arg Pro Ile Cys Leu Pro Ala Ala
 195 200 205
 Asn Ala Ser Phe Pro Asn Gly Leu His Cys Thr Val Thr Gly Trp Gly
 210 215 220
 His Val Ala Pro Ser Val Ser Leu Leu Thr Pro Lys Pro Leu Gln Gln
 225 230 235 240
 Leu Glu Val Pro Leu Ile Ser Arg Glu Thr Trp
 245 250

<210> 1051

<211> 171

<212> PRT

<213> Homo sapiens

<400> 1051

His Tyr Arg Arg Tyr Ala Cys Arg Tyr Arg Ser Gly Ile Arg Gly Arg
 1 5 10 15
 Val Asp Ile Arg Arg Arg Ser Ser Arg Arg Pro Arg Glu Pro Pro Gly
 20 25 30
 Pro Ser Arg Arg Arg Arg Arg Arg Pro Asp Pro Arg Thr Met Pro
 35 40 45
 Ser Glu Lys Thr Phe Lys Gln Arg Arg Thr Phe Glu Gln Arg Val Glu
 50 55 60
 Asp Val Arg Leu Ile Arg Glu Gln His Pro Thr Lys Ile Pro Val Ile

1035

65 70 75 80
 Ile Glu Arg Tyr Lys Gly Glu Lys Gln Leu Pro Val Leu Asp Lys Thr
 85 90 95
 Lys Phe Leu Val Pro Asp His Val Asn Met Ser Glu Leu Ile Lys Ile
 100 105 110
 Ile Arg Arg Arg Leu Gln Leu Asn Ala Asn Gln Ala Phe Phe Leu Leu
 115 120 125
 Val Asn Gly His Ser Met Val Ser Val Ser Thr Pro Ile Ser Glu Val
 130 135 140
 Tyr Glu Ser Glu Lys Asp Glu Asp Gly Phe Leu Tyr Met Val Tyr Ala
 145 150 155 160
 Ser Gln Glu Thr Phe Gly Met Lys Leu Ser Val
 165 170

<210> 1052

<211> 189

<212> PRT

<213> Homo sapiens

<400> 1052

Gly Gly Pro Thr Cys Ser Ala Arg Cys Glu Pro Val Arg Pro Pro Pro
 1 5 10 15
 Ala Pro Glu Gln Pro Ala Ser Leu His Arg Leu Leu Ser Val Leu Ser
 20 25 30
 Pro Arg Ala Ala Ile Ala Val Met Leu Gly Ala Ala Leu Arg Arg Cys
 35 40 45
 Ala Val Ala Ala Thr Thr Arg Ala Asp Pro Arg Gly Leu Leu His Ser
 50 55 60
 Ala Arg Thr Pro Gly Pro Ala Val Ala Ile Gln Ser Val Arg Cys Tyr
 65 70 75 80
 Ser His Gly Ser Gln Glu Thr Asp Glu Glu Phe Asp Ala Arg Trp Val
 85 90 95
 Thr Tyr Phe Asn Lys Pro Asp Ile Asp Ala Trp Glu Leu Arg Lys Gly
 100 105 110
 Ile Asn Thr Leu Val Thr Tyr Asp Met Val Pro Glu Pro Lys Ile Ile
 115 120 125

1036

Asp Ala Ala Leu Arg Ala Cys Arg Arg Leu Asn Asp Phe Ala Ser Thr
 130 135 140

Val Arg Ile Leu Glu Val Val Lys Asp Lys Ala Gly Pro His Lys Glu
 145 150 155 160

Ile Tyr Pro Tyr Val Ile Gln Glu Leu Arg Pro Thr Leu Asn Glu Leu
 165 170 175

Gly Ile Ser Thr Pro Glu Glu Leu Gly Leu Asp Lys Val
 180 185

<210> 1053

<211> 315

<212> PRT

<213> Homo sapiens

<400> 1053

Arg His Ser Ala Ser Pro Arg Cys Arg Leu Pro Pro Thr Glu Pro Val
 1 5 10 15

Ser Gly Leu Arg Ala Ser Gly Glu Met Leu Leu Pro Leu Leu Leu Leu
 20 25 30

Leu Pro Met Cys Trp Ala Val Glu Val Lys Arg Pro Arg Gly Val Ser
 35 40 45

Leu Thr Asn His His Phe Tyr Asp Glu Ser Lys Pro Phe Thr Cys Leu
 50 55 60

Asp Gly Ser Ala Thr Ile Pro Phe Asp Gln Val Asn Asp Asp Tyr Cys
 65 70 75 80

Asp Cys Lys Asp Gly Ser Asp Glu Pro Gly Thr Ala Ala Cys Pro Asn
 85 90 95

Gly Ser Phe His Cys Thr Asn Thr Gly Tyr Lys Pro Leu Tyr Ile Pro
 100 105 110

Ser Asn Arg Val Asn Asp Gly Val Cys Asp Cys Cys Asp Gly Thr Asp
 115 120 125

Glu Tyr Asn Ser Gly Val Ile Cys Glu Asn Thr Cys Lys Glu Lys Gly
 130 135 140

Arg Lys Glu Arg Glu Ser Leu Gln Gln Met Ala Glu Val Thr Arg Glu
 145 150 155 160

1037

Gly Phe Arg Leu Lys Lys Ile Leu Ile Glu Asp Trp Lys Lys Ala Arg
 165 170 175
 Glu Glu Lys Gln Lys Lys Leu Ile Glu Leu Gln Ala Gly Lys Lys Ser
 180 185 190
 Leu Glu Asp Gln Val Glu Met Leu Arg Thr Val Lys Glu Glu Ala Glu
 195 200 205
 Lys Pro Glu Arg Glu Ala Lys Glu Gln His Gln Lys Leu Trp Glu Glu
 210 215 220
 Gln Leu Ala Ala Ala Lys Ala Gln Gln Glu Gln Glu Leu Ala Ala Asp
 225 230 235 240
 Ala Phe Lys Glu Leu Asp Asp Asp Met Asp Gly Thr Val Ser Val Thr
 245 250 255
 Glu Leu Gln Thr His Pro Glu Leu Asp Thr Asp Gly Asp Gly Ala Leu
 260 265 270
 Ser Glu Ala Glu Ala Gln Ala Leu Leu Ser Gly Asp Thr Gln Thr Asp
 275 280 285
 Ala Thr Ser Phe Tyr Asp Arg Val Trp Gly Pro Gly Gly Ala Gly Pro
 290 295 300
 His Ser Gln Ala Pro Thr Ala Phe Lys Asp Gly
 305 310 315

<210> 1054

<211> 138

<212> PRT

<213> Homo sapiens

<400> 1054

Val Trp Lys Val Ile Val Trp Ser His Ser Ser Leu Ile Thr Leu Leu
 1 5 10 15
 Gly Ile Leu Glu Glu Lys Gly Ser Lys Thr Tyr Thr His Thr Pro Thr
 20 25 30
 Gln Ser Asn Ser Val Phe Lys Gln Ile Pro Arg Ile Leu Gly Pro Gly
 35 40 45
 Leu Asn Lys Ala Gly Lys Phe Pro Ser Leu Leu Thr His Asn Glu Asn
 50 55 60
 Met Val Ala Lys Val Asp Glu Val Lys Ser Thr Ile Lys Phe Gln Met

1038

65 70 75 80
 Lys Lys Val Leu Cys Leu Ala Val Ala Val Gly His Val Lys Met Thr
 85 90 95
 Asp Asp Glu Leu Val Tyr Asn Ile His Leu Ala Val Asn Phe Leu Val
 100 105 110
 Ser Leu Leu Lys Lys Asn Trp Gln Asn Val Arg Ala Leu Tyr Ile Lys
 115 120 125
 Ser Thr Met Gly Lys Pro Gln Arg Leu Tyr
 130 135

<210> 1055
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 1055
 Gly Thr Arg Glu Glu Ala Gly Val Asp Leu Val Ser Pro Thr Pro Leu
 1 5 10 15
 Thr Pro Pro Asp Pro Gly Ala Ala Ser Ala Thr Ala Thr Ala Pro Ala
 20 25 30
 Pro Ala Ala Ala Arg Arg Gly Glu Ala Met Ala Lys Val Ser Val Leu
 35 40 45
 Asn Val Ala Val Leu Glu Asn Pro Ser Pro Phe His Ser Pro Phe Arg
 50 55 60
 Phe Glu Ile Ser Phe Glu Cys Ser Glu Ala Leu Ala Asp Asp Leu Glu
 65 70 75 80
 Trp Lys Ile Ile Tyr Val Gly Ser Ala Glu Ser Glu Glu Phe Asp Gln
 85 90 95
 Ile Leu Asp Ser Val Leu Val Gly Pro Val Pro Ala Gly Arg His Met
 100 105 110
 Phe Val Phe Gln Ala Asp Ala Pro Asn Pro Ser Leu Ile Pro Glu Thr
 115 120 125
 Asp Ala Val Gly Val Thr Val Val Leu Ile Thr Cys Thr Tyr His Gly
 130 135 140
 Gln Glu Phe Ile Arg Val Gly Tyr Tyr Val Asn Asn Glu Tyr Leu Asn
 145 150 155 160

1039

Pro Glu Leu Arg Glu Asn Pro Pro Met Lys Pro Asp Phe Ser Gln Leu
 165 170 175

Gln Arg Asn Ile Leu Ala Ser Asn Pro Arg Val Thr Arg Phe His Ile
 180 185 190

Asn Trp Asp Asn Asn Met Asp Arg Leu Glu Ala Ile Glu Thr Gln Asp
 195 200 205

Pro Ser Leu Gly Cys Gly Leu Pro Leu Asn Cys Thr Pro Ile Lys Gly
 210 215 220

Leu Gly Leu Pro Gly Cys Ile Pro Gly Leu Leu Pro Glu Asn Ser Met
 225 230 235 240

Asp Cys Ile

<210> 1056

<211> 211

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1056

His Glu Pro Arg Arg Leu Leu Xaa Asp Ala Glu Gly Pro Glu Glu Thr
 1 5 10 15

Val Arg Leu Trp Pro Ala Ala Arg Ala Ala Met Asp Ala Ala Glu Val
 20 25 30

Glu Phe Leu Ala Glu Lys Glu Leu Val Thr Ile Ile Pro Asn Phe Ser
 35 40 45

Leu Asp Lys Ile Tyr Leu Ile Gly Gly Asp Leu Gly Pro Phe Asn Pro
 50 55 60

Gly Leu Pro Val Glu Val Pro Leu Trp Leu Ala Ile Asn Leu Lys Gln
 65 70 75 80

Arg Gln Lys Cys Arg Leu Leu Pro Pro Glu Trp Met Asp Val Glu Lys
 85 90 95

Leu Glu Lys Met Arg Asp His Glu Arg Lys Glu Glu Thr Phe Thr Pro

1040

100	105	110
Met Pro Ser Pro Tyr Tyr Met Glu Leu Thr Lys Leu Leu Leu Asn His		
115	120	125
Ala Ser Asp Asn Ile Pro Lys Ala Asp Glu Ile Arg Thr Leu Val Lys		
130	135	140
Asp Met Trp Asp Thr Arg Ile Ala Lys Leu Arg Val Ser Ala Asp Ser		
145	150	155 160
Phe Val Arg Gln Gln Glu Ala His Ala Lys Leu Asp Asn Leu Thr Leu		
165	170	175
Met Glu Ile Asn Thr Ser Gly Thr Phe Leu Thr Gln Ala Leu Asn His		
180	185	190
Met Tyr Lys Leu Arg Thr Asn Leu Gln Pro Leu Glu Ser Thr Gln Ser		
195	200	205
Gln Asp Phe		
210		

<210> 1057

<211> 407

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (343)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1057

Val Ile Leu Gly Ala Gly Leu Arg Asp Lys Asp Met Trp Ile Pro Val
1 5 10 15

Val Gly Leu Pro Arg Arg Leu Arg Leu Ser Ala Leu Ala Gly Ala Gly
20 25 30

Arg Phe Cys Ile Leu Gly Ser Glu Ala Ala Thr Arg Lys His Leu Pro
35 40 45

Ala Arg Asn His Cys Gly Leu Ser Asp Ser Ser Pro Gln Leu Trp Pro
50 55 60

Glu Pro Asp Phe Arg Asn Pro Pro Arg Lys Ala Ser Lys Ala Ser Leu
65 70 75 80

1041

Asp Phe Lys Arg Tyr Val Thr Asp Arg Arg Leu Ala Glu Thr Leu Ala
85 90 95

Gln Ile Tyr Leu Gly Lys Pro Ser Arg Pro Pro His Leu Leu Leu Glu
100 105 110

Cys Asn Pro Gly Pro Gly Ile Leu Thr Gln Ala Leu Leu Glu Ala Gly
115 120 125

Ala Lys Val Val Ala Leu Glu Ser Asp Lys Thr Phe Ile Pro His Leu
130 135 140

Glu Ser Leu Gly Lys Asn Leu Asp Gly Lys Leu Arg Val Ile His Cys
145 150 155 160

Asp Phe Phe Lys Leu Asp Pro Arg Ser Gly Gly Val Ile Lys Pro Pro
165 170 175

Ala Met Ser Ser Arg Gly Leu Phe Lys Asn Leu Gly Ile Glu Ala Val
180 185 190

Pro Trp Thr Ala Asp Ile Pro Leu Lys Val Val Gly Met Phe Pro Ser
195 200 205

Arg Gly Glu Lys Arg Ala Leu Trp Lys Leu Ala Tyr Asp Leu Tyr Ser
210 215 220

Cys Thr Ser Ile Tyr Lys Phe Gly Arg Ile Glu Val Asn Met Phe Ile
225 230 235 240

Gly Glu Lys Glu Phe Gln Lys Leu Met Ala Asp Pro Gly Asn Pro Asp
245 250 255

Leu Tyr His Val Leu Ser Val Ile Trp Gln Leu Ala Cys Glu Ile Lys
260 265 270

Val Leu His Met Glu Pro Trp Ser Ser Phe Asp Ile Tyr Thr Arg Lys
275 280 285

Gly Pro Leu Glu Asn Pro Lys Arg Arg Glu Leu Leu Asp Gln Leu Gln
290 295 300

Gln Lys Leu Tyr Leu Ile Gln Met Ile Pro Arg Gln Asn Leu Phe Thr
305 310 315 320

Lys Asn Leu Thr Pro Met Asn Tyr Asn Ile Phe Phe His Leu Leu Lys
325 330 335

His Cys Phe Gly Arg Arg Xaa Ala Thr Val Ile Asp His Leu Arg Ser
340 345 350

1042

Leu Thr Pro Leu Asp Ala Arg Asp Ile Leu Met Gln Ile Gly Lys Gln
355 360 365

Glu Asp Glu Lys Val Val Asn Met His Pro Gln Asp Phe Lys Thr Leu
370 375 380

Phe Glu Thr Ile Glu Arg Ser Lys Asp Cys Ala Tyr Lys Trp Leu Tyr
385 390 395 400

Asp Glu Thr Leu Glu Asp Arg
405

<210> 1058
<211> 89
<212> PRT
<213> Homo sapiens

<400> 1058
Ser Ser Trp Val Gly Gly Ser Leu Arg Gln Ala Ala Thr Leu Glu Gly
1 5 10 15

Glu Gln Gly Ser Ala Val Ser Ala Ala Ser His Ala Arg Ser Asp Leu
20 25 30

Ser Leu Gly Thr Pro Gln Glu Pro Glu Asp Ser Ser Gly Gln Cys Arg
35 40 45

Trp Gly Val Gly Gly Glu Ser Gly Arg Glu Ala Leu Arg Ala Pro Ser
50 55 60

Pro Thr Thr Asn Leu Ala Leu Val Val Ile Phe Arg Gln Asn Phe Val
65 70 75 80

Val Phe Phe Pro Phe Tyr Asp Gly Phe
85

<210> 1059
<211> 457
<212> PRT
<213> Homo sapiens

<400> 1059
Gly Thr Arg Pro Ser Ser Cys Ser Gln Thr Glu Ala Gln Pro Pro Ser
1 5 10 15

Pro Val Ser Ile Thr Ser Ala Ala Ser Met Ser Asp Lys Leu Pro Tyr
20 25 30

1043

Lys Val Ala Asp Ile Gly Leu Ala Ala Trp Gly Arg Lys Ala Leu Asp
 35 40 45
 Ile Ala Glu Asn Glu Met Pro Gly Leu Met Arg Met Arg Glu Arg Tyr
 50 55 60
 Ser Ala Ser Lys Pro Leu Lys Gly Ala Arg Ile Ala Gly Cys Leu His
 65 70 75 80
 Met Thr Val Glu Thr Ala Val Leu Ile Glu Thr Leu Val Thr Leu Gly
 85 90 95
 Ala Glu Val Gln Trp Ser Ser Cys Asn Ile Phe Ser Thr Gln Asp His
 100 105 110
 Ala Ala Ala Ala Ile Ala Lys Ala Gly Ile Pro Val Tyr Ala Trp Lys
 115 120 125
 Gly Glu Thr Asp Glu Glu Tyr Leu Trp Cys Ile Glu Gln Thr Leu Tyr
 130 135 140
 Phe Lys Asp Gly Pro Leu Asn Met Ile Leu Asp Asp Gly Gly Asp Leu
 145 150 155 160
 Thr Asn Leu Ile His Thr Lys Tyr Pro Gln Leu Leu Pro Gly Ile Arg
 165 170 175
 Gly Ile Ser Glu Glu Thr Thr Thr Gly Val His Asn Leu Tyr Lys Met
 180 185 190
 Met Ala Asn Gly Ile Leu Lys Val Pro Ala Ile Asn Val Asn Asp Ser
 195 200 205
 Val Thr Lys Ser Lys Phe Asp Asn Leu Tyr Gly Cys Arg Glu Ser Leu
 210 215 220
 Ile Asp Gly Ile Lys Arg Ala Thr Asp Val Met Ile Ala Gly Lys Val
 225 230 235 240
 Ala Val Val Ala Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Gln Ala
 245 250 255
 Leu Arg Gly Phe Gly Ala Arg Val Ile Ile Thr Glu Ile Asp Pro Ile
 260 265 270
 Asn Ala Leu Gln Ala Ala Met Glu Gly Tyr Glu Val Thr Thr Met Asp
 275 280 285
 Glu Ala Cys Gln Glu Gly Asn Ile Phe Val Thr Thr Thr Gly Cys Ile
 290 295 300

1044

Asp Ile Ile Leu Gly Arg His Phe Glu Gln Met Lys Asp Asp Ala Ile
 305 310 315 320

Val Cys Asn Ile Gly His Phe Asp Val Glu Ile Asp Val Lys Trp Leu
 325 330 335

Asn Glu Asn Ala Val Glu Lys Val Asn Ile Lys Pro Gln Val Asp Arg
 340 345 350

Tyr Arg Leu Lys Asn Gly Arg Arg Ile Ile Leu Leu Ala Glu Gly Arg
 355 360 365

Leu Val Asn Leu Gly Cys Ala Met Gly His Pro Ser Phe Val Met Ser
 370 375 380

Asn Ser Phe Thr Asn Gln Val Met Ala Gln Ile Glu Leu Trp Thr His
 385 390 395 400

Pro Asp Lys Tyr Pro Val Gly Val His Phe Leu Pro Lys Lys Leu Asp
 405 410 415

Glu Ala Val Ala Glu Ala His Leu Gly Lys Leu Asn Val Lys Leu Thr
 420 425 430

Lys Leu Thr Glu Lys Gln Ala Gln Tyr Leu Gly Met Ser Cys Asp Gly
 435 440 445

Pro Phe Lys Pro Asp His Tyr Arg Tyr
 450 455

<210> 1060

<211> 511

<212> PRT

<213> Homo sapiens

<400> 1060

Glu Gly Val Met Ala Asp Gly Gln Val Ala Glu Leu Leu Leu Arg Arg
 1 5 10 15

Leu Glu Ala Ser Asp Gly Gly Leu Asp Ser Ala Glu Leu Ala Ala Glu
 20 25 30

Leu Gly Met Glu His Gln Ala Val Val Gly Ala Val Lys Ser Leu Gln
 35 40 45

Ala Leu Gly Glu Val Ile Glu Ala Glu Leu Arg Ser Thr Lys His Trp
 50 55 60

1045

Glu Leu Thr Ala Glu Gly Glu Glu Ile Ala Arg Glu Gly Ser His Glu
65 70 75 80

Ala Arg Val Phe Arg Ser Ile Pro Pro Glu Gly Leu Ala Gln Ser Glu
85 90 95

Leu Met Arg Leu Pro Ser Gly Lys Val Gly Phe Ser Lys Ala Met Ser
100 105 110

Asn Lys Trp Ile Arg Val Asp Lys Ser Ala Ala Asp Gly Pro Arg Val
115 120 125

Phe Arg Val Val Asp Ser Met Glu Asp Glu Val Gln Arg Arg Leu Gln
130 135 140

Leu Val Arg Gly Gly Gln Ala Glu Lys Leu Gly Glu Lys Glu Arg Ser
145 150 155 160

Glu Leu Arg Lys Arg Lys Leu Leu Ala Glu Val Thr Leu Lys Thr Tyr
165 170 175

Trp Val Ser Lys Gly Ser Ala Phe Ser Thr Ser Ile Ser Lys Gln Glu
180 185 190

Thr Glu Leu Ser Pro Glu Met Ile Ser Ser Gly Ser Trp Arg Asp Arg
195 200 205

Pro Phe Lys Pro Tyr Asn Phe Leu Ala His Gly Val Leu Pro Asp Ser
210 215 220

Gly His Leu His Pro Leu Leu Lys Val Arg Ser Gln Phe Arg Gln Ile
225 230 235 240

Phe Leu Glu Met Gly Phe Thr Glu Met Pro Thr Asp Asn Phe Ile Glu
245 250 255

Ser Ser Phe Trp Asn Phe Asp Ala Leu Phe Gln Pro Gln Gln His Pro
260 265 270

Ala Arg Asp Gln His Asp Thr Phe Phe Leu Arg Asp Pro Ala Glu Ala
275 280 285

Leu Gln Leu Pro Met Asp Tyr Val Gln Arg Val Lys Arg Thr His Ser
290 295 300

Gln Gly Gly Tyr Gly Ser Gln Gly Tyr Lys Tyr Asn Trp Lys Leu Asp
305 310 315 320

Glu Ala Arg Lys Asn Leu Leu Arg Thr His Thr Thr Ser Ala Ser Ala
325 330 335

1046

Arg Ala Leu Tyr Arg Leu Ala Gln Lys Lys Pro Phe Thr Pro Val Lys
340 345 350

Tyr Phe Ser Ile Asp Arg Val Phe Arg Asn Glu Thr Leu Asp Ala Thr
355 360 365

His Leu Ala Glu Phe His Gln Ile Glu Gly Val Val Ala Asp His Gly
370 375 380

Leu Thr Leu Gly His Leu Met Gly Val Leu Arg Glu Phe Phe Thr Lys
385 390 395 400

Leu Gly Ile Thr Gln Leu Arg Phe Lys Pro Ala Tyr Asn Pro Tyr Thr
405 410 415

Glu Pro Ser Met Glu Val Phe Ser Tyr His Gln Gly Leu Lys Lys Trp
420 425 430

Val Glu Val Gly Asn Ser Gly Val Phe Arg Pro Glu Met Leu Leu Pro
435 440 445

Met Gly Leu Pro Glu Asn Val Ser Val Ile Ala Trp Gly Leu Ser Leu
450 455 460

Glu Arg Pro Thr Met Ile Lys Tyr Gly Ile Asn Asn Ile Arg Glu Leu
465 470 475 480

Val Gly His Lys Val Asn Leu Gln Met Val Tyr Asp Ser Pro Leu Cys
485 490 495

Arg Leu Asp Ala Glu Pro Arg Pro Pro Pro Thr Gln Glu Ala Ala
500 505 510

<210> 1061

<211> 228

<212> PRT

<213> Homo sapiens

<400> 1061

Arg Ala Ala Ser Thr Pro Arg Ala Ala Pro Gly Ala Ala Leu Leu Ser
1 5 10 15

Pro Pro Gly Leu Arg Ala Ala Pro Ala Ala Leu Val Met Gly Glu Gly
20 25 30

Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala Ser Pro Glu Gln
35 40 45

Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly Leu Val Glu Asn

1047

50 55 60
 His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly Gly Ser Ala Gly
 65 70 75 80
 Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala Val Phe Arg Glu
 85 90 95
 Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly Gly Lys His His
 100 105 110
 Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro Pro Ala Arg Thr
 115 120 125
 Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg Ile Ser Thr Met
 130 135 140
 Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu Tyr Ser Leu His
 145 150 155 160
 Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu Lys Gln Cys Lys
 165 170 175
 Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys Val Asn Pro Asn
 180 185 190
 Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg Gly Asp Pro Glu
 195 200 205
 Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Arg Gly Val His Thr
 210 215 220
 Gln Arg Met Gln
 225

<210> 1062

<211> 324

<212> PRT

<213> Homo sapiens

<400> 1062

Pro Arg Val Met Ala Met Ala Thr Lys Gly Gly Thr Val Lys Ala Ala
 1 5 10 15

Ser Gly Phe Asn Ala Met Glu Asp Ala Gln Thr Leu Arg Lys Ala Met
 20 25 30

Lys Gly Leu Gly Thr Asp Glu Asp Ala Ile Ile Ser Val Leu Ala Tyr
 35 40 45

1048

Arg Asn Thr Ala Gln Arg Gln Glu Ile Arg Thr Ala Tyr Lys Ser Thr
 50 55 60

Ile Gly Arg Asp Leu Ile Asp Asp Leu Lys Ser Glu Leu Ser Gly Asn
 65 70 75 80

Phe Glu Gln Val Ile Val Gly Met Met Thr Pro Thr Val Leu Tyr Asp
 85 90 95

Val Gln Glu Leu Arg Arg Ala Met Lys Gly Ala Gly Thr Asp Glu Gly
 100 105 110

Cys Leu Ile Glu Ile Leu Ala Ser Arg Thr Pro Glu Glu Ile Arg Arg
 115 120 125

Ile Ser Gln Thr Tyr Gln Gln Gln Tyr Gly Arg Ser Leu Glu Asp Asp
 130 135 140

Ile Arg Ser Asp Thr Ser Phe Met Phe Gln Arg Val Leu Val Ser Leu
 145 150 155 160

Ser Ala Gly Gly Arg Asp Glu Gly Asn Tyr Leu Asp Asp Ala Leu Val
 165 170 175

Arg Gln Asp Ala Gln Asp Leu Tyr Glu Ala Gly Glu Lys Lys Trp Gly
 180 185 190

Thr Asp Glu Val Lys Phe Leu Thr Val Leu Cys Ser Arg Asn Arg Asn
 195 200 205

His Leu Leu His Val Phe Asp Glu Tyr Lys Arg Ile Ser Gln Lys Asp
 210 215 220

Ile Glu Gln Ser Ile Lys Ser Glu Thr Ser Gly Ser Phe Glu Asp Ala
 225 230 235 240

Leu Leu Ala Ile Val Lys Cys Met Arg Asn Lys Ser Ala Tyr Phe Ala
 245 250 255

Glu Lys Leu Tyr Lys Ser Met Lys Gly Leu Gly Thr Asp Asp Asn Thr
 260 265 270

Leu Ile Arg Val Met Val Ser Arg Ala Glu Ile Asp Met Leu Asp Ile
 275 280 285

Arg Ala His Phe Lys Arg Leu Tyr Gly Lys Ser Leu Tyr Ser Phe Ile
 290 295 300

Lys Gly Asp Thr Ser Gly Asp Tyr Arg Lys Val Leu Leu Val Leu Cys
 305 310 315 320

1049

Gly Gly Asp Asp

<210> 1063

<211> 355

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (37)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1063

Xaa Tyr Xaa Ile Pro Gly Ser Thr His Ala Ser Gly Lys Ile Leu Gly

1

5

10

15

Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys Lys

20

25

30

Glu Thr Glu Val Xaa Val Thr Ser Val Lys Asp Ala Lys Ile Ala Val

35

40

45

Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr Val

50

55

60

Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu Glu

65

70

75

80

Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala Asn

85

90

95

Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr Ala

100

105

110

Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp Leu

115

120

125

1050

Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu Thr
 130 135 140

Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu Ser
 145 150 155 160

Glu Val Gly Asp Thr Gln Val Val Val Phe Lys His Glu Lys Glu Asp
 165 170 175

Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu Met
 180 185 190

Asp Asp Ile Glu Arg Ala Val Asp Asp Gly Val Asn Thr Phe Lys Val
 195 200 205

Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu Ile
 210 215 220

Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly Leu
 225 230 235 240

Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile Pro
 245 250 255

Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile Ser
 260 265 270

Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu Asp
 275 280 285

Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly Ile
 290 295 300

Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr Asn
 305 310 315 320

Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys Pro
 325 330 335

Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp Asp
 340 345 350

Gln Asn Asp
 355

<210> 1064

<211> 113

<212> PRT

<213> Homo sapiens

1051

<400> 1064

Ser Pro Phe Thr Leu His Cys Cys His Ser Thr Leu Tyr Asp Gly Arg
1 5 10 15

Thr Gly Ser Ser Arg Glu Asn Cys Thr Val Thr Thr Val Phe Phe Thr
20 25 30

Leu Phe Gln Gly Ser Leu Ser Pro Asp Ile Glu Glu Ile Ser Phe Arg
35 40 45

Pro Glu Thr Gln Arg Pro His Ser Pro Val Ile Lys Pro Arg Phe His
50 55 60

Ser Gly Pro Arg Ser Gly Ala Trp Pro Leu Leu Phe Gly Ser His Trp
65 70 75 80

Glu Ala His Trp Pro Trp Ile Ile Ser Ser Cys Thr Pro Gly Val Leu
85 90 95

Pro Ala Cys Leu Leu Ser Trp Thr Ala Val Cys Lys Lys Val Thr Lys
100 105 110

Thr

<210> 1065

<211> 634

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (325)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1065

Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr Phe Lys Ser Gly
1 5 10 15

Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe Lys His Val Val
20 25 30

Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val Lys Gly Arg Arg
35 40 45

Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu Ser Phe Asn Asn
50 55 60

1052

Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile His Gln Trp Cys
65 70 75 80

Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala Thr Gln Val Ser
85 90 95

Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala Arg Val His Val
100 105 110

Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln Val Leu Gly Pro
115 120 125

Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala Lys Glu Asp Ala
130 135 140

Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser Asn Gly Ala Gly
145 150 155 160

Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro Phe Ala Gln Gly
165 170 175

Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His Gly Lys Asp Gly
180 185 190

Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr Glu Glu Arg Lys
195 200 205

Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys Met Asp Tyr Pro
210 215 220

Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly Glu Thr Pro Leu
225 230 235 240

Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp Gln Thr Asp Gly
245 250 255

Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn Val Glu Arg Val
260 265 270

Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala Met Ala Ala Gln
275 280 285

His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln Ile Trp Arg Ile
290 295 300

Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr Tyr Gly Gln Phe
305 310 315 320

Tyr Gly Gly Asp Xaa Tyr Ile Ile Leu Tyr Asn Tyr Arg His Gly Gly
325 330 335

1053

Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala Gln Ser Thr Gln
 340 345 350
 Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln Leu Asp Glu Glu
 355 360 365
 Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln Gly Lys Glu Pro
 370 375 380
 Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met Ile Ile Tyr Lys
 385 390 395 400
 Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro Ala Ser Thr Arg
 405 410 415
 Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr Arg Ala Val Glu
 420 425 430
 Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp Ala Phe Val Leu
 435 440 445
 Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr Gly Ala Ser Glu
 450 455 460
 Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val Leu Arg Ala Gln
 465 470 475 480
 Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly Phe Trp Glu Ala
 485 490 495
 Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg Leu Lys Asp Lys
 500 505 510
 Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys Ser Asn Lys Ile
 515 520 525
 Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu Met Gln Glu Asp
 530 535 540
 Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp Asp Gln Val Phe
 545 550 555 560
 Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys Thr Glu Ala Leu
 565 570 575
 Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala Asn Arg Asp Arg
 580 585 590
 Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu Pro Pro Ser Phe
 595 600 605

1054

Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp Ser Val Asp Pro
610 615 620

Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
625 630

<210> 1066

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1066

Arg Ala Arg Gly Arg Cys Arg Arg Ser Pro Asp Gly Val Gly Ile Glu
1 5 10 15

Ala Pro Arg Lys Lys Val Lys Tyr Gln Glu Ile Gln Val Glu Glu Pro
20 25 30

Tyr Tyr Asp Cys His Glu Cys Thr Glu Thr Phe Thr Ser Ser Thr Ala
35 40 45

Phe Ser Glu His Leu Lys Thr His Ala Ser Met Ile Ile Phe Glu Pro
50 55 60

Ala Asn Ala Phe Gly Glu Cys Ser Gly Tyr Ile Glu Arg Ala Ser Thr
65 70 75 80

Ser Thr Gly Gly Ala Asn Gln Ala Asp Glu Lys Tyr Phe Lys Cys Asp
85 90 95

Val Cys Gly Gln Leu Phe Asn Asp Arg Leu Ser Leu Ala Arg His Gln
100 105 110

Asn Thr His Thr Gly
115

<210> 1067

<211> 192

<212> PRT

<213> Homo sapiens

<400> 1067

Pro Glu Gln Arg Gly Ser Ser Met Ala His Gly Pro Gly Ala Leu Met
1 5 10 15

Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu
20 25 30

1055

Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Ser Thr Cys Pro Pro
 35 40 45

Ser Ser Thr Thr Thr Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser
 50 55 60

Tyr Pro Met Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn Pro
 65 70 75 80

Ala Ser Phe Gln Asn Val Lys Glu Glu Trp Val Pro Glu Leu Lys Glu
 85 90 95

Tyr Ala Pro Asn Val Pro Phe Leu Leu Ile Gly Thr Gln Ile Asp Leu
 100 105 110

Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Asn Asp Met Lys Glu Lys
 115 120 125

Pro Ile Cys Val Glu Gln Gly Gln Lys Leu Ala Lys Glu Ile Gly Ala
 130 135 140

Cys Cys Tyr Val Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys Thr
 145 150 155 160

Val Phe Asp Glu Ala Ile Ile Ala Ile Leu Thr Pro Lys Lys His Thr
 165 170 175

Val Lys Lys Arg Ile Gly Ser Arg Cys Ile Asn Cys Cys Leu Ile Thr
 180 185 190

<210> 1068

<211> 360

<212> PRT

<213> Homo sapiens

<400> 1068

Ser Arg Trp Ala Arg Arg Asp Pro Gln Glu Arg Arg Glu Arg Gly Thr
 1 5 10 15

Arg Val Gln Ser Ser Gly Thr Trp Ile Gly Ala Gly Ala Met Gly Gly
 20 25 30

Glu Gln Glu Glu Glu Arg Phe Asp Gly Met Leu Leu Ala Met Ala Gln
 35 40 45

1056

Gln His Glu Gly Gly Val Gln Glu Leu Val Asn Thr Phe Phe Ser Phe
50 55 60

Leu Arg Arg Lys Thr Asp Phe Phe Ile Gly Gly Glu Glu Gly Met Ala
65 70 75 80

Glu Lys Leu Ile Thr Gln Thr Phe Ser His His Asn Gln Leu Ala Gln
85 90 95

Lys Thr Arg Arg Glu Lys Arg Ala Arg Gln Glu Ala Glu Arg Arg Glu
100 105 110

Lys Ala Glu Arg Ala Ala Arg Leu Ala Lys Glu Ala Lys Ser Glu Thr
115 120 125

Ser Gly Pro Gln Ile Lys Glu Leu Thr Asp Glu Glu Ala Glu Arg Leu
130 135 140

Gln Leu Glu Ile Asp Gln Lys Lys Asp Ala Glu Asn His Glu Ala Gln
145 150 155 160

Leu Lys Asn Gly Ser Leu Asp Ser Pro Gly Lys Gln Asp Thr Glu Glu
165 170 175

Asp Glu Glu Glu Asp Glu Lys Asp Lys Gly Lys Leu Lys Pro Asn Leu
180 185 190

Gly Asn Gly Ala Asp Leu Pro Asn Tyr Arg Trp Thr Gln Thr Leu Ser
195 200 205

Glu Leu Asp Leu Ala Val Pro Phe Cys Val Asn Phe Arg Leu Lys Gly
210 215 220

Lys Asp Met Val Val Asp Ile Gln Arg Arg His Leu Arg Val Gly Leu
225 230 235 240

Lys Gly Gln Pro Ala Ile Ile Asp Gly Glu Leu Tyr Asn Glu Val Lys
245 250 255

Val Glu Glu Ser Ser Trp Leu Ile Glu Asp Gly Lys Val Val Thr Val
260 265 270

His Leu Glu Lys Ile Asn Lys Met Glu Trp Trp Ser Arg Leu Val Ser
275 280 285

Ser Asp Pro Glu Ile Asn Thr Lys Lys Ile Asn Pro Glu Asn Ser Lys
290 295 300

Leu Ser Asp Leu Asp Ser Glu Thr Arg Ser Met Val Glu Lys Met Met
305 310 315 320

1057

Tyr Asp Gln Arg Gln Lys Ser Met Gly Leu Pro Thr Ser Asp Glu Gln
 325 330 335

Lys Lys Gln Glu Ile Leu Lys Lys Phe Met Asp Gln His Pro Glu Met
 340 345 350

Asp Phe Ser Lys Ala Lys Phe Asn
 355 360

<210> 1069

<211> 174

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (52)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1069

Val Trp Leu Ser Trp Asp Gln Glu Lys Ile Pro Val Leu Asp Gln Glu
 1 5 10 15

Ala Ala Asp Gly Ser Ser Thr Leu Gly Gly Gly Ala Gly Thr Met Gly
 20 25 30

Leu Ser Ala Arg Tyr Gly Pro Gln Phe Thr Leu Gln His Val Pro Asp
 35 40 45

Tyr Arg Gln Xaa Val Tyr Ile Pro Gly Ser Asn Ala Thr Leu Thr Asn
 50 55 60

Ala Ala Gly Lys Arg Gly Trp Gln Gly Pro Ser Arg Trp Gln Trp Gln
 65 70 75 80

Gln Glu Glu Val Gly Gln Glu Gly Glu Val Thr Trp Arg Pro Gly
 85 90 95

Gln Glu Pro Gln Gly Gly Leu Ser Pro Thr Ser Pro Ala Ser Pro Tyr
 100 105 110

Leu His Pro Gly Leu Arg Val Ser Gly Leu Thr Pro Arg Ile Leu Val
 115 120 125

Gly Ala Lys Ala Met Leu Pro Leu Gly Asn Arg Asn Lys Cys Pro Val
 130 135 140

Ser Thr Tyr Pro Phe Pro Pro Arg Gly Leu Asn Met Gln Lys Gln Phe
 145 150 155 160

1058

Arg Trp Glu Pro Pro Ser Asn Gln Leu Leu Tyr Pro Trp Gly
 165 170

<210> 1070

<211> 445

<212> PRT

<213> Homo sapiens

<400> 1070

Pro Arg Gly Leu Thr Gly Leu Trp Arg Ser Ser Leu Pro Ile Arg Lys
 1 5 10 15

Leu Gln Leu Pro Pro Asp Ala Leu Lys Met Ala Thr Ser Leu Gly Ser
 20 25 30

Asn Thr Tyr Asn Arg Gln Asn Trp Glu Asp Ala Asp Phe Pro Ile Leu
 35 40 45

Cys Gln Thr Cys Leu Gly Glu Asn Pro Tyr Ile Arg Met Thr Lys Glu
 50 55 60

Lys Tyr Gly Lys Glu Cys Lys Ile Cys Ala Arg Pro Phe Thr Val Phe
 65 70 75 80

Arg Trp Cys Pro Gly Val Arg Met Arg Phe Lys Lys Thr Glu Val Cys
 85 90 95

Gln Thr Cys Ser Lys Leu Lys Asn Val Cys Gln Thr Cys Leu Leu Asp
 100 105 110

Leu Glu Tyr Gly Leu Pro Ile Gln Val Arg Asp Ala Gly Leu Ser Phe
 115 120 125

Lys Asp Asp Met Pro Lys Ser Asp Val Asn Lys Glu Tyr Tyr Thr Gln
 130 135 140

Asn Met Glu Arg Glu Ile Ser Asn Ser Asp Gly Thr Arg Pro Val Gly
 145 150 155 160

Met Leu Gly Lys Ala Thr Ser Thr Ser Asp Met Leu Leu Lys Leu Ala
 165 170 175

Arg Thr Thr Pro Tyr Tyr Lys Arg Asn Arg Pro His Ile Cys Ser Phe
 180 185 190

Trp Val Lys Gly Glu Cys Lys Arg Gly Glu Glu Cys Pro Tyr Arg His
 195 200 205

1059

Glu Lys Pro Thr Asp Pro Asp Asp Pro Leu Ala Asp Gln Asn Ile Lys
 210 215 220
 Asp Arg Tyr Tyr Gly Ile Asn Asp Pro Val Ala Asp Lys Leu Leu Lys
 225 230 235 240
 Arg Ala Ser Thr Met Pro Arg Leu Asp Pro Pro Glu Asp Lys Thr Ile
 245 250 255
 Thr Thr Leu Tyr Val Gly Gly Leu Gly Asp Thr Ile Thr Glu Thr Asp
 260 265 270
 Leu Arg Asn His Phe Tyr Gln Phe Gly Glu Ile Arg Thr Ile Thr Val
 275 280 285
 Val Gln Arg Gln Gln Cys Ala Phe Ile Gln Phe Ala Thr Arg Gln Ala
 290 295 300
 Ala Glu Val Ala Ala Glu Lys Ser Phe Asn Lys Leu Ile Val Asn Gly
 305 310 315 320
 Arg Arg Leu Asn Val Lys Trp Gly Arg Ser Gln Ala Ala Arg Gly Lys
 325 330 335
 Glu Lys Glu Lys Asp Gly Thr Thr Asp Ser Gly Ile Lys Leu Glu Pro
 340 345 350
 Val Pro Gly Leu Pro Gly Ala Leu Pro Pro Pro Pro Ala Ala Glu Glu
 355 360 365
 Glu Ala Ser Ala Asn Tyr Phe Asn Leu Pro Pro Ser Gly Pro Pro Ala
 370 375 380
 Val Val Asn Ile Ala Leu Pro Pro Pro Pro Gly Ile Ala Pro Pro Pro
 385 390 395 400
 Pro Pro Gly Phe Gly Pro His Met Phe His Pro Met Gly Pro Pro Pro
 405 410 415
 Pro Phe Met Arg Ala Pro Gly Pro Ile His Tyr Pro Ser Gln Asp Pro
 420 425 430
 Gln Arg Met Gly Ala His Ala Gly Lys His Ser Ser Pro
 435 440 445

<210> 1071

<211> 346

<212> PRT

<213> Homo sapiens

1060

<220>

<221> SITE

<222> (286)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (287)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (291)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (294)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1071

Trp	Ser	Arg	Leu	Cys	Leu	Leu	Lys	Gln	Tyr	Leu	Phe	Thr	Met	Lys	Leu
1				5					10					15	

Gln	Ser	Pro	Glu	Phe	Gln	Ser	Leu	Phe	Thr	Glu	Gly	Leu	Lys	Ser	Leu
			20					25					30		

Thr	Glu	Leu	Phe	Val	Lys	Glu	Asn	His	Glu	Leu	Arg	Ile	Ala	Gly	Gly
	35						40					45			

Ala	Val	Arg	Asp	Leu	Leu	Asn	Gly	Val	Lys	Pro	Gln	Asp	Ile	Asp	Phe
	50					55					60				

Ala	Thr	Thr	Ala	Thr	Pro	Thr	Gln	Met	Lys	Glu	Met	Phe	Gln	Ser	Ala
65					70					75				80	

Gly	Ile	Arg	Met	Ile	Asn	Asn	Arg	Gly	Glu	Lys	His	Gly	Thr	Ile	Thr
			85						90					95	

Ala	Arg	Leu	His	Glu	Glu	Asn	Phe	Glu	Ile	Thr	Thr	Leu	Arg	Ile	Asp
		100						105					110		

Val	Thr	Thr	Asp	Gly	Arg	His	Ala	Glu	Val	Glu	Phe	Thr	Thr	Asp	Trp
		115					120					125			

Gln	Lys	Asp	Ala	Glu	Arg	Arg	Asp	Leu	Thr	Ile	Asn	Ser	Met	Phe	Leu
	130						135					140			

Gly	Phe	Asp	Gly	Thr	Leu	Phe	Asp	Tyr	Phe	Asn	Gly	Tyr	Glu	Asp	Leu
145					150					155				160	

1061

Lys Asn Lys Lys Val Arg Phe Val Gly His Ala Lys Gln Arg Ile Gln
165 170 175

Glu Asp Tyr Leu Arg Ile Leu Arg Tyr Phe Arg Phe Tyr Gly Arg Ile
180 185 190

Val Asp Lys Pro Gly Asp His Asp Pro Glu Thr Leu Glu Ala Ile Ala
195 200 205

Glu Asn Ala Lys Gly Leu Ala Gly Ile Ser Gly Glu Arg Ile Trp Val
210 215 220

Glu Leu Lys Lys Ile Leu Val Gly Asn His Val Asn His Leu Ile His
225 230 235 240

Leu Ile Tyr Asp Leu Asp Val Ala Pro Tyr Ile Gly Leu Pro Ala Asn
245 250 255

Ala Ser Leu Glu Glu Phe Asp Lys Val Ser Lys Asn Val Asp Gly Phe
260 265 270

Ser Pro Lys Pro Val Thr Leu Leu Ala Ser Leu Phe Lys Xaa Xaa Asp
275 280 285

Asp Val Xaa Lys Leu Xaa Leu Arg Leu Lys Ile Ala Lys Glu Glu Lys
290 295 300

Asn Leu Gly Leu Phe Ile Val Lys Asn Arg Lys Asp Leu Ile Lys Ala
305 310 315 320

Thr Asp Ser Ser Asp Pro Leu Lys Pro Tyr Gln Asp Phe Ile Ile Asp
325 330 335

Ser Arg Glu Pro Asp Ala His Ser Cys Met
340 345

<210> 1072

<211> 404

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (77)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1062

<222> (81)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1072

Glu Asp Ser Leu Asn Leu Asp Leu Thr Pro Arg Met Leu Arg Arg Leu
 1 5 10 15

Leu Glu Arg Pro Cys Thr Leu Ala Leu Leu Val Gly Ser Gln Leu Ala
 20 25 30

Val Met Met Tyr Leu Ser Leu Gly Gly Phe Arg Ser Leu Ser Ala Leu
 35 40 45

Phe Gly Arg Asp Gln Gly Pro Thr Phe Asp Tyr Ser His Pro Arg Asp
 50 55 60

Val Tyr Ser Asn Leu Ser His Leu Pro Gly Ala Pro Xaa Gly Pro Pro
 65 70 75 80

Xaa Pro Gln Gly Leu Pro Tyr Cys Pro Glu Arg Ser Pro Leu Leu Val
 85 90 95

Gly Pro Val Ser Val Ser Phe Ser Pro Val Pro Ser Leu Ala Glu Ile
 100 105 110

Val Glu Arg Asn Pro Arg Val Glu Pro Gly Gly Arg Tyr Arg Pro Ala
 115 120 125

Gly Cys Glu Pro Arg Ser Arg Thr Ala Ile Ile Val Pro His Arg Ala
 130 135 140

Arg Glu His His Leu Arg Leu Leu Leu Tyr His Leu His Pro Phe Leu
 145 150 155 160

Gln Arg Gln Gln Leu Ala Tyr Gly Ile Tyr Val Ile His Gln Ala Gly
 165 170 175

Asn Gly Thr Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Val Arg Glu
 180 185 190

Ala Leu Arg Asp Glu Glu Trp Asp Cys Leu Phe Leu His Asp Val Asp
 195 200 205

Leu Leu Pro Glu Asn Asp His Asn Leu Tyr Val Cys Asp Pro Arg Gly
 210 215 220

Pro Arg His Val Ala Val Ala Met Asn Lys Phe Gly Tyr Ser Leu Pro
 225 230 235 240

Tyr Pro Gln Tyr Phe Gly Gly Val Ser Ala Leu Thr Pro Asp Gln Tyr
 245 250 255

1063

Leu Lys Met Asn Gly Phe Pro Asn Glu Tyr Trp Gly Trp Gly Gly Glu
 260 265 270
 Asp Asp Asp Ile Ala Thr Arg Val Arg Leu Ala Gly Met Lys Ile Ser
 275 280 285
 Arg Pro Pro Thr Ser Val Gly His Tyr Lys Met Val Lys His Arg Gly
 290 295 300
 Asp Lys Gly Asn Glu Glu Asn Pro His Arg Phe Asp Leu Leu Val Arg
 305 310 315 320
 Thr Gln Asn Ser Trp Thr Gln Asp Gly Met Asn Ser Leu Thr Tyr Gln
 325 330 335
 Leu Leu Ala Arg Glu Leu Gly Pro Leu Tyr Thr Asn Ile Thr Ala Asp
 340 345 350
 Ile Gly Thr Asp Pro Arg Gly Pro Arg Ala Pro Ser Gly Pro Arg Tyr
 355 360 365
 Pro Pro Gly Ser Ser Gln Ala Phe Arg Gln Glu Met Leu Gln Arg Arg
 370 375 380
 Pro Pro Ala Arg Pro Gly Pro Leu Ser Thr Ala Asn His Thr Ala Leu
 385 390 395 400
 Arg Gly Ser His

<210> 1073

<211> 217

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (68)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1073

Asn Lys Glu Gln Leu Met Asp Lys Ser Gly Ile Asp Ser Leu Asp His
 1 5 10 15

Val Thr Ser Asp Ala Val Glu Leu Ala Asn Arg Ser Asp Asn Ser Ser
 20 25 30

Asp Ser Ser Leu Phe Lys Thr Gln Cys Ile Pro Tyr Ser Pro Lys Gly

1064

35	40	45
Glu Lys Arg Asn Pro Ile Arg Lys Phe Val Arg Thr Pro Glu Ser Val		
50	55	60
His Ala Ser Xaa Ser Ser Ser Asp Ser Ser Phe Glu Pro Ile Pro Leu		
65	70	75 80
Thr Ile Lys Ala Ile Phe Glu Arg Phe Lys Asn Arg Lys Lys Arg Tyr		
	85	90 95
Lys Lys Lys Lys Lys Arg Arg Tyr Gln Pro Thr Gly Arg Pro Arg Gly		
	100	105 110
Arg Pro Glu Gly Arg Arg Asn Pro Ile Tyr Ser Leu Ile Asp Lys Lys		
	115	120 125
Lys Gln Phe Arg Ser Arg Gly Ser Gly Phe Pro Phe Leu Glu Ser Glu		
	130	135 140
Asn Glu Lys Asn Ala Pro Trp Arg Lys Ile Leu Thr Phe Glu Gln Ala		
145	150	155 160
Val Ala Arg Gly Phe Phe Asn Tyr Ile Glu Lys Leu Lys Tyr Glu His		
	165	170 175
His Leu Lys Glu Ser Leu Lys Gln Met Asn Val Gly Glu Asp Leu Glu		
	180	185 190
Asn Glu Asp Phe Asp Ser Arg Arg Tyr Lys Phe Leu Asp Asp Asp Gly		
	195	200 205
Ser Ile Ser Pro Ile Glu Glu Ser Thr		
210	215	

<210> 1074

<211> 161

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (110)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (122)

<223> Xaa equals any of the naturally occurring L-amino acids

1065

<220>

<221> SITE

<222> (123)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (125)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (128)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (147)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1074

Thr	His	Tyr	Arg	Ala	Lys	Leu	Val	Arg	Leu	Pro	Gly	Thr	Gly	Ser	Gly
1				5					10					15	

Asn	Ser	Arg	Val	Asp	Pro	Arg	Val	Arg	Glu	Gln	Pro	Ser	Pro	Ala	Ser
		20						25					30		

Ser	Ala	Pro	Gly	Gln	Leu	Asn	Ser	Cys	Gln	Asp	Val	Leu	Pro	Ala	Glu
	35					40						45			

Pro	Ala	Ala	Val	Pro	Thr	Pro	Thr	Gln	Val	Ser	Leu	Thr	Gln	Val	Ser
	50					55					60				

Pro	Lys	Glu	Pro	Ser	Thr	Val	Ser	Ala	Ser	Ser	Phe	Leu	Trp	Leu	Cys
65					70					75				80	

Pro	Lys	Leu	Trp	Gly	Leu	Trp	Pro	Ser	Ser	Glu	Gly	Gly	Cys	Phe	Leu
		85						90					95		

Asn	His	His	Arg	Arg	His	His	Arg	Cys	Arg	Arg	Gln	Arg	Xaa	Asn	Ser
		100						105					110		

Cys	Asp	Arg	Ala	Val	Val	Ser	Lys	Ala	Xaa	Xaa	Leu	Xaa	Ala	Ala	Xaa
	115						120					125			

Phe	Trp	Gly	Leu	Leu	Leu	Ile	Gln	Ile	Leu	Met	Leu	Arg	Gln	Ala	Ile
	130					135					140				

Phe	Gly	Xaa	Asn	Lys	Asn	Ser	Gln	Glu	Ala	Lys	Asn	Ser	Pro	Ile	Trp
145				150						155				160	

1066

Lys

<210> 1075

<211> 221

<212> PRT

<213> Homo sapiens

<400> 1075

Ser Ser Ser Trp His Ala Arg Tyr Thr Val Leu Thr Tyr Leu Gln Thr
 1 5 10 15

Met Val Phe Tyr Asn Leu Phe Ile Phe Leu Asn Asn Glu Asp Ala Val
 20 25 30

Lys Asp Ile Arg Trp Leu Val Ile Ser Leu Leu Glu Asp Glu Gln Leu
 35 40 45

Glu Val Arg Glu Met Ala Ala Thr Thr Leu Ser Gly Leu Leu Gln Cys
 50 55 60

Asn Phe Leu Thr Met Asp Ser Pro Met Gln Ile His Phe Glu Gln Leu
 65 70 75 80

Cys Lys Thr Lys Leu Pro Lys Lys Arg Lys Arg Asp Pro Gly Ser Val
 85 90 95

Gly Asp Thr Ile Pro Ser Ala Glu Leu Val Lys Arg His Ala Gly Val
 100 105 110

Leu Gly Leu Gly Ala Cys Val Leu Ser Ser Pro Tyr Asp Val Pro Thr
 115 120 125

Trp Met Pro Gln Leu Leu Met Asn Leu Ser Ala His Leu Asn Asp Pro
 130 135 140

Gln Pro Ile Glu Met Thr Val Lys Lys Thr Leu Ser Asn Phe Arg Arg
 145 150 155 160

Leu Thr Met Thr Thr Gly Arg Asn Ile Asn Ser Asn Ser Leu Met Thr
 165 170 175

Asn Cys Leu Phe Ser Pro Ile Phe Leu Cys His His Ala Ile Met His
 180 185 190

Arg Lys Met Thr Ser Pro His Phe Arg Leu Phe Ser Ser Lys Ile Pro
 195 200 205

1067

His Pro Gln Val Pro Ser Val Val Ala Leu Cys Lys Phe
 210 215 220

<210> 1076

<211> 166

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (56)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (135)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (163)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (166)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1076

Ala Arg Gly Ala Arg Val Arg Ala Cys Ala Ser Leu Gly Ser Trp Arg
 1 5 10 15

Gly Pro Arg Gly Glu Gly Trp Lys Met Ser Met Asp Val Thr Phe Leu
 20 25 30

Gly Thr Gly Ala Ala Tyr Pro Ser Pro Thr Arg Gly Ala Ser Ala Val
 35 40 45

Val Leu Arg Cys Glu Gly Glu Xaa Trp Leu Phe Asp Cys Gly Glu Gly
 50 55 60

Thr Gln Thr Gln Leu Met Lys Ser Gln Leu Lys Ala Gly Arg Ile Thr
 65 70 75 80

Lys Ile Phe Ile Thr His Leu His Gly Asp His Phe Phe Gly Leu Pro
 85 90 95

Gly Leu Leu Cys Thr Ile Ser Leu Gln Ser Gly Ser Met Val Ser Lys
 100 105 110

1068

Gln Pro Ile Glu Ile Tyr Gly Pro Val Gly Phe Gly Thr Leu Ser Gly
 115 120 125

Glu Pro Trp Asn Ser Leu Xaa Arg Glu Leu Val Phe His Tyr Val Val
 130 135 140

His Glu Leu Val Pro Thr Ala Asp Gln Cys Pro Ala Glu Gly Thr Lys
 145 150 155 160

Arg Ile Xaa Ala Cys Xaa
 165

<210> 1077

<211> 239

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (25)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1077

Gly Leu Arg Ala Leu Ser Gln His Thr Asp Leu Ser Pro Leu Ser Pro
 1 5 10 15

Lys Thr Pro Ala Pro Ser Met Arg Xaa Lys Met Gly Asn Gly Thr Glu
 20 25 30

Glu Asp Tyr Asn Phe Val Phe Lys Val Val Leu Ile Gly Glu Ser Gly
 35 40 45

Val Gly Lys Thr Asn Leu Leu Ser Arg Phe Thr Arg Asn Glu Phe Ser
 50 55 60

His Asp Ser Arg Thr Thr Ile Gly Val Glu Phe Ser Thr Arg Thr Val
 65 70 75 80

Met Leu Gly Thr Ala Ala Val Lys Ala Gln Ile Trp Asp Thr Ala Gly
 85 90 95

Leu Glu Arg Tyr Arg Ala Ile Thr Ser Ala Tyr Tyr Arg Gly Ala Val
 100 105 110

Gly Ala Leu Leu Val Phe Asp Leu Thr Lys His Gln Thr Tyr Ala Val
 115 120 125

Val Glu Arg Trp Leu Lys Glu Leu Tyr Asp His Ala Glu Ala Thr Ile

1069

130	135	140
Val Val Met Leu Val Gly Asn Lys Ser Asp Leu Ser Gln Ala Arg Glu		
145	150	155 160
Val Pro Thr Glu Glu Ala Arg Met Phe Ala Glu Asn Asn Gly Leu Leu		
165	170	175
Phe Leu Glu Thr Ser Ala Leu Asp Ser Thr Asn Val Glu Leu Ala Phe		
180	185	190
Glu Thr Val Leu Lys Glu Ile Phe Ala Lys Val Ser Lys Gln Arg Gln		
195	200	205
Asn Ser Ile Arg Thr Asn Ala Ile Thr Ser Gly Ser Ala Gln Ala Gly		
210	215	220
Gln Glu Pro Gly Pro Gly Glu Lys Arg Ala Cys Cys Ile Ser Leu		
225	230	235

<210> 1078

<211> 171

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (123)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1078

Ile Leu Lys Gly Ser Ser Gly Ser Val Trp Leu Arg Asn Leu Gln Leu
1 5 10 15

Gly Leu Phe Gly Thr Ala Leu Gly Leu Val Gly Leu Trp Trp Ala Glu
20 25 30

Gly Thr Ala Val Ala Thr Arg Gly Phe Phe Phe Gly Tyr Thr Pro Ala
35 40 45

Val Trp Gly Val Val Leu Asn Gln Ala Phe Gly Gly Leu Leu Val Ala
50 55 60

Val Val Val Lys Tyr Ala Asp Asn Ile Leu Lys Gly Phe Ala Thr Ser
65 70 75 80

Leu Ser Ile Val Leu Ser Thr Val Ala Ser Ile Arg Leu Phe Gly Phe
85 90 95

1070

His Val Asp Pro Leu Phe Ala Leu Gly Ala Gly Leu Val Ile Gly Ala
 100 105 110

Val Tyr Leu Tyr Ser Leu Pro Arg Gly Ala Xaa Lys Ala Ile Ala Ser
 115 120 125

Ala Ser Ala Ser Ala Ser Gly Pro Cys Val His Gln Gln Pro Pro Gly
 130 135 140

Gln Pro Pro Pro Pro Gln Leu Ser Ser His Arg Gly Asp Leu Ile Thr
 145 150 155 160

Glu Pro Phe Leu Pro Lys Ser Val Leu Val Lys
 165 170

<210> 1079

<211> 141

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1079

Arg Arg Val Cys His Ser Ser Pro His Leu Ser Ser Pro Arg Ala Ala
 1 5 10 15

Cys Glu Gln Gln Ala Val Ala Leu Thr Leu Gln Glu Asp Arg Ala Ser
 20 25 30

Leu Thr Leu Ser Gly Gly Pro Ser Ala Leu Ala Phe Asp Leu Ser Lys
 35 40 45

Val Pro Gly Pro Glu Ala Ala Pro Arg Leu Xaa Ala Leu Thr Leu Gly
 50 55 60

Leu Ala Lys Arg Val Trp Ser Leu Glu Arg Arg Leu Ala Ala Ala Glu
 65 70 75 80

Glu Thr Ala Val Ser Pro Arg Lys Ser Pro Arg Pro Ala Gly Pro Gln
 85 90 95

Leu Phe Leu Pro Asp Pro Asp Pro Gln Arg Gly Gly Pro Gly Pro Gly
 100 105 110

Val Arg Arg Arg Cys Pro Gly Glu Ser Leu Ile Asn Pro Gly Phe Lys
 115 120 125

1071

Ser Lys Lys Pro Ala Gly Gly Val Asp Phe Asp Glu Thr
 130 135 140

<210> 1080

<211> 359

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1080

Ala Val Glu Ser Arg Xaa Pro Gly Trp Asn His His Gly Ile Gln Phe
 1 5 10 15

Pro Cys Gly Ser Val Trp Leu Glu His Ala Ile Ala Met Ile Cys Gly
 20 25 30

Asn Val Cys Leu Trp Lys Gly Ala Pro Thr Thr Ser Leu Ile Ser Val
 35 40 45

Ala Val Thr Lys Ile Ile Ala Lys Val Leu Glu Asp Asn Lys Leu Pro
 50 55 60

Gly Ala Ile Cys Ser Leu Thr Cys Gly Gly Ala Asp Ile Gly Thr Ala
 65 70 75 80

Met Ala Lys Asp Glu Arg Val Asn Leu Leu Ser Phe Thr Gly Ser Thr
 85 90 95

Gln Val Gly Lys Gln Val Gly Leu Met Val Gln Glu Arg Phe Gly Arg
 100 105 110

Ser Leu Leu Glu Leu Gly Gly Asn Asn Ala Ile Ile Ala Phe Glu Asp
 115 120 125

Ala Asp Leu Ser Leu Val Val Pro Ser Ala Leu Phe Ala Ala Val Gly
 130 135 140

Thr Ala Gly Gln Arg Cys Thr Thr Ala Arg Arg Leu Phe Ile His Glu
 145 150 155 160

Ser Ile His Asp Glu Val Val Asn Arg Leu Lys Lys Ala Tyr Ala Gln
 165 170 175

Ile Arg Val Gly Asn Pro Trp Asp Pro Asn Val Leu Tyr Gly Pro Leu

1072

180	185	190
His Thr Lys Gln Ala Val Ser Met Phe Leu Gly Ala Val Glu Glu Ala		
195	200	205
Lys Lys Glu Gly Gly Thr Val Val Tyr Gly Gly Lys Val Met Asp Arg		
210	215	220
Pro Gly Asn Tyr Val Glu Pro Thr Ile Val Thr Gly Leu Gly His Asp		
225	230	235
Ala Ser Ile Ala His Thr Glu Thr Phe Ala Pro Ile Leu Tyr Val Phe		
245	250	255
Lys Phe Lys Asn Glu Glu Glu Val Phe Ala Trp Asn Asn Glu Val Lys		
260	265	270
Gln Gly Leu Ser Ser Ser Ile Phe Thr Lys Asp Leu Gly Arg Ile Phe		
275	280	285
Arg Trp Leu Gly Pro Lys Gly Ser Asp Cys Gly Ile Val Asn Val Asn		
290	295	300
Ile Pro Thr Ser Gly Ala Glu Ile Gly Gly Ala Phe Gly Gly Glu Lys		
305	310	315
His Thr Gly Gly Gly Arg Glu Ser Gly Ser Asp Ala Trp Lys Gln Tyr		
325	330	335
Met Arg Arg Ser Thr Cys Thr Ile Asn Tyr Ser Lys Asp Leu Pro Leu		
340	345	350
Ala Gln Gly Ile Lys Phe Gln		
355		

<210> 1081

<211> 138

<212> PRT

<213> Homo sapiens

<400> 1081

Ala Val Pro Leu Leu Gly Arg Pro Thr Arg Pro Val Gly Pro Arg Ala
1 5 10 15

Ala Leu Thr Met Thr Gln Gln Gly Ala Ala Leu Gln Asn Tyr Asn Asn
20 25 30

Glu Leu Val Lys Cys Ile Glu Glu Leu Cys Gln Lys Arg Glu Glu Leu
35 40 45

1073

Cys Arg Gln Ile Gln Glu Glu Glu Asp Glu Lys Gln Arg Leu Gln Asn
 50 55 60

Glu Val Arg Gln Leu Thr Glu Lys Leu Ala Arg Val Asn Glu Asn Leu
 65 70 75 80

Ala Arg Lys Ile Ala Ser Arg Asn Glu Phe Asp Arg Thr Ile Ala Glu
 85 90 95

Thr Glu Ala Ala Tyr Leu Lys Ile Leu Glu Ser Ser Gln Thr Leu Leu
 100 105 110

Ser Val Leu Lys Arg Glu Ala Gly Asn Leu Thr Lys Ala Thr Ala Pro
 115 120 125

Asp Gln Lys Ser Ser Gly Gly Arg Asp Ser
 130 135

<210> 1082

<211> 339

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1082

Ser Pro Ile Ser Asn Cys Glu Ile Thr Ile Thr Asp Pro Gly Lys Phe
 1 5 10 15

Tyr Asn Ser Asn Ser Val Phe Ser Arg Gly Asn Met Ala Lys Val Phe
 20 25 30

Ser Phe Ile Leu Val Thr Thr Ala Leu Xaa Met Gly Arg Glu Ile Ser
 35 40 45

Ala Leu Glu Asp Cys Ala Gln Glu Gln Met Arg Leu Arg Ala Gln Val
 50 55 60

Arg Leu Leu Glu Thr Arg Val Lys Gln Gln Gln Val Lys Ile Lys Gln
 65 70 75 80

Leu Leu Gln Glu Asn Glu Val Gln Phe Leu Asp Lys Gly Asp Glu Asn
 85 90 95

Thr Val Val Asp Leu Gly Ser Lys Arg Gln Tyr Ala Asp Cys Ser Glu

1074

100	105	110
Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly Phe Tyr Lys Ile Lys Pro 115 120 125		
Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr Cys Asp Met Ser Asp Gly 130 135 140		
Gly Gly Trp Thr Val Ile Gln Arg Arg Ser Asp Gly Ser Glu Asn Phe 145 150 155 160		
Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly Phe Gly Asn Phe Val Gln 165 170 175		
Lys His Gly Glu Tyr Trp Leu Gly Asn Lys Asn Leu His Phe Leu Thr 180 185 190		
Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp Leu Ala Asp Phe Glu Lys 195 200 205		
Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe Lys Val Gly Asp Glu Lys 210 215 220		
Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr Ser Gly Thr Ala Gly Asp 225 230 235 240		
Ser Leu Ala Gly Asn Phe His Pro Glu Val Gln Trp Trp Ala Ser His 245 250 255		
Gln Arg Met Lys Phe Ser Thr Trp Asp Arg Asp His Asp Asn Tyr Glu 260 265 270		
Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly Trp Trp Phe Asn Arg Cys 275 280 285		
His Ser Ala Asn Leu Asn Gly Val Tyr Tyr Ser Gly Pro Tyr Thr Ala 290 295 300		
Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr Trp His Gly Trp Trp Tyr 305 310 315 320		
Ser Leu Lys Ser Val Val Met Lys Ile Arg Pro Asn Asp Phe Ile Pro 325 330 335		
Asn Val Ile		

<210> 1083

<211> 256

1075

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (56)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1083

Lys Ser Leu Asn Gly Pro Ala Asp Phe Glu Lys Arg Val Glu Gly Gly
 1 5 10 15

Gly Arg Pro Arg Ala Pro Leu Val Asn Ala Leu Leu Thr Ala Pro Glu
 20 25 30

Phe Leu Ile Tyr Thr Gly Cys Met Val Cys Val Phe Leu Phe Cys Phe
 35 40 45

Ser Pro Pro Ala Gly Leu Phe Xaa Gly Trp Gly Gly Gly Phe Ala Met
 50 55 60

Ser Asp Asp Asp Ser Arg Ala Ser Thr Ser Ser Ser Ser Ser Ser
 65 70 75 80

Ser Asn Gln Gln Thr Glu Lys Glu Thr Asn Thr Pro Lys Lys Lys Glu
 85 90 95

Ser Lys Val Ser Met Ser Lys Asn Ser Lys Leu Leu Ser Thr Ser Ala
 100 105 110

Lys Arg Ile Gln Lys Glu Leu Ala Asp Ile Thr Leu Asp Pro Pro Pro
 115 120 125

Asn Cys Ser Ala Gly Pro Lys Gly Asp Asn Ile Tyr Glu Trp Arg Ser
 130 135 140

Thr Ile Leu Gly Pro Pro Gly Ser Val Tyr Glu Gly Gly Val Phe Phe
 145 150 155 160

Leu Asp Ile Thr Phe Thr Pro Glu Tyr Pro Phe Lys Pro Pro Lys Val
 165 170 175

Thr Phe Arg Thr Arg Ile Tyr His Cys Asn Ile Asn Ser Gln Gly Val
 180 185 190

Ile Cys Leu Asp Ile Leu Lys Asp Asn Trp Ser Pro Ala Leu Thr Ile
 195 200 205

Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Cys Asn Pro
 210 215 220

1076

Ala Asp Pro Leu Val Gly Ser Ile Ala Thr Gln Tyr Met Thr Asn Arg
225 230 235 240

Ala Glu His Asp Arg Met Ala Arg Gln Trp Thr Lys Arg Tyr Ala Thr
245 250 255

<210> 1084

<211> 176

<212> PRT

<213> Homo sapiens

<400> 1084

Glu Lys Cys Val Ser Phe Ser Ala Val Leu Lys Ser Leu Ser Pro Val
1 5 10 15

Asp Pro Val Glu Pro Ile Ser Asn Ser Glu Pro Ser Met Asn Ser Asp
20 25 30

Met Gly Lys Val Ser Lys Asn Asp Thr Glu Glu Glu Ser Asn Lys Ser
35 40 45

Ala Thr Thr Asp Asn Glu Ile Ser Arg Thr Glu Tyr Leu Cys Glu Asn
50 55 60

Ser Leu Glu Gly Lys Asn Lys Asp Asn Ser Ser Asn Glu Val Phe Pro
65 70 75 80

Gln Gly Ala Glu Glu Arg Met Cys Tyr Gln Cys Glu Ser Glu Asp Glu
85 90 95

Pro Gln Ala Asp Gly Ser Gly Leu Thr Thr Ala Pro Pro Thr Pro Arg
100 105 110

Asp Ser Leu Gln Pro Ser Ile Lys Gln Arg Leu Ala Arg Leu Gln Leu
115 120 125

Ser Pro Asp Phe Thr Phe Thr Ala Gly Leu Ala Ala Glu Val Ala Ala
130 135 140

Arg Ser Leu Ser Phe Thr Thr Met Gln Glu Gln Thr Phe Gly Asp Glu
145 150 155 160

Glu Glu Glu Gln Ile Ile Glu Glu Asn Lys Asn Glu Ile Glu Glu Lys
165 170 175

1077

<210> 1085

<211> 220

<212> PRT

<213> Homo sapiens

<400> 1085

His Arg Lys Ser Arg Pro Ala Asn His Cys Val Tyr Phe Tyr Gly Asp
 1 5 10 15

Glu Ile Ser Phe Ser Cys His Glu Thr Ser Arg Phe Ser Ala Ile Cys
 20 25 30

Gln Gly Asp Gly Thr Trp Ser Pro Arg Thr Pro Ser Cys Gly Asp Ile
 35 40 45

Cys Asn Phe Pro Pro Lys Ile Ala His Gly His Tyr Lys Gln Ser Ser
 50 55 60

Ser Tyr Ser Phe Phe Lys Glu Glu Ile Ile Tyr Glu Cys Asp Lys Gly
 65 70 75 80

Tyr Ile Leu Val Gly Gln Ala Lys Leu Ser Cys Ser Tyr Ser His Trp
 85 90 95

Ser Ala Pro Ala Pro Gln Cys Lys Ala Leu Cys Arg Lys Pro Glu Leu
 100 105 110

Val Asn Gly Arg Leu Ser Val Asp Lys Asp Gln Tyr Val Glu Pro Glu
 115 120 125

Asn Val Thr Ile Gln Cys Asp Ser Gly Tyr Gly Val Val Gly Pro Gln
 130 135 140

Ser Ile Thr Cys Ser Gly Asn Arg Thr Trp Tyr Pro Glu Val Pro Lys
 145 150 155 160

Cys Glu Trp Glu Thr Pro Glu Gly Cys Glu Gln Val Leu Thr Gly Lys
 165 170 175

Arg Leu Met Gln Cys Leu Pro Asn Pro Glu Asp Val Lys Met Ala Leu
 180 185 190

Glu Val Tyr Lys Leu Ser Leu Glu Ile Glu Gln Leu Glu Leu Gln Arg
 195 200 205

Asp Ser Ala Arg Gln Ser Thr Leu Asp Lys Glu Leu
 210 215 220

1078

<210> 1086

<211> 133

<212> PRT

<213> Homo sapiens

<400> 1086

Val Lys Pro Ser Gly Gly Glu Gly Asp Val Ala Gln Arg Pro Arg Asp
1 5 10 15

Arg Leu Ser Ser Arg Leu Leu Gly Ser Pro Ala Trp Arg Arg Arg Leu
20 25 30

Met Thr Glu Gly Pro Leu Ala Gly Ala Pro Val Cys Ile Phe Glu Gly
35 40 45

Pro Gly Pro Pro Gly Gly Ala Gly Ser Tyr Ser Trp Gly Leu Gly Phe
50 55 60

Arg Arg Ala Gly Gly Gly Ala Gly Leu Lys Ala Ala Leu Val Tyr Gly
65 70 75 80

Val Val Thr Gln Ser His Trp Gln Arg Trp Gly Leu Ala Val Ala Trp
85 90 95

Gln Tyr Leu Gly Ile Ala Ser Thr Gly Asn Lys Asp Gly His Glu Gln
100 105 110

Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
115 120 125

Lys Lys Lys Lys Lys
130

<210> 1087

<211> 289

<212> PRT

<213> Homo sapiens

<400> 1087

Ile Leu Thr Tyr Lys Met Lys Gln Asp Ala Ser Arg Asn Ala Ala Tyr
1 5 10 15

Thr Val Asp Cys Glu Asp Tyr Val His Val Val Glu Phe Asn Pro Phe
20 25 30

Glu Asn Gly Asp Ser Gly Asn Leu Ile Ala Tyr Gly Gly Asn Asn Tyr

1079

35	40	45
Val Val Ile Gly Thr Cys Thr Phe Gln Glu Glu Glu Ala Asp Val Glu		
50	55	60
Gly Ile Gln Tyr Lys Thr Leu Arg Thr Phe His His Gly Val Arg Val		
65	70	75 80
Asp Gly Ile Ala Trp Ser Pro Glu Thr Arg Leu Asp Ser Leu Pro Pro		
	85	90 95
Val Ile Lys Phe Cys Thr Ser Ala Ala Asp Met Lys Ile Arg Leu Phe		
	100	105 110
Thr Ser Asp Leu Gln Asp Lys Asn Glu Tyr Lys Val Leu Glu Gly His		
	115	120 125
Thr Asp Phe Ile Asn Gly Leu Val Phe Asp Pro Lys Glu Gly Gln Glu		
	130	135 140
Ile Ala Ser Val Ser Asp Asp His Thr Cys Arg Ile Trp Asn Leu Glu		
	145	150 155 160
Gly Val Gln Thr Ala His Phe Val Leu His Ser Pro Gly Met Ser Val		
	165	170 175
Cys Trp His Pro Glu Glu Thr Phe Lys Leu Met Val Ala Glu Lys Asn		
	180	185 190
Gly Thr Ile Arg Phe Tyr Asp Leu Leu Ala Gln Gln Ala Ile Leu Ser		
	195	200 205
Leu Glu Ser Glu Gln Val Pro Leu Met Ser Ala His Trp Cys Leu Lys		
	210	215 220
Asn Thr Phe Lys Val Gly Ala Val Ala Gly Asn Asp Trp Leu Ile Trp		
	225	230 235 240
Asp Ile Thr Arg Ser Ser Tyr Pro Gln Asn Lys Arg Pro Val His Met		
	245	250 255
Asp Arg Ala Cys Leu Phe Arg Trp Ser Thr Ile Ser Glu Asn Leu Phe		
	260	265 270
Ala Thr Thr Gly Tyr Pro Gly Lys Met Gln Ala Ser Phe Lys Phe Ile		
	275	280 285
Ile		

1080

<210> 1088

<211> 836

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (677)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1088

Pro Thr Arg Pro Asn Trp Thr Gly Met Thr Asn Leu Leu Asp Ile Pro
 1 5 10 15

Gly Leu Ser Ser Leu Ser Asp Thr Met Ile Met Asp Ser Ile Ala Ala
 20 25 30

Phe Leu Val Leu Pro Asn Arg Leu Leu Val Pro Leu Val Pro Asp Leu
 35 40 45

Gln Asp Val Ala Gln Leu Arg Ser Pro Leu Pro Arg Gly Ile Ile Arg
 50 55 60

Ile His Leu Leu Ala Ala Arg Gly Leu Ser Ser Lys Asp Lys Tyr Val
 65 70 75 80

Lys Gly Leu Ile Glu Gly Lys Ser Asp Pro Tyr Ala Leu Val Arg Leu
 85 90 95

Gly Thr Gln Thr Phe Cys Ser Arg Val Ile Asp Glu Glu Leu Asn Pro
 100 105 110

Gln Trp Gly Glu Thr Tyr Glu Val Met Val His Glu Val Pro Gly Gln
 115 120 125

Glu Ile Glu Val Glu Val Phe Asp Lys Asp Pro Asp Lys Asp Asp Phe
 130 135 140

Leu Gly Arg Met Lys Leu Asp Val Gly Lys Val Leu Gln Ala Ser Val
 145 150 155 160

Leu Asp Asp Trp Phe Pro Leu Gln Gly Gly Gln Gly Gln Val His Leu
 165 170 175

Arg Leu Glu Trp Leu Ser Leu Leu Ser Asp Ala Glu Lys Leu Glu Gln
 180 185 190

Val Leu Gln Trp Asn Trp Gly Val Ser Ser Arg Pro Asp Pro Pro Ser
 195 200 205

1081

Ala Ala Ile Leu Val Val Tyr Leu Asp Arg Ala Gln Asp Leu Pro Leu
210 215 220

Lys Lys Gly Asn Lys Glu Pro Asn Pro Met Val Gln Leu Ser Ile Gln
225 230 235 240

Asp Val Thr Gln Glu Ser Lys Ala Val Tyr Ser Thr Asn Cys Pro Val
245 250 255

Trp Glu Glu Ala Phe Arg Phe Phe Leu Gln Asp Pro Gln Ser Gln Glu
260 265 270

Leu Asp Val Gln Val Lys Asp Asp Ser Arg Ala Leu Thr Leu Gly Ala
275 280 285

Leu Thr Leu Pro Leu Ala Arg Leu Leu Thr Ala Pro Glu Leu Ile Leu
290 295 300

Asp Gln Trp Phe Gln Leu Ser Ser Ser Gly Pro Asn Ser Arg Leu Tyr
305 310 315 320

Met Lys Leu Val Met Arg Ile Leu Tyr Leu Asp Ser Ser Glu Ile Cys
325 330 335

Phe Pro Thr Val Pro Gly Cys Pro Gly Ala Trp Asp Val Asp Ser Glu
340 345 350

Asn Pro Gln Arg Gly Ser Ser Val Asp Ala Pro Pro Arg Pro Cys His
355 360 365

Thr Thr Pro Asp Ser Gln Phe Gly Thr Glu His Val Leu Arg Ile His
370 375 380

Val Leu Glu Ala Gln Asp Leu Ile Ala Lys Asp Arg Phe Leu Gly Gly
385 390 395 400

Leu Val Lys Gly Lys Ser Asp Pro Tyr Val Lys Leu Lys Leu Ala Gly
405 410 415

Arg Ser Phe Arg Ser His Val Val Arg Glu Asp Leu Asn Pro Arg Trp
420 425 430

Asn Glu Val Phe Glu Val Ile Val Thr Ser Val Pro Gly Gln Glu Leu
435 440 445

Glu Val Glu Val Phe Asp Lys Asp Leu Asp Lys Asp Asp Phe Leu Gly
450 455 460

Arg Cys Lys Val Arg Leu Thr Thr Val Leu Asn Ser Gly Phe Leu Asp
465 470 475 480

1082

Glu Trp Leu Thr Leu Glu Asp Val Pro Ser Gly Arg Leu His Leu Arg
485 490 495

Leu Glu Arg Leu Thr Pro Arg Pro Thr Ala Ala Glu Leu Glu Glu Val
500 505 510

Leu Gln Val Asn Ser Leu Ile Gln Thr Gln Lys Ser Ala Glu Leu Ala
515 520 525

Ala Ala Leu Leu Ser Ile Tyr Met Glu Arg Ala Glu Asp Leu Pro Leu
530 535 540

Arg Lys Gly Thr Lys His Leu Ser Pro Tyr Ala Thr Leu Thr Val Gly
545 550 555 560

Asp Ser Ser His Lys Thr Lys Thr Ile Ser Gln Thr Ser Ala Pro Val
565 570 575

Trp Asp Glu Ser Ala Ser Phe Leu Ile Arg Lys Pro His Thr Glu Ser
580 585 590

Leu Glu Leu Gln Val Arg Gly Glu Gly Thr Gly Val Leu Gly Ser Leu
595 600 605

Ser Leu Pro Leu Ser Glu Leu Leu Val Ala Asp Gln Leu Cys Leu Asp
610 615 620

Arg Trp Phe Thr Leu Ser Ser Gly Gln Gly Gln Val Leu Leu Arg Ala
625 630 635 640

Gln Leu Gly Ile Leu Val Ser Gln His Ser Gly Val Glu Ala His Ser
645 650 655

His Ser Tyr Ser His Ser Ser Ser Ser Leu Ser Glu Glu Pro Glu Leu
660 665 670

Ser Gly Gly Pro Xaa His Ile Thr Ser Ser Ala Pro Glu Leu Arg Gln
675 680 685

Arg Leu Thr His Val Asp Ser Pro Leu Glu Ala Pro Ala Gly Pro Leu
690 695 700

Gly Gln Val Lys Leu Thr Leu Trp Tyr Tyr Ser Glu Glu Arg Lys Leu
705 710 715 720

Val Ser Ile Val His Gly Cys Arg Ser Leu Arg Gln Asn Gly Arg Asp
725 730 735

Pro Pro Asp Pro Tyr Val Ser Leu Leu Leu Leu Pro Asp Lys Asn Arg
740 745 750

1083

Gly Thr Lys Arg Arg Thr Ser Gln Lys Lys Arg Thr Leu Ser Pro Glu
755 760 765

Phe Asn Glu Arg Phe Glu Trp Glu Leu Pro Leu Asp Glu Ala Gln Arg
770 775 780

Arg Lys Leu Asp Val Ser Val Lys Ser Asn Ser Ser Phe Met Ser Arg
785 790 795 800

Glu Arg Glu Leu Leu Gly Lys Val Gln Leu Asp Leu Ala Glu Thr Asp
805 810 815

Leu Ser Gln Gly Val Ala Arg Trp Tyr Asp Leu Met Asp Asn Lys Asp
820 825 830

Lys Gly Ser Ser
835

<210> 1089

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (65)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (393)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (406)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1089

Arg Ser Ser Val Ala Ser Val His Thr Trp Arg Gln Arg Arg Gln Val
1 5 10 15

Xaa Val Phe Val Leu Pro Ser Thr Ala Asn Met Lys Arg Pro Lys Leu
20 25 30

1084

Lys Lys Ala Ser Lys Arg Met Thr Cys His Lys Arg Tyr Lys Ile Gln
 35 40 45
 Lys Lys Val Arg Glu His His Arg Lys Leu Arg Lys Glu Ala Lys Lys
 50 55 60
 Xaa Gly His Lys Lys Pro Arg Lys Asp Pro Gly Val Pro Asn Ser Ala
 65 70 75 80
 Pro Phe Lys Glu Ala Leu Leu Arg Glu Ala Glu Leu Arg Lys Gln Arg
 85 90 95
 Leu Glu Glu Leu Lys Gln Gln Gln Lys Leu Asp Arg Gln Lys Glu Leu
 100 105 110
 Glu Lys Lys Arg Lys Leu Glu Thr Asn Pro Asp Ile Lys Pro Ser Asn
 115 120 125
 Val Glu Pro Met Glu Lys Glu Phe Gly Leu Cys Lys Thr Glu Asn Lys
 130 135 140
 Ala Lys Ser Gly Lys Gln Asn Ser Lys Lys Leu Tyr Cys Gln Glu Leu
 145 150 155 160
 Lys Lys Val Ile Glu Ala Ser Asp Val Val Leu Glu Val Leu Asp Ala
 165 170 175
 Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln Val Glu Glu Ala Ile Val
 180 185 190
 Gln Ser Gly Gln Lys Lys Leu Val Leu Ile Leu Asn Lys Ser Asp Leu
 195 200 205
 Val Pro Lys Glu Asn Leu Glu Ser Trp Leu Asn Tyr Leu Lys Lys Glu
 210 215 220
 Leu Pro Thr Val Val Phe Arg Ala Ser Thr Lys Pro Lys Asp Lys Gly
 225 230 235 240
 Lys Ile Thr Lys Arg Val Lys Ala Lys Lys Asn Ala Ala Pro Phe Arg
 245 250 255
 Ser Glu Val Cys Phe Gly Lys Glu Gly Leu Trp Lys Leu Leu Gly Gly
 260 265 270
 Phe Gln Glu Thr Cys Ser Lys Ala Ile Arg Val Gly Val Ile Gly Phe
 275 280 285
 Pro Asn Val Gly Lys Ser Ser Ile Ile Asn Ser Leu Lys Gln Glu Gln
 290 295 300

1085

Met Cys Asn Val Gly Val Ser Met Gly Leu Thr Arg Ser Met Gln Val
 305 310 315 320

Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser Pro Ser Phe Ile
 325 330 335

Val Ser Pro Leu Asn Ser Ser Ser Ala Leu Ala Leu Arg Ser Pro Ala
 340 345 350

Ser Ile Glu Val Val Lys Pro Met Glu Ala Ala Ser Ala Ile Leu Ser
 355 360 365

Gln Ala Asp Ala Arg Gln Val Val Leu Lys Tyr Thr Val Pro Gly Tyr
 370 375 380

Arg Asn Ser Leu Gly Ile Phe Tyr Xaa Ala Cys Ser Glu Lys Arg Tyr
 385 390 395 400

Ala Pro Lys Arg Trp Xaa Pro Lys Cys
 405

<210> 1090

<211> 161

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (56)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1090

Pro Lys Asn Trp Xaa Thr Ala Arg Ala Asp His His Ala Ser Met Asn
 1 5 10 15

Trp Val Pro Cys Gly His Ser Tyr Phe Gly Ala Thr Leu Asn Ser Phe
 20 25 30

Ile His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ser Val Pro Ser
 35 40 45

Met Arg Pro Tyr Leu Trp Trp Xaa Glu Val His His Ser Gly Ala Ala
 50 55 60

1086

Ala Ser Val Cys Ala Asp Asn His Pro Asp Gln Leu Arg Gly His Leu
65 70 75 80

Ala Val His Ile Pro Ser Trp Leu Val Val Phe Pro Asp Trp Ile His
85 90 95

Asp Phe Pro Asp Cys Ser Leu His Lys Leu Leu His Ser Asp Leu Gln
100 105 110

Gln Glu Arg Gly Leu Pro Lys Glu Arg Pro Pro Glu Gly Pro Pro Glu
115 120 125

Trp Val His Gly Cys Cys Glu Trp Thr His Gln Gln Leu Phe Thr Pro
130 135 140

Gly Lys Gln Cys Glu Ala Lys Glu Ala Ala Glu Gly Leu Lys Ser Lys
145 150 155 160

Asn

<210> 1091
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1091
Ser Lys Asn Ser Ala Arg Glu Glu Met Ala Ala Ser Ser Ser Ser Ser
1 5 10 15

Ser Ala Gly Gly Val Ser Gly Ser Ser Val Thr Gly Ser Gly Phe Ser
20 25 30

Val Ser Asp Leu Ala Pro Pro Arg Lys Ala Leu Phe Thr Tyr Pro Lys
35 40 45

Gly Ala Gly Glu Met Leu Glu Asp Gly Ser Glu Arg Phe Leu Cys Glu
50 55 60

Ser Val Phe Ser Tyr Gln Val Ala Ser Thr Leu Lys Gln Val Lys His
65 70 75 80

Asp Gln Gln Val Ala Arg Met Glu Lys Leu Ala Gly Leu Val Glu Glu
85 90 95

Leu Glu Ala Asp Glu Trp Arg Phe Lys Pro Ile Glu Gln Leu Leu Gly
100 105 110

1087

Phe Thr Pro Ser Ser Gly
115

<210> 1092

<211> 198

<212> PRT

<213> Homo sapiens

<400> 1092

Ala Pro Phe Leu Ala Ala Gly Val Ser Met Gly Gly Met Leu Leu Leu
1 5 10 15

Asn Tyr Leu Gly Lys Ile Gly Ser Lys Thr Pro Leu Met Ala Ala Ala
20 25 30

Thr Phe Ser Val Gly Trp Asn Thr Phe Ala Cys Ser Glu Ser Leu Glu
35 40 45

Lys Pro Leu Asn Trp Leu Leu Phe Asn Tyr Tyr Leu Thr Thr Cys Leu
50 55 60

Gln Ser Ser Val Asn Lys His Arg His Met Phe Val Lys Gln Val Asp
65 70 75 80

Met Asp His Val Met Lys Ala Lys Ser Ile Arg Glu Phe Asp Lys Arg
85 90 95

Phe Thr Ser Val Met Phe Gly Tyr Gln Thr Ile Asp Asp Tyr Tyr Thr
100 105 110

Asp Ala Ser Pro Ser Pro Arg Leu Lys Ser Val Gly Ile Pro Val Leu
115 120 125

Cys Leu Asn Ser Val Asp Asp Val Phe Ser Pro Ser His Ala Ile Pro
130 135 140

Ile Glu Thr Ala Lys Gln Asn Pro Asn Val Ala Leu Val Leu Thr Ser
145 150 155 160

Tyr Gly Gly His Ile Gly Phe Leu Glu Gly Ile Trp Pro Arg Gln Ser
165 170 175

Thr Tyr Met Asp Arg Val Phe Lys Gln Phe Val Gln Ala Met Val Glu
180 185 190

His Gly His Glu Leu Ser
195

1088

<210> 1093

<211> 36

<212> PRT

<213> Homo sapiens

<400> 1093

Pro Gly Trp Ser Arg Ser Pro Gly Trp Ser Arg Ser Pro Gly Trp Ser
1 5 10 15

Arg Ser Pro Asp Val Val Ile His Pro Pro Arg Pro Pro Lys Met Leu
20 25 30

Gly Leu Gln Val
35

<210> 1094

<211> 615

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (21)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (113)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (132)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (155)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (156)

1089

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (157)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1094

Tyr Xaa Gln Leu Val Leu Leu Gln Val Pro Val Arg Ile Pro Gly Ser
1 5 10 15

Thr His Ala Ser Xaa Asp Ala Trp Val Ala Arg Gln Leu Ala Lys Pro
20 25 30

Asp Asn Thr Leu Phe Val Asn Arg Thr Leu Phe Asp Gln Val Leu Glu
35 40 45

Phe Leu Cys Ser Pro Asp Asp Asp Ser Arg His Ser Glu Arg Gln Gln
50 55 60

Val Leu Leu Glu Leu Leu Gln Ala Gly Gly Ile Val Gln Phe Glu Glu
65 70 75 80

Ser Arg Leu Ile Arg Met Ala Glu Lys Ala Glu Phe Tyr Gln Ile Cys
85 90 95

Glu Phe Met Tyr Glu Arg Glu His Gln Tyr Asp Lys Ile Ile Asp Cys
100 105 110

Xaa Leu Arg Asp Pro Leu Arg Glu Glu Val Phe Asn Tyr Ile His
115 120 125

Asn Ile Leu Xaa Ile Pro Gly His Ser Ala Glu Glu Lys Gln Ser Val
130 135 140

Trp Gln Lys Ala Met Asp His Ile Glu Glu Xaa Xaa Xaa Leu Lys Pro
145 150 155 160

Cys Lys Ala Ala Glu Leu Val Ala Thr His Phe Ser Gly His Ile Glu
165 170 175

Thr Val Ile Lys Lys Leu Gln Asn Gln Val Leu Leu Phe Lys Phe Leu
180 185 190

Arg Ser Leu Leu Asp Pro Arg Glu Gly Ile His Val Asn Gln Glu Leu
195 200 205

Leu Gln Ile Ser Pro Cys Ile Thr Glu Gln Phe Ile Glu Leu Leu Cys
210 215 220

Gln Phe Asn Pro Thr Gln Val Ile Glu Thr Leu Gln Val Leu Glu Cys

1090

225 230 235 240
Tyr Arg Leu Glu Glu Thr Ile Gln Ile Thr Gln Lys Tyr Gln Leu His
 245 250 255
Glu Val Thr Ala Tyr Leu Leu Glu Lys Lys Gly Asp Ile His Gly Ala
 260 265 270
Phe Leu Ile Met Leu Glu Arg Leu Gln Ser Lys Leu Gln Glu Val Thr
 275 280 285
His Gln Gly Glu Asn Thr Lys Glu Asp Pro Ser Leu Lys Asp Val Glu
 290 295 300
Asp Thr Met Val Glu Thr Ile Ala Leu Cys Gln Arg Asn Ser His Asn
305 310 315 320
Leu Asn Gln Gln Gln Arg Glu Ala Leu Trp Phe Pro Leu Leu Glu Ala
 325 330 335
Met Met Ala Pro Gln Lys Leu Ser Ser Ser Ala Ile Pro His Leu His
 340 345 350
Ser Glu Ala Leu Lys Ser Leu Thr Met Gln Val Leu Asn Ser Met Ala
 355 360 365
Ala Phe Ile Ala Leu Pro Ser Ile Leu Gln Arg Ile Leu Gln Asp Pro
 370 375 380
Val Tyr Gly Lys Gly Lys Leu Gly Glu Ile Gln Gly Leu Ile Leu Gly
385 390 395 400
Met Leu Asp Thr Phe Asn Tyr Glu Gln Thr Leu Leu Glu Thr Thr Thr
 405 410 415
Ser Leu Leu Asn Gln Asp Leu His Trp Ser Leu Cys Asn Leu Arg Ala
 420 425 430
Ser Val Thr Arg Gly Leu Asn Pro Lys Gln Asp Tyr Cys Ser Ile Cys
 435 440 445
Leu Gln Gln Tyr Lys Arg Arg Gln Glu Met Ala Asp Glu Ile Ile Val
 450 455 460
Phe Ser Cys Gly His Leu Tyr His Ser Phe Cys Leu Gln Asn Lys Glu
465 470 475 480
Cys Thr Val Glu Phe Glu Gly Gln Thr Arg Trp Thr Cys Tyr Lys Cys
 485 490 495
Ser Ser Ser Asn Lys Val Gly Lys Leu Ser Glu Asn Ser Ser Glu Ile

His Gln Ser Lys Gly Asp Pro Thr Ala Lys Lys Gly Thr Ser Glu Pro
530 535 540

Val Leu Asp Pro Gln Gln Ile Gln Ala Phe Asp Gln Leu Cys Arg Leu
545 550 555 560

Tyr Arg Gly Ser Ser Arg Leu Ala Leu Leu Thr Glu Leu Ser Gln Asn
565 570 575

Arg Ser Ser Glu Ser Tyr Arg Pro Phe Ser Gly Ser Gln Ser Ala Pro
580 585 590

Ala Phe Asn Ser Ile Phe Gln Asn Glu Asn Phe Gln Leu Gln Leu Ile
595 600 605

Pro Pro Pro Val Thr Glu Asp
610 615

<210> 1095

<211> 264

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (27)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1095

Trp Xaa Ser Thr Thr Ile Trp Lys Ala Gly Pro Pro Ala Gly Thr Gly
1 5 10 15

Pro Glu Phe Pro Gly Arg Pro Thr Arg Pro Xaa Thr Arg Gly Phe Trp
20 25 30

Phe Cys Ser Ser Val Trp Val Ser Ser Arg Leu Leu Lys Met Asn Arg
35 40 45

Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

1092

50	55	60
Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile		
65	70	75 80
Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys		
	85	90 95
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg		
	100	105 110
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala		
	115	120 125
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu		
	130	135 140
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu		
	145	150 155 160
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu		
	165	170 175
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu		
	180	185 190
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu		
	195	200 205
Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp		
	210	215 220
Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly		
	225	230 235 240
Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe		
	245	250 255
Gly Leu Pro Gln Ile Pro Ala Ser		
	260	

<210> 1096

<211> 244

<212> PRT

<213> Homo sapiens

<400> 1096

Ser Cys Cys Phe Leu Lys Arg Leu Gln Ala Ser Phe Pro Arg Thr Ala
1 5 10 15

1093

Val Ser Phe Glu Pro Leu Ala Gly Asp Met Pro Arg Gly Arg Lys Ser
 20 25 30
 Arg Arg Arg Arg Asn Ala Arg Ala Ala Glu Glu Asn Arg Asn Asn Arg
 35 40 45
 Lys Ile Gln Ala Ser Glu Ala Ser Glu Thr Pro Met Ala Ala Ser Val
 50 55 60
 Val Ala Ser Thr Pro Glu Asp Asp Leu Ser Gly Pro Glu Glu Asp Pro
 65 70 75 80
 Ser Thr Pro Glu Glu Ala Ser Thr Thr Pro Glu Glu Ala Ser Ser Thr
 85 90 95
 Ala Gln Ala Gln Lys Pro Ser Val Pro Arg Ser Asn Phe Gln Gly Thr
 100 105 110
 Lys Lys Ser Leu Leu Met Ser Ile Leu Ala Leu Ile Phe Ile Met Gly
 115 120 125
 Asn Ser Ala Lys Glu Ala Leu Val Trp Lys Val Leu Gly Lys Leu Gly
 130 135 140
 Met Gln Pro Gly Arg Gln His Ser Ile Phe Gly Asp Pro Lys Lys Ile
 145 150 155 160
 Val Thr Glu Glu Phe Val Arg Arg Gly Tyr Leu Ile Tyr Lys Pro Val
 165 170 175
 Pro Arg Ser Ser Pro Val Glu Tyr Glu Phe Phe Trp Gly Pro Arg Ala
 180 185 190
 His Val Glu Ser Ser Lys Leu Lys Val Met His Phe Val Ala Arg Val
 195 200 205
 Arg Asn Arg Cys Ser Lys Asp Trp Pro Cys Asn Tyr Asp Trp Asp Ser
 210 215 220
 Asp Asp Asp Ala Glu Val Glu Ala Ile Leu Asn Ser Gly Ala Arg Gly
 225 230 235 240
 Tyr Ser Ala Pro

<210> 1097

<211> 132

<212> PRT

1094

<213> Homo sapiens

<400> 1097

Ala Thr Met Val Arg Met Asn Val Leu Ala Asp Ala Leu Lys Ser Ile
1 5 10 15

Asn Asn Ala Glu Lys Arg Gly Lys Arg Gln Val Leu Ile Arg Pro Cys
20 25 30

Ser Lys Val Ile Val Arg Phe Leu Thr Val Met Met Lys His Gly Tyr
35 40 45

Ile Gly Glu Phe Glu Ile Ile Asp Asp His Arg Ala Gly Lys Ile Val
50 55 60

Val Asn Leu Thr Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg
65 70 75 80

Phe Asp Val Gln Leu Lys Asp Leu Glu Lys Trp Gln Asn Asn Leu Leu
85 90 95

Pro Ser Arg Gln Phe Gly Phe Ile Val Leu Thr Thr Ser Ala Gly Ile
100 105 110

Met Asp His Glu Glu Ala Arg Arg Lys His Thr Gly Gly Lys Ile Leu
115 120 125

Gly Phe Phe Phe
130

<210> 1098

<211> 371

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (44)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (186)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1098

Ala Arg His Thr Pro Ala Gln Arg His Asp His Pro Gln Glu Gly Asn
1 5 10 15

1095

Ile Pro Val Cys Val Gln Leu Ala Val Cys Ala Leu Pro Leu Pro Val
20 25 30

Val Pro Gly Pro Glu His Cys Gly Pro Gln Arg Xaa Leu Gln Pro Leu
35 40 45

Val Tyr Pro Leu Ala Gln Val Ile Ile Gly Cys Ile Lys Leu Ile Pro
50 55 60

Thr Ala Arg Phe Tyr Pro Leu Arg Met His Cys Ile Arg Ala Leu Thr
65 70 75 80

Leu Leu Ser Gly Ser Ser Gly Ala Phe Ile Pro Val Leu Pro Phe Ile
85 90 95

Leu Glu Met Phe Gln Gln Val Asp Phe Asn Arg Lys Pro Gly Arg Met
100 105 110

Ser Ser Lys Pro Ile Asn Phe Ser Val Ile Leu Lys Leu Ser Asn Val
115 120 125

Asn Leu Gln Glu Lys Ala Tyr Arg Asp Gly Leu Val Glu Gln Leu Tyr
130 135 140

Asp Leu Thr Leu Glu Tyr Leu His Ser Gln Ala His Cys Ile Gly Phe
145 150 155 160

Pro Glu Leu Val Leu Pro Val Val Leu Gln Leu Lys Ser Phe Leu Arg
165 170 175

Glu Cys Lys Val Ala Asn Tyr Cys Arg Xaa Val Gln Gln Leu Leu Gly
180 185 190

Lys Val Gln Glu Asn Ser Ala Tyr Ile Cys Ser Arg Arg Gln Arg Val
195 200 205

Ser Phe Gly Val Ser Glu Gln Gln Ala Val Glu Ala Trp Glu Lys Leu
210 215 220

Thr Arg Glu Glu Gly Thr Pro Leu Thr Leu Tyr Tyr Ser His Trp Arg
225 230 235 240

Lys Leu Arg Asp Arg Glu Ile Gln Leu Glu Ile Ser Gly Lys Glu Arg
245 250 255

Leu Glu Asp Leu Asn Phe Pro Glu Ile Lys Arg Arg Lys Met Ala Asp
260 265 270

Arg Lys Asp Glu Asp Arg Lys Gln Phe Lys Asp Leu Phe Asp Leu Asn
275 280 285

1096

Ser Ser Glu Glu Asp Asp Thr Glu Gly Phe Ser Glu Arg Gly Ile Leu
 290 295 300

Arg Pro Leu Ser Thr Arg His Gly Val Glu Asp Asp Glu Glu Asp Glu
 305 310 315 320

Glu Glu Gly Glu Glu Asp Ser Ser Asn Ser Glu Gly Glu Trp Ser Trp
 325 330 335

Asp Gly Asp Pro Asp Ala Glu Ala Gly Leu Ala Pro Gly Glu Leu Gln
 340 345 350

Gln Leu Ala Gln Gly Pro Glu Asp Glu Leu Glu Asp Leu Gln Leu Ser
 355 360 365

Glu Asp Asp
 370

<210> 1099

<211> 321

<212> PRT

<213> Homo sapiens

<400> 1099

Glu Arg Thr Leu Gly Gln Pro Gly Phe Leu Gly Cys Pro Arg Gln Pro
 1 5 10 15

His Thr Ala Met His Tyr Pro Thr Ala Leu Leu Phe Leu Ile Leu Ala
 20 25 30

Asn Gly Ala Gln Ala Phe Arg Ile Cys Ala Phe Asn Ala Gln Arg Leu
 35 40 45

Thr Leu Ala Lys Val Ala Arg Glu Gln Val Met Asp Thr Leu Val Arg
 50 55 60

Ile Leu Ala Arg Cys Asp Ile Met Val Leu Gln Glu Val Val Asp Ser
 65 70 75 80

Ser Gly Ser Ala Ile Pro Leu Leu Leu Arg Glu Leu Asn Arg Phe Asp
 85 90 95

Gly Ser Gly Pro Tyr Ser Thr Leu Ser Ser Pro Gln Leu Gly Arg Ser
 100 105 110

Thr Tyr Met Glu Thr Tyr Val Tyr Phe Tyr Arg Ser His Lys Thr Gln
 115 120 125

Val Leu Ser Ser Tyr Val Tyr Asn Asp Glu Asp Asp Val Phe Ala Arg

1097

130	135	140
Glu Pro Phe Val Ala Gln Phe Ser Leu Pro Ser Asn Val Leu Pro Ser		
145	150	155 160
Leu Val Leu Val Pro Leu His Thr Thr Pro Lys Ala Val Glu Lys Glu		
	165	170 175
Leu Asn Ala Leu Tyr Asp Val Phe Leu Glu Val Ser Gln His Trp Gln		
	180	185 190
Ser Lys Asp Val Ile Leu Leu Gly Asp Phe Asn Ala Asp Cys Ala Ser		
	195	200 205
Leu Thr Lys Lys Arg Leu Asp Lys Leu Glu Leu Arg Thr Glu Pro Gly		
	210	215 220
Phe His Trp Val Ile Ala Asp Gly Glu Asp Thr Thr Val Arg Ala Ser		
	225	230 235 240
Thr His Cys Thr Tyr Asp Arg Val Val Leu His Gly Glu Arg Cys Arg		
	245	250 255
Ser Leu Leu His Thr Ala Ala Ala Phe Asp Phe Pro Thr Ser Phe Gln		
	260	265 270
Leu Thr Glu Glu Glu Ala Leu Asn Ile Ser Asp His Tyr Pro Val Glu		
	275	280 285
Val Glu Leu Lys Leu Ser Gln Ala His Ser Val Gln Pro Leu Ser Leu		
	290	295 300
Thr Val Leu Leu Leu Leu Ser Leu Leu Ser Pro Gln Leu Cys Pro Ala		
	305	310 315 320
Ala		

<210> 1100

<211> 60

<212> PRT

<213> Homo sapiens

<400> 1100

Leu Leu Leu Cys Val Phe Tyr Ile Ala Cys Phe Cys Lys Asn Met Leu
1 5 10 15

Gly Asp Glu Arg Leu Val Leu Glu Arg Lys Cys Ser Ser Val Gln Arg
20 25 30

1098

Met His Phe Leu Pro Leu Ile Leu Glu Lys Thr Phe Thr Val Ile Tyr
 35 40 45

Met Val Phe Cys Lys Arg Thr Ile Asn Arg Thr Phe
 50 55 60

<210> 1101

<211> 254

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (162)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (170)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1101

Phe Gly Thr Ser Tyr Ile Gly Gly Leu Leu Ser Ala Phe Tyr Leu Thr
 1 5 10 15

Gly Glu Glu Val Phe Arg Ile Lys Ala Ile Arg Leu Gly Glu Lys Leu
 20 25 30

Leu Pro Ala Phe Asn Thr Pro Thr Gly Ile Pro Lys Gly Val Val Ser
 35 40 45

Phe Lys Ser Gly Asn Trp Gly Trp Ala Thr Ala Gly Ser Ser Ser Ile
 50 55 60

Leu Ala Glu Phe Gly Ser Leu His Leu Glu Phe Leu His Leu Thr Glu
 65 70 75 80

Leu Ser Gly Asn Gln Val Phe Ala Glu Lys Val Arg Asn Ile Arg Lys
 85 90 95

Val Leu Arg Lys Ile Glu Lys Pro Phe Gly Leu Tyr Pro Asn Phe Leu
 100 105 110

Ser Pro Val Ser Gly Asn Trp Val Gln His His Val Ser Val Gly Gly
 115 120 125

Leu Gly Asp Ser Phe Tyr Glu Tyr Leu Ile Lys Ser Trp Leu Met Ser
 130 135 140

1099

Gly Lys Thr Asp Met Glu Ala Lys Asn Met Tyr Tyr Glu Ala Leu Glu
145 150 155 160

Ala Xaa Arg Asp Leu Leu Ala Glu Cys Xaa Ser Arg Gly Ala Asp Leu
165 170 175

His Cys Arg Val Ala Arg Gly Asp Ser Gly Pro Gln Asp Gly Ala Pro
180 185 190

Gly Leu Phe Leu Arg Gly His Asp Arg Pro Trp Pro Glu Asp Ala Lys
195 200 205

Glu Glu Lys Arg Ala His Tyr Arg Glu Leu Ala Ala Gln Ile Thr Lys
210 215 220

Thr Cys His Glu Ser Tyr Ala Arg Ser Asp Thr Lys Leu Gly Pro Glu
225 230 235 240

Ala Ser Gly Leu Thr Pro Ala Glu Arg Pro Trp Pro Pro Ser
245 250

<210> 1102

<211> 233

<212> PRT

<213> Homo sapiens

<400> 1102

Gly Pro Gly Trp Tyr Pro Ala Pro Leu Arg Leu Phe His Ser Asp Pro
1 5 10 15

Trp Gly His Ala Gln Pro Gly Ala Lys Arg His Arg Ile Pro Glu Pro
20 25 30

Glu Ala Ala Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys
35 40 45

His Gln His Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val
50 55 60

Phe Ala Asp Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp
65 70 75 80

Ser Cys Val Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala
85 90 95

Cys Pro Ala Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr
100 105 110

1100

Ser Gly Lys Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr
 115 120 125
 Met Leu Ala Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu
 130 135 140
 Phe Gly Lys Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser
 145 150 155 160
 Ala Pro Ala Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala
 165 170 175
 Glu Arg Leu Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln
 180 185 190
 Asp Pro Met Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala
 195 200 205
 Gln Val Val Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu
 210 215 220
 Gly Asp Arg Glu Val Val Leu Tyr Gly
 225 230

<210> 1103
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 1103
 Cys Gln Leu Arg Ser Ala Ala Gly Val Pro Ser Ser Val Ser Val Ser
 1 5 10 15
 Pro Arg Asp Pro Ile Ala Met Glu Leu Ser Asp Ala Asn Leu Gln Thr
 20 25 30
 Leu Thr Glu Tyr Leu Lys Lys Thr Leu Asp Pro Asp Pro Ala Ile Arg
 35 40 45
 Arg Pro Ala Glu Lys Phe Leu Glu Ser Val Glu Gly Asn Gln Asn Tyr
 50 55 60
 Pro Leu Leu Leu Leu Thr Leu Leu Glu Lys Ser Gln Asp Asn Val Ile
 65 70 75 80
 Lys Val Cys Ala Ser Val Thr Phe Lys Asn Tyr Ile Lys Arg Asn Trp
 85 90 95
 Arg Ile Val Glu Asp Glu Pro Asn Lys Ile Cys Glu Ala Asp Arg Val

1101

100	105	110
Ala Ile Lys Ala Asn Ile Val His Leu Met Leu Ser Ser Pro Glu Gln		
115	120	125
Ile Gln Lys Gln Leu Ser Asp Ala Ile Ser Ile Ile Gly Arg Glu Asp		
130	135	140
Phe Pro Gln Lys Trp Pro Asp Leu Leu Thr Glu Met Val Asn Arg Phe		
145	150	155
		160
Gln Ser Gly Asp Phe His Val Ile Asn Gly Val Leu Arg Thr Ala His		
165	170	175
Ser Leu Phe Lys Arg Tyr Arg His Glu Phe Lys Ser Asn Glu Leu Trp		
180	185	190
Thr Glu Ile Lys Leu Val Leu Asp Ala Phe Ala Leu Pro Leu Thr Asn		
195	200	205
Leu Phe Lys Ala Thr Ile Glu Leu Cys Ser Thr His Ala Asn Asp Ala		
210	215	220
Ser Ala Leu Arg Ile Leu Phe Ser Ser Leu Ile Leu Ile Ser Lys Leu		
225	230	235
		240
Phe Tyr Ser Leu Asn Phe Gln Asp Leu Pro Glu Phe Phe Glu Asp Asn		
245	250	255
Met Glu Thr Trp Met Asn Asn Phe His Thr Leu Leu Thr Leu Asp Asn		
260	265	270
Lys Leu Leu Gln Thr Asp Asp Glu Glu Glu Ala Gly Leu Leu Glu Leu		
275	280	285
Leu Lys Ser Gln Ile Cys Asp Asn Ala Ala Leu Tyr Ala Gln Lys Tyr		
290	295	300
Asp Glu Glu Phe Gln Arg Tyr Leu Pro Arg Phe Val Thr Ala Ile Trp		
305	310	315
		320
Glu Phe Thr Ser Tyr Asn Gly Ser Arg Gly		
325	330	

<210> 1104

<211> 180

<212> PRT

<213> Homo sapiens

1102

<220>

<221> SITE

<222> (9)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (150)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (167)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (171)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (175)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (177)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (180)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1104

Gly Thr Ser Pro Gly Arg Gly Gly Xaa Gly Val Gly Leu Arg Gly Leu
1 5 10 15

Ser Ser Leu Gln Ala Pro Gln Pro Ser Arg Val Pro Trp Pro Met Ala
20 25 30

Ala Tyr Ser Tyr Arg Pro Gly Pro Gly Ala Gly Pro Gly Pro Ala Ala
35 40 45

Gly Ala Ala Leu Pro Asp Gln Ser Phe Leu Trp Asn Val Phe Gln Arg
50 55 60

Val Asp Lys Asp Arg Ser Gly Val Ile Ser Asp Thr Glu Leu Gln Gln
65 70 75 80

1103

Ala Leu Ser Asn Gly Thr Trp Thr Pro Phe Asn Pro Val Thr Val Arg
 85 90 95

Ser Ile Ile Ser Met Phe Asp Arg Glu Asn Lys Ala Gly Val Asn Phe
 100 105 110

Ser Glu Phe Thr Gly Val Trp Lys Tyr Ile Thr Asp Trp Gln Asn Val
 115 120 125

Phe Arg Thr Tyr Asp Arg Asp Asn Ser Gly Met Ile Asp Lys Asn Glu
 130 135 140

Leu Lys Gln Ala Leu Xaa Val Ser Ala Thr Gly Ser Leu Thr Ser Ser
 145 150 155 160

Thr Thr Ser Ser Phe Glu Xaa Leu Thr Gly Xaa Gly Arg Gly Xaa Ser
 165 170 175

Xaa Ser Thr Xaa
 180

<210> 1105

<211> 241

<212> PRT

<213> Homo sapiens

<400> 1105

Thr Thr Arg Phe Pro Ser Gly Gln Pro Leu Lys Pro Arg Pro Thr Leu
 1 5 10 15

Thr Ala Ala Gly Pro Arg Pro Gly Leu Leu Cys Phe Thr Ile Tyr Ile
 20 25 30

Met Asn Pro Ser Met Lys Gln Lys Gln Glu Glu Ile Lys Glu Asn Ile
 35 40 45

Lys Asn Ser Ser Val Pro Arg Arg Thr Leu Lys Met Ile Gln Pro Ser
 50 55 60

Ala Ser Gly Ser Leu Val Gly Arg Glu Asn Glu Leu Ser Ala Gly Leu
 65 70 75 80

Ser Lys Arg Lys His Arg Asn Asp His Leu Thr Ser Thr Thr Ser Ser
 85 90 95

Pro Gly Val Ile Val Pro Glu Ser Ser Glu Asn Lys Asn Leu Gly Gly
 100 105 110

Val Thr Gln Glu Ser Phe Asp Leu Met Ile Lys Glu Asn Pro Ser Ser

1104

115	120	125
Gln Tyr Trp Lys Glu Val	Ala Glu Lys Arg Arg Lys Ala Leu Tyr Glu	
130	135	140
Ala Leu Lys Glu Asn Glu Lys Leu His Lys Glu Ile Glu Gln Lys Asp		
145	150	155 160
Asn Glu Ile Ala Arg Leu Lys Lys Glu Asn Lys Glu Leu Ala Glu Val		
	165	170 175
Ala Glu His Val Gln Tyr Met Ala Glu Leu Ile Glu Arg Leu Asn Gly		
	180	185 190
Glu Pro Leu Asp Asn Phe Glu Ser Leu Asp Asn Gln Glu Phe Asp Ser		
195	200	205
Glu Glu Glu Thr Val Glu Asp Ser Leu Val Glu Asp Ser Glu Ile Gly		
210	215	220
Thr Cys Ala Glu Gly Thr Val Ser Ser Ser Thr Asp Ala Lys Pro Cys		
225	230	235 240
Ile		

<210> 1106
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 1106
 Phe His Thr Glu Phe Ile Thr Ile Trp Asp Val Arg Gln Cys Ser Asn
 1 5 10 15
 Lys His Cys Gln His Val Asn Phe Leu Lys Ser Val Gly His Ile Ala
 20 25 30
 Lys Asn Leu Leu Lys His Asn Cys Ile Phe Cys Phe Arg Ala Leu Leu
 35 40 45
 Met Phe Cys Arg Ser Asn Val Cys Ile Phe Leu Leu Asn Lys Leu Val
 50 55 60
 Leu Ile Leu Glu Leu Ser Asp Asp Phe Val Leu Glu Arg Thr Thr Gln
 65 70 75 80
 Arg Arg Gln Cys Lys Ser Lys Ser
 85

1105

<210> 1107

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1107

Leu Val Val Leu Lys Arg Arg Pro Glu Lys Ser Gln Gly His Glu His
1 5 10 15

Arg Ala Met Pro Phe Leu Asp Ile Gln Lys Arg Phe Gly Leu Asn Ile
20 25 30

Asp Arg Trp Leu Thr Ile Gln Ser Gly Glu Gln Pro Tyr Lys Met Ala
35 40 45

Gly Arg Cys His Ala Phe Glu Lys Glu Trp Ile Glu Cys Ala His Gly
50 55 60

Ile Gly Tyr Thr Arg Ala Glu Lys Glu Cys Lys Ile Glu Tyr Asp Asp
65 70 75 80

Phe Val Glu Cys Leu Leu Arg Gln Lys Thr Met Arg Arg Ala Gly Thr
85 90 95

Ile Arg Lys Gln Arg Asp Lys Leu Ile Lys Glu Gly Lys Tyr Thr Pro
100 105 110

Pro Pro His His Ile Gly Lys Gly Glu Pro Arg Pro
115 120

<210> 1108

<211> 299

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (32)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (186)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1108

1106

His Leu Leu Cys Cys Arg Ala Gln Arg Arg Pro Gln Thr Pro Pro Ala
 1 5 10 15
 Ala Arg Gly Leu Glu Pro Ala Gln Arg Cys Phe Glu Asp Ala Gly Xaa
 20 25 30
 Pro Pro Leu Leu Leu Ala Ala Val Leu Leu Gly Leu Val Leu Leu Val
 35 40 45
 Val Leu Leu Leu Leu Leu Arg His Trp Gly Trp Gly Leu Cys Leu Ile
 50 55 60
 Gly Trp Asn Glu Phe Ile Leu Gln Pro Ile His Asn Leu Leu Met Gly
 65 70 75 80
 Asp Thr Lys Glu Gln Arg Ile Leu Asn His Val Leu Gln His Ala Glu
 85 90 95
 Pro Gly Asn Ala Gln Ser Val Leu Glu Ala Ile Asp Thr Tyr Cys Glu
 100 105 110
 Gln Lys Glu Trp Ala Met Asn Val Gly Asp Lys Lys Gly Lys Ile Val
 115 120 125
 Asp Ala Val Ile Gln Glu His Gln Pro Ser Val Leu Leu Glu Leu Gly
 130 135 140
 Ala Tyr Cys Gly Tyr Ser Ala Val Arg Met Ala Arg Leu Leu Ser Pro
 145 150 155 160
 Gly Ala Arg Leu Ile Thr Ile Glu Ile Asn Pro Asp Cys Ala Ala Ile
 165 170 175
 Thr Gln Arg Met Val Asp Phe Ala Gly Xaa Lys Asp Lys Val Thr Leu
 180 185 190
 Val Val Gly Ala Ser Gln Asp Ile Ile Pro Gln Leu Lys Lys Lys Tyr
 195 200 205
 Asp Val Asp Thr Leu Asp Met Val Phe Leu Asp His Trp Lys Asp Arg
 210 215 220
 Tyr Leu Pro Asp Thr Leu Leu Leu Glu Glu Cys Gly Leu Leu Arg Lys
 225 230 235 240
 Gly Thr Val Leu Leu Ala Asp Asn Val Ile Cys Pro Gly Ala Pro Asp
 245 250 255
 Phe Leu Ala His Val Arg Gly Ser Ser Cys Phe Glu Cys Thr His Tyr
 260 265 270

1107

Gln Ser Phe Leu Glu Tyr Arg Glu Val Val Asp Gly Leu Glu Lys Ala
 275 280 285

Ile Tyr Lys Gly Pro Gly Ser Glu Ala Gly Pro
 290 295

<210> 1109

<211> 300

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (43)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1109

Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu Arg Leu Arg Asp Leu
 1 5 10 15

Leu Thr Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser
 20 25 30

Leu Arg Leu Thr Gly Ser Ser Ala Gln Glu Xaa Ala Ser Gly Val Ala
 35 40 45

Leu Gly Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser
 50 55 60

Ala Gln Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg
 65 70 75 80

Asn Ala Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn
 85 90 95

Lys Ile Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala
 100 105 110

Gly Lys Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp
 115 120 125

Ile Leu Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu
 130 135 140

Arg Asp Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg
 145 150 155 160

Cys Pro Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly
 165 170 175

1108

Gly Val Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp
 180 185 190
 Ala Phe Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val
 195 200 205
 Gly Thr Leu Gln Arg Leu Pro Lys Val Ile Gly Asn Gln Ser Leu Val
 210 215 220
 Asn Glu Leu Ala Phe Thr Ala Arg Lys Met Met Ala Asp Glu Ala Leu
 225 230 235 240
 Gly Ser Gly Leu Val Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu
 245 250 255
 Asp Ala Ala Leu Ala Leu Ala Ala Glu Ile Ser Ser Lys Ser Pro Val
 260 265 270
 Ala Cys Arg Ala Pro Arg Ser Thr Cys Cys Ile Pro Ala Thr Ile Arg
 275 280 285
 Trp Pro Arg Ala Ser Thr Thr Trp Arg Pro Gly Thr
 290 295 300

<210> 1110
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 1110
 Arg Ser Cys Ala Leu Val Cys Lys His Trp Tyr Arg Cys Leu His Gly
 1 5 10 15
 Asp Glu Asn Ser Glu Val Trp Arg Ser Leu Cys Ala Arg Ser Leu Ala
 20 25 30
 Glu Glu Ala Leu Arg Thr Asp Ile Leu Cys Asn Leu Pro Ser Tyr Lys
 35 40 45
 Ala Lys Ile Arg Ala Phe Gln His Ala Phe Ser Thr Asn Asp Cys Ser
 50 55 60
 Arg Asn Val Tyr Ile Lys Lys Asn Gly Phe Thr Leu His Arg Asn Pro
 65 70 75 80
 Ile Ala Gln Ser Thr Asp Gly Ala Arg Thr Lys Ile Gly Phe Ser Glu
 85 90 95

1109

Gly Arg His Ala Trp Glu Val Trp Trp Glu Gly Pro Leu Gly Thr Val
 100 105 110
 Ala Val Ile Gly Ile Ala Thr Lys Arg Ala Pro Met Gln Cys Gln Gly
 115 120 125
 Tyr Val Ala Leu Leu Gly Ser Asp Asp Gln Ser Trp Gly Trp Asn Leu
 130 135 140
 Val Asp Asn Asn Leu Leu His Asn Gly Glu Val Asn Gly Ser Phe Pro
 145 150 155 160
 Gln Cys Asn Asn Ala Pro Lys Tyr Gln Ile Gly Glu Arg Ile Arg Val
 165 170 175
 Ile Leu Asp Met Glu Asp Lys Thr Leu Ala Phe Glu Arg Gly Tyr Glu
 180 185 190
 Phe Leu Gly Val Ala Phe Arg Gly Leu Pro Lys Val Cys Leu Tyr Pro
 195 200 205
 Ala Val Ser Ala Val Tyr Gly Asn Thr Glu Val Thr Leu Val Tyr Leu
 210 215 220
 Gly Lys Pro Leu Asp Gly
 225 230

<210> 1111

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (11)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (16)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1111

Pro Xaa Leu Thr Lys Gly Asn Lys Ser Trp Xaa Ser Thr Ala Val Xaa

1110

1 5 10 15
 Thr Ala Leu Glu Leu Val Asp Pro Pro Gly Cys Arg Asn Ser Ala Pro
 20 25 30
 Gln Lys Asn Leu Lys Asn Thr Val Phe Cys Ile Asp Ile Cys Thr Val
 35 40 45
 Cys Val Cys Val Cys Glu Ile Lys Ile Arg Phe
 50 55

<210> 1112
 <211> 425
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (3)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (88)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (228)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1112
 Cys Ile Xaa Gly Phe Tyr Phe Ala Val Leu Ala Pro Gln Glu Leu Leu
 1 5 10 15
 Ile Tyr Glu Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val
 20 25 30
 Ala Met Asn Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser
 35 40 45
 Val Asn Glu Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val
 50 55 60
 Leu Trp Arg Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile
 65 70 75 80
 Leu Val Ile Leu Lys Glu Trp Xaa Ser Lys Leu Trp His Arg Gln Ser
 85 90 95

1111

Ile Val Val Ser Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr
 100 105 110
 Tyr Val Glu Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln
 115 120 125
 Phe Leu Leu Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val
 130 135 140
 Gly Leu Gly Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His
 145 150 155 160
 Ile Ala Ser Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe
 165 170 175
 Pro Glu Pro Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly
 180 185 190
 Thr Glu Gly Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile
 195 200 205
 Glu Ala Cys Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro
 210 215 220
 Tyr Phe Met Xaa Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp
 225 230 235 240
 Glu Glu Tyr Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala
 245 250 255
 Gln Asp Phe Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln
 260 265 270
 Lys Val Gly Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro
 275 280 285
 Leu Phe Asp Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe
 290 295 300
 Trp Thr Phe Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met
 305 310 315 320
 His Ile Gln Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val
 325 330 335
 Glu Gln Met Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser
 340 345 350
 Leu Gln Lys Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu
 355 360 365

1112

His His Lys Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser
 370 375 380

Trp Met Phe Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu
 385 390 395 400

Ser Ile Ile Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln
 405 410 415

Arg Leu Asn Ser Glu Glu Lys Thr Lys
 420 425

<210> 1113

<211> 254

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1113

Xaa Ile Glu Ile Asn Pro His Val Lys Gly Thr Lys Ala Gly Ala Pro
 1 5 10 15

Pro Arg Cys Gly Arg Ser Arg Thr Ser Gly Ser Pro Gly Leu Gln Glu
 20 25 30

Phe Gly Thr Ser Ser Ser Thr Pro Ala Arg Pro Ser Ser His His Ser
 35 40 45

Ala Cys Phe Leu Gly Pro Glu Ile Met Pro Leu Gly Leu Leu Trp Leu
 50 55 60

Gly Leu Ala Leu Leu Gly Ala Leu His Ala Gln Ala Gln Asp Ser Thr
 65 70 75 80

Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val Pro Leu Gln Gln
 85 90 95

Asn Phe Gln Asp Asn Gln Phe Gln Gly Lys Trp Tyr Val Val Gly Leu
 100 105 110

Ala Gly Asn Ala Ile Leu Arg Glu Asp Lys Asp Pro Gln Lys Met Tyr
 115 120 125

Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr Asn Val Thr Ser

1113

130 135 140
 Val Leu Phe Arg Lys Lys Lys Cys Asp Tyr Trp Ile Arg Thr Phe Val
 145 150 155 160
 Pro Gly Cys Gln Pro Gly Glu Phe Thr Leu Gly Asn Ile Lys Ser Tyr
 165 170 175
 Pro Gly Leu Thr Ser Tyr Leu Val Arg Val Val Ser Thr Asn Tyr Asn
 180 185 190
 Gln His Ala Met Val Phe Phe Lys Lys Val Ser Gln Asn Arg Glu Tyr
 195 200 205
 Phe Lys Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu Thr Ser Glu Leu
 210 215 220
 Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly Leu Pro Glu Asn
 225 230 235 240
 His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile Asp Gly
 245 250

<210> 1114
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 1114
 Ala Ser Glu Glu Ala Asn Pro Ala Gly Ile Arg Ala Ile Arg Thr Ala
 1 5 10 15
 Thr Met Thr Val Gly Lys Ser Ser Lys Met Leu Gln His Ile Asp Tyr
 20 25 30
 Arg Met Arg Cys Ile Leu Gln Asp Gly Arg Ile Phe Ile Gly Thr Phe
 35 40 45
 Lys Ala Phe Asp Lys His Met Asn Leu Ile Leu Cys Asp Cys Asp Glu
 50 55 60
 Phe Arg Lys Ile Lys Pro Lys Asn Ser Lys Gln Ala Glu Arg Glu Glu
 65 70 75 80
 Lys Arg Val Leu Gly Leu Val Leu Leu Arg Gly Glu Asn Leu Val Ser
 85 90 95
 Met Thr Val Glu Gly Pro Pro Pro Lys Asp Thr Gly Ile Ala Arg Val
 100 105 110

1114

Pro Leu Ala Gly Ala Ala Gly Gly Pro Gly Ile Gly Arg Ala Ala Gly
115 120 125

Arg Gly Ile Pro Ala Gly Val Pro Met Pro Gln Ala Pro Ala Gly Leu
130 135 140

Ala Gly Pro Val Arg Gly Val Gly Gly Pro Ser Gln Gln Val Met Thr
145 150 155 160

Pro Gln Gly Arg Gly Thr Val Ala Ala Ala Ala Ala Ala Thr Ala
165 170 175

Ser Ile Ala Gly Ala Pro Thr Gln Tyr Pro Pro Gly Arg Gly Gly Pro
180 185 190

Pro Pro Pro Met Gly Arg Gly Ala Pro Pro Pro Gly Met Met Gly Pro
195 200 205

Pro Pro Gly Met Arg Pro Pro Met Gly Pro Pro Met Gly Ile Pro Pro
210 215 220

Gly Arg Gly Thr Pro Met Gly Met Pro Pro Pro Gly Met Arg Pro Pro
225 230 235 240

Pro Pro Gly Met Arg Gly Leu Leu
245

<210> 1115

<211> 777

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (9)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (14)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1115

<221> SITE

<222> (21)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (32)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1115

Leu Thr Lys Gly Xaa Lys Ser Trp Xaa Ser Thr Ala Val Xaa Thr Ala
 1 5 10 15

Leu Glu Leu Val Xaa Pro Pro Gly Cys Arg Asn Ser Ala Arg Ala Xaa
 20 25 30

Pro Pro Leu Gly Ser Ser Pro Leu Gly Arg Arg Phe Arg Val Leu Ser
 35 40 45

Ser Leu Arg Arg Ser Pro Met Phe Glu Glu Lys Ala Ser Ser Pro Ser
 50 55 60

Gly Lys Met Gly Gly Glu Glu Lys Pro Ile Gly Ala Gly Glu Glu Lys
 65 70 75 80

Gln Lys Glu Gly Gly Lys Lys Lys Asn Lys Glu Gly Ser Gly Asp Gly
 85 90 95

Gly Arg Ala Glu Leu Asn Pro Trp Pro Glu Tyr Ile Tyr Thr Arg Leu
 100 105 110

Glu Met Tyr Asn Ile Leu Lys Ala Glu His Asp Ser Ile Leu Ala Glu
 115 120 125

Lys Ala Glu Lys Asp Ser Lys Pro Ile Lys Val Thr Leu Pro Asp Gly
 130 135 140

Lys Gln Val Asp Ala Glu Ser Trp Lys Thr Thr Pro Tyr Gln Ile Ala
 145 150 155 160

Cys Gly Ile Ser Gln Gly Leu Ala Asp Asn Thr Val Ile Ala Lys Val
 165 170 175

Asn Asn Val Val Trp Asp Leu Asp Arg Pro Leu Glu Glu Asp Cys Thr
 180 185 190

Leu Glu Leu Leu Lys Phe Glu Asp Glu Glu Ala Gln Ala Val Tyr Trp
 195 200 205

His Ser Ser Ala His Ile Met Gly Glu Ala Met Glu Arg Val Tyr Gly
 210 215 220

1116

Gly Cys Leu Cys Tyr Gly Pro Pro Ile Glu Asn Gly Phe Tyr Tyr Asp
 225 230 235 240
 Met Tyr Leu Glu Glu Gly Gly Val Ser Ser Asn Asp Phe Ser Ser Leu
 245 250 255
 Glu Ala Leu Cys Lys Lys Ile Ile Lys Glu Lys Gln Ala Phe Glu Arg
 260 265 270
 Leu Glu Val Lys Lys Glu Thr Leu Leu Ala Met Phe Lys Tyr Asn Lys
 275 280 285
 Phe Lys Cys Arg Ile Leu Asn Glu Lys Val Asn Thr Pro Thr Thr Thr
 290 295 300
 Val Tyr Arg Cys Gly Pro Leu Ile Asp Leu Cys Arg Gly Pro His Val
 305 310 315 320
 Arg His Thr Gly Lys Ile Lys Ala Leu Lys Ile His Lys Asn Ser Ser
 325 330 335
 Thr Tyr Trp Glu Gly Lys Ala Asp Met Glu Thr Leu Gln Arg Ile Tyr
 340 345 350
 Gly Ile Ser Phe Pro Asp Pro Lys Met Leu Lys Glu Trp Glu Lys Phe
 355 360 365
 Gln Glu Glu Ala Lys Asn Arg Asp His Arg Lys Ile Gly Arg Asp Gln
 370 375 380
 Glu Leu Tyr Phe Phe His Glu Leu Ser Pro Gly Ser Cys Phe Phe Leu
 385 390 395 400
 Pro Lys Gly Ala Tyr Ile Tyr Asn Ala Leu Ile Glu Phe Ile Arg Ser
 405 410 415
 Glu Tyr Arg Lys Arg Gly Phe Gln Glu Val Val Thr Pro Asn Ile Phe
 420 425 430
 Asn Ser Arg Leu Trp Met Thr Ser Gly His Trp Gln His Tyr Ser Glu
 435 440 445
 Asn Met Phe Ser Phe Glu Val Glu Lys Glu Leu Phe Ala Leu Lys Pro
 450 455 460
 Met Asn Cys Pro Gly His Cys Leu Met Phe Asp His Arg Pro Arg Ser
 465 470 475 480
 Trp Arg Glu Leu Pro Leu Arg Leu Ala Asp Phe Gly Val Leu His Arg
 485 490 495

1117

Asn Glu Leu Ser Gly Ala Leu Thr Gly Leu Thr Arg Val Arg Arg Phe
500 505 510

Gln Gln Asp Asp Ala His Ile Phe Cys Ala Met Glu Gln Ile Glu Asp
515 520 525

Glu Ile Lys Gly Cys Leu Asp Phe Leu Arg Thr Val Tyr Ser Val Phe
530 535 540

Gly Phe Ser Phe Lys Leu Asn Leu Ser Thr Arg Pro Glu Lys Phe Leu
545 550 555 560

Gly Asp Ile Glu Val Trp Asp Gln Ala Glu Lys Gln Leu Glu Asn Ser
565 570 575

Leu Asn Glu Phe Gly Glu Lys Trp Glu Leu Asn Ser Gly Asp Gly Ala
580 585 590

Phe Tyr Gly Pro Lys Ile Asp Ile Gln Ile Lys Asp Ala Ile Gly Arg
595 600 605

Tyr His Gln Cys Ala Thr Ile Gln Leu Asp Phe Gln Leu Pro Ile Arg
610 615 620

Phe Asn Leu Thr Tyr Val Ser His Asp Gly Asp Asp Lys Lys Arg Pro
625 630 635 640

Val Ile Val His Arg Ala Ile Leu Gly Ser Val Glu Arg Met Ile Ala
645 650 655

Ile Leu Thr Glu Asn Tyr Gly Gly Lys Trp Pro Phe Trp Leu Ser Pro
660 665 670

Arg Gln Val Met Val Val Pro Val Gly Pro Thr Cys Asp Glu Tyr Ala
675 680 685

Gln Lys Val Arg Gln Gln Phe His Asp Ala Lys Phe Met Ala Asp Ile
690 695 700

Asp Leu Asp Pro Gly Cys Thr Leu Asn Lys Lys Ile Arg Asn Ala Gln
705 710 715 720

Leu Ala Gln Tyr Asn Phe Ile Leu Val Val Gly Glu Lys Glu Lys Ile
725 730 735

Ser Gly Thr Val Asn Ile Arg Thr Arg Asp Asn Lys Val His Gly Glu
740 745 750

Arg Thr Ile Ser Glu Thr Ile Glu Arg Leu Gln Gln Leu Lys Glu Phe
755 760 765

1118

Arg Ser Lys Gln Ala Glu Glu Glu Phe
770 775

<210> 1116

<211> 360

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (29)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (38)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1116

Thr Thr Ser Ala Xaa Arg Trp Asp Gly Thr Arg Gly Arg Thr Arg Gly
1 5 10 15

Arg Thr Xaa Gly Phe Gly Asn Leu Ser Ile Thr Gln Xaa Trp Met Met
20 25 30

Trp Ala Met Val Ser Xaa Met Glu Ile Asp Gln Pro Ala Gly Thr Gly
35 40 45

Thr Leu Ser Arg Thr Asn Pro Pro Thr Gln Lys Pro Pro Ser Pro Pro
50 55 60

Met Ser Gly Arg Gly Thr Leu Gly Arg Asn Thr Pro Tyr Lys Thr Leu
65 70 75 80

Glu Pro Val Lys Pro Pro Thr Val Pro Asn Asp Tyr Met Thr Ser Pro
85 90 95

Ala Arg Leu Gly Ser Gln His Ser Pro Gly Arg Thr Ala Ser Leu Asn

1119

100	105	110
Gln Arg Pro Arg Thr His Ser Gly Ser Ser Gly Gly Ser Gly Ser Arg		
115	120	125
Glu Asn Ser Gly Ser Ser Ser Ile Gly Ile Pro Ile Ala Val Pro Thr		
130	135	140
Pro Ser Pro Pro Thr Ile Gly Pro Ala Ala Pro Gly Ser Ala Pro Gly		
145	150	155
Ser Gln Tyr Gly Thr Met Thr Arg Gln Ile Ser Arg His Asn Ser Thr		
165	170	175
Thr Ser Ser Thr Ser Ser Gly Gly Tyr Arg Arg Thr Pro Ser Val Thr		
180	185	190
Ala Gln Phe Ser Ala Gln Pro His Val Asn Gly Gly Pro Leu Tyr Ser		
195	200	205
Gln Asn Ser Ile Ser Ile Ala Pro Pro Pro Pro Pro Met Pro Gln Leu		
210	215	220
Thr Pro Gln Ile Pro Leu Thr Gly Phe Val Ala Arg Val Gln Glu Asn		
225	230	235
Ile Ala Asp Ser Pro Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp Ile		
245	250	255
Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro Pro Pro Val Asp		
260	265	270
Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Asn Asp Pro Tyr Ala		
275	280	285
Asp Gly Asp Pro Ala Trp Ala Pro Lys Asn Tyr Ile Glu Lys Val Val		
290	295	300
Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu Leu Ser Phe Met		
305	310	315
Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp Tyr		
325	330	335
Glu Gly Val Cys Asn Arg Val Thr Gly Leu Phe Pro Gly Asn Tyr Val		
340	345	350
Glu Ser Ile Met His Tyr Thr Asp		
355	360	

1120

<210> 1117

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (86)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1117

Pro	Ala	Arg	Leu	Gly	Ile	Thr	Cys	His	Ser	Pro	Ala	Ile	Leu	Ser	Thr
1				5					10					15	

Ala	Leu	Trp	Gly	Gly	Ser	Ser	Pro	Ile	Pro	Asp	Ala	Pro	Thr	Thr	Gln
			20					25						30	

Trp	Lys	Val	Thr	Lys	Pro	Ala	Pro	Cys	Pro	Arg	Pro	Arg	Arg	Val	Glu
		35						40					45		

Pro	Val	Cys	Ser	Gly	Leu	Gln	Ala	Gln	Ile	Leu	His	Cys	Tyr	Arg	Asp
	50					55						60			

Arg	Pro	His	Glu	Val	Leu	Leu	Cys	Ser	Asp	Leu	Val	Lys	Ala	Tyr	Gln
	65					70					75				80

Arg	Cys	Val	Ser	Ala	Xaa	His	Lys	Gly
							85	

<210> 1118

<211> 347

<212> PRT

<213> Homo sapiens

<400> 1118

Arg	Gly	Val	Val	Asp	Ser	Glu	Asp	Leu	Pro	Leu	Asn	Ile	Ser	Arg	Glu
1				5					10					15	

Met	Leu	Gln	Gln	Ser	Lys	Ile	Leu	Lys	Val	Ile	Arg	Lys	Asn	Ile	Val
			20					25						30	

Lys	Lys	Cys	Leu	Glu	Leu	Phe	Ser	Glu	Leu	Ala	Glu	Asp	Lys	Glu	Asn
		35					40					45			

Tyr	Lys	Lys	Phe	Tyr	Glu	Ala	Phe	Ser	Lys	Asn	Leu	Lys	Leu	Gly	Ile
		50					55					60			

His	Glu	Asp	Ser	Thr	Asn	Arg	Arg	Arg	Leu	Ser	Glu	Leu	Leu	Arg	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1121

65		70		75		80
His Thr Ser Gln Ser Gly Asp Glu Met Thr Ser Leu Ser Glu Tyr Val						
	85			90		95
Ser Arg Met Lys Glu Thr Gln Lys Ser Ile Tyr Tyr Ile Thr Gly Glu						
	100		105		110	
Ser Lys Glu Gln Val Ala Asn Ser Ala Phe Val Glu Arg Val Arg Lys						
	115		120		125	
Arg Gly Phe Glu Val Val Tyr Met Thr Glu Pro Ile Asp Glu Tyr Cys						
	130		135		140	
Val Gln Gln Leu Lys Glu Phe Asp Gly Lys Ser Leu Val Ser Val Thr						
	145		150		155	160
Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Lys Lys Lys Met						
	165		170		175	
Glu Glu Ser Lys Ala Lys Phe Glu Asn Leu Cys Lys Leu Met Lys Glu						
	180		185		190	
Ile Leu Asp Lys Lys Val Glu Lys Val Thr Ile Ser Asn Arg Leu Val						
	195		200		205	
Ser Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala Asn						
	210		215		220	
Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr Met						
	225		230		235	240
Gly Tyr Met Met Ala Lys Lys His Leu Glu Ile Asn Pro Asp His Pro						
	245		250		255	
Ile Val Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp Lys						
	260		265		270	
Ala Val Lys Asp Leu Val Val Leu Leu Phe Glu Thr Ala Leu Leu Ser						
	275		280		285	
Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ser Asn Arg Ile Tyr						
	290		295		300	
Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Glu Val Ala Ala						
	305		310		315	320
Glu Glu Pro Asn Ala Ala Val Pro Asp Glu Ile Pro Pro Leu Glu Gly						
	325		330		335	
Asp Glu Asp Ala Ser Arg Met Glu Glu Val Asp						

1122

340

345

<210> 1119

<211> 293

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (170)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1119

Pro Gly Ser Pro Asp Val Asn Arg Ala Val Val Arg Pro Pro Pro Pro
1 5 10 15

Pro Pro Pro Pro Pro Pro Ala Pro Gln Pro Thr Met Ser Arg Arg Lys
20 25 30

Gln Gly Lys Pro Gln His Leu Ser Lys Arg Glu Phe Ser Pro Glu Pro
35 40 45

Leu Glu Ala Ile Leu Thr Asp Asp Glu Pro Asp His Gly Pro Leu Gly
50 55 60

Ala Pro Glu Gly Asp His Asp Leu Leu Thr Cys Gly Gln Cys Gln Met
65 70 75 80

Asn Phe Pro Leu Gly Asp Ile Leu Ile Phe Ile Glu His Lys Arg Lys
85 90 95

Gln Cys Asn Gly Ser Leu Cys Leu Glu Lys Ala Val Asp Lys Pro Pro
100 105 110

Ser Pro Ser Pro Ile Glu Met Lys Lys Ala Ser Asn Pro Val Glu Val
115 120 125

Gly Ile Gln Val Thr Pro Glu Asp Asp Asp Cys Leu Ser Thr Ser Ser
130 135 140

Arg Gly Ile Cys Pro Lys Gln Glu His Ile Ala Asp Lys Leu Leu His
145 150 155 160

Trp Arg Gly Leu Ser Ser Pro Arg Ser Xaa Thr Trp Ser Ser Asn Pro
165 170 175

His Ala Trp Asp Glu Cys Arg Ile Cys Pro Ala Gly Ile Cys Lys Asp
180 185 190

1123

Glu Pro Ser Ser Tyr Thr Cys Thr Thr Cys Lys Gln Pro Phe Thr Ser
195 200 205

Ala Trp Phe Leu Leu Gln His Ala Gln Asn Thr His Gly Leu Arg Ile
210 215 220

Tyr Leu Glu Ser Glu His Gly Ser Pro Leu Thr Pro Arg Val Gly Ile
225 230 235 240

Pro Ser Gly Leu Gly Ala Glu Cys Pro Ser Gln Pro Pro Leu His Gly
245 250 255

Ile His Ile Ala Asp Asn Asn Pro Phe Asn Leu Leu Arg Ile Pro Gly
260 265 270

Ser Val Ser Arg Glu Ala Ser Gly Leu Gly Arg Arg Ala Leu Ser Thr
275 280 285

His Ser Pro Pro Val
290

<210> 1120

<211> 190

<212> PRT

<213> Homo sapiens

<400> 1120

Ala Ala Ala Ala Ala Gly Asp Pro Gly Ala Met Gly Arg Ala Arg Asp
1 5 10 15

Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys
20 25 30

Phe Lys Leu Lys Leu Leu Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg
35 40 45

Ile Pro Arg Gly Ala Leu Leu Ser Met Asp Ala Leu Asp Leu Thr Asp
50 55 60

Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala
65 70 75 80

Asn Val Leu Arg Asp Met Gly Leu Gln Glu Met Ala Gly Gln Leu Gln
85 90 95

Ala Ala Thr His Gln Gly Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala
100 105 110

Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu His Phe Ile Asp Gln His

1124

115	120	125
Arg Ala Ala Leu Ile Ala Arg Val Thr Asn Val Glu Trp Leu Leu Asp		
130	135	140
Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg		
145	150	155
Pro Ser Pro Pro Thr Gln Ala Arg Cys Gly Ser Ser Ser Val Ser His		
165	170	175
Gln Pro Gly Thr Gly Pro Ala Arg Thr Cys Ser Ser Arg Pro		
180	185	190

<210> 1121

<211> 217

<212> PRT

<213> Homo sapiens

<400> 1121

Gly Arg Lys Trp Phe Cys Pro Tyr Lys Thr Trp Arg Lys Ala Phe Leu		
1	5	10
Ser Pro Arg Lys Arg His Val Met Ser Gln Ser Cys Gly Ala Arg Ala		
20	25	30
Glu Val Gln Ala Thr Gly Ser Asp Gly Ala Pro Thr Lys Ala Leu Gly		
35	40	45
Leu Val Arg Val Ala Ala Val Ser Ser Asp Ser Cys Val Val Pro Met		
50	55	60
Val Glu Lys Lys Thr Ser Val Arg Ser Gln Asp Pro Gly Gln Arg Arg		
65	70	75
Val Leu Asp Arg Ala Ala Arg Gln Arg Arg Ile Asn Arg Gln Leu Glu		
85	90	95
Ala Leu Glu Asn Asp Asn Phe Gln Asp Asp Pro His Ala Gly Leu Pro		
100	105	110
Gln Leu Gly Lys Arg Leu Pro Gln Phe Asp Asp Asp Ala Asp Thr Gly		
115	120	125
Lys Lys Lys Lys Lys Thr Arg Gly Asp His Phe Lys Leu Arg Phe Arg		
130	135	140
Lys Asn Phe Gln Ala Leu Leu Glu Glu Gln Asn Leu Ser Val Ala Glu		
145	150	155
		160

1125

Gly Pro Asn Tyr Leu Thr Ala Cys Ala Gly Pro Pro Ser Arg Pro Gln
165 170 175

Arg Pro Phe Cys Ala Val Cys Gly Phe Pro Ser Pro Tyr Thr Cys Val
180 185 190

Ser Cys Gly Ala Arg Tyr Cys Thr Val Arg Cys Leu Gly Thr His Gln
195 200 205

Glu Thr Arg Cys Leu Lys Trp Thr Val
210 215

<210> 1122

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1122

Gly Asn Cys Gln Lys Cys Ala Phe Gly Tyr Ser Gly Leu Asp Cys Lys
1 5 10 15

Asp Lys Phe Gln Leu Ile Leu Thr Ile Val Gly Thr Ile Ala Gly Ile
20 25 30

Val Ile Leu Ser Met Ile Ile Ala Leu Ile Val Thr Ala Arg Ser Asn
35 40 45

Asn Lys Thr Lys His Ile Glu Glu Asn Leu Ile Asp Glu Asp Phe
50 55 60

Gln Asn Leu Lys Leu Arg Ser Thr Gly Phe Thr Asn Leu Gly Ala Glu
65 70 75 80

Gly Ser Val Phe Pro Lys Val Arg Ile Thr Ala Ser Arg Asp Ser Gln
85 90 95

Met Gln Asn Pro Tyr Ser Ser His Ser Ser Met Pro Arg Pro Asp Tyr
100 105 110

<210> 1123

<211> 216

<212> PRT

<213> Homo sapiens

1126

<400> 1123

Gly Lys Leu Val Cys Gly Met Val Ser Tyr Leu Asn Asp Leu Pro Ser
1 5 10 15

Gln Arg Ile Gln Pro Gln Gln Val Ala Val Trp Pro Thr Met Val Asp
20 25 30

Ile Asn Ser Pro Glu Ser Leu Thr Glu Ala Tyr Lys Leu Arg Ala Ala
35 40 45

Arg Leu Val Glu Ile Ala Ala Lys Asn Leu Gln Lys Glu Val Ile His
50 55 60

Arg Lys Ser Lys Glu Val Ala Trp Asn Leu Thr Ser Val Asp Leu Val
65 70 75 80

Arg Ala Ser Glu Ala His Cys His Tyr Val Val Val Lys Leu Phe Ser
85 90 95

Glu Lys Leu Leu Lys Ile Gln Asp Lys Ala Ile Gln Ala Val Leu Arg
100 105 110

Ser Leu Cys Leu Leu Tyr Ser Leu Tyr Gly Ile Ser Gln Asn Ala Gly
115 120 125

Asp Phe Leu Gln Gly Ser Ile Met Thr Glu Pro Gln Ile Thr Gln Val
130 135 140

Asn Gln Arg Val Lys Glu Leu Leu Thr Leu Ile Arg Ser Asp Ala Val
145 150 155 160

Ala Leu Val Asp Ala Phe Asp Phe Gln Asp Val Thr Leu Gly Ser Val
165 170 175

Leu Gly Arg Tyr Asp Gly Asn Val Tyr Glu Asn Leu Phe Glu Trp Ala
180 185 190

Lys Asn Ser Pro Leu Asn Lys Ala Glu Val His Glu Ser Tyr Lys His
195 200 205

Leu Lys Ser Leu Gln Ser Lys Leu
210 215

<210> 1124

<211> 218

<212> PRT

<213> Homo sapiens

1127

<400> 1124

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Pro Ser Pro Arg Pro Pro Asp Pro Glu Ser Ser Gln Leu Arg Pro Gly
 1             5             10             15

Gly Asp Gly Ala Glu Leu Arg Val Leu Val Asp Met Asp Gly Val Leu
      20             25             30

Ala Asp Phe Glu Ala Gly Leu Leu Arg Gly Phe Arg Arg Arg Phe Pro
      35             40             45

Glu Glu Pro His Val Pro Leu Glu Gln Arg Arg Gly Phe Leu Ala Arg
      50             55             60

Glu Gln Tyr Arg Ala Leu Arg Pro Asp Leu Ala Asp Lys Val Ala Ser
      65             70             75             80

Val Tyr Glu Ala Pro Gly Phe Phe Leu Asp Leu Glu Pro Ile Pro Gly
      85             90             95

Ala Leu Asp Ala Val Arg Glu Met Asn Asp Leu Pro Asp Thr Gln Val
      100            105            110

Phe Ile Cys Thr Ser Pro Leu Leu Lys Tyr His His Cys Val Gly Glu
      115            120            125

Lys Tyr Arg Trp Val Glu Gln His Leu Gly Pro Gln Phe Val Glu Arg
      130            135            140

Ile Ile Leu Thr Arg Asp Lys Thr Val Val Leu Gly Asp Leu Leu Ile
      145            150            155            160

Asp Asp Lys Asp Thr Val Arg Gly Gln Glu Glu Thr Pro Ser Trp Glu
      165            170            175

His Ile Leu Phe Thr Cys Cys His Asn Arg His Leu Val Leu Pro Pro
      180            185            190

Thr Arg Arg Arg Leu Leu Ser Trp Ser Asp Asn Trp Arg Glu Ile Leu
      195            200            205

Asp Ser Lys Arg Gly Ala Ala Gln Arg Glu
      210            215

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<210> 1125

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1125

1128

Met Arg Arg Arg Val Phe Phe Leu His Arg Cys Ser Ile Leu Val Phe
 1 5 10 15
 Leu Phe Pro Cys Lys Cys Asn Gln Met Pro Phe Tyr Met Trp Thr Tyr
 20 25 30
 Leu Tyr Trp Pro Asn Ile Phe Phe Leu Leu Ser Leu Phe Phe Phe Pro
 35 40 45
 Phe Phe Leu Leu Pro Leu Phe Leu Tyr Ser Phe Leu Phe Leu Phe Phe
 50 55 60
 Phe Phe Phe Ser Phe Phe Phe Gly Ser Cys Cys Tyr Pro Arg His Phe
 65 70 75 80
 Thr Ser Pro Ser Leu Lys Gly
 85

<210> 1126

<211> 174

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (173)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1126

Pro Pro Leu Gly Lys Lys Xaa Glu Leu His Arg Gly Gly Gly Arg Ser
 1 5 10 15
 Arg Leu Glu Glu Phe Gln Met Arg Ala Arg Pro Arg Pro Arg Pro Leu
 20 25 30
 Trp Ala Thr Val Leu Ala Leu Gly Ala Leu Ala Gly Val Gly Val Gly
 35 40 45
 Gly Pro Asn Ile Cys Thr Thr Arg Gly Val Ser Ser Cys Gln Gln Cys
 50 55 60
 Leu Ala Val Ser Pro Met Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro
 65 70 75 80

1129

Leu Gly Ser Pro Arg Cys Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn
 85 90 95
 Cys Ala Pro Glu Ser Ile Glu Phe Pro Val Ser Glu Ala Arg Val Leu
 100 105 110
 Glu Asp Arg Pro Leu Ser Asp Lys Gly Ser Gly Asp Ser Ser Gln Val
 115 120 125
 Thr Gln Val Ser Pro Gln Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp
 130 135 140
 Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val
 145 150 155 160
 Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Xaa Gly
 165 170

<210> 1127

<211> 359

<212> PRT

<213> Homo sapiens

<400> 1127

Pro Gln Pro Phe Gln Gly Ser Gly Cys Val Ile Ala Ile Leu Gly Lys
 1 5 10 15
 Arg Cys Ser Arg Pro Trp Arg Thr Trp Arg Gly Arg Thr Pro Ser Thr
 20 25 30
 Arg His Ile Cys Ser Trp Cys Thr Met Val Ser Gly Thr Ser Ala Ala
 35 40 45
 Val Glu Glu Tyr Ser Cys Glu Phe Gly Ser Ala Lys Tyr Tyr Ala Leu
 50 55 60
 Cys Gly Phe Gly Gly Val Leu Ser Cys Gly Leu Thr His Thr Ala Val
 65 70 75 80
 Val Pro Leu Asp Leu Val Lys Cys Arg Met Gln Val Asp Pro Gln Lys
 85 90 95
 Tyr Lys Gly Ile Phe Asn Gly Phe Ser Val Thr Leu Lys Glu Asp Gly
 100 105 110
 Val Arg Gly Leu Ala Lys Gly Trp Ala Pro Thr Phe Leu Gly Tyr Ser
 115 120 125
 Met Gln Gly Leu Cys Lys Phe Gly Phe Tyr Glu Val Phe Lys Val Leu

1130

130	135	140
Tyr Ser Asn Met Leu Gly Glu Glu Asn Thr Tyr Leu Trp Arg Thr Ser		
145	150	155 160
Leu Tyr Leu Ala Ala Ser Ala Ser Ala Glu Phe Phe Ala Asp Ile Ala		
	165	170 175
Leu Ala Pro Met Glu Ala Ala Lys Val Arg Ile Gln Thr Gln Pro Gly		
	180	185 190
Tyr Ala Asn Thr Leu Arg Asp Ala Ala Pro Lys Met Tyr Lys Glu Glu		
	195	200 205
Gly Leu Lys Ala Phe Tyr Lys Gly Val Ala Pro Leu Trp Met Arg Gln		
	210	215 220
Ile Pro Tyr Thr Met Met Lys Phe Ala Cys Phe Glu Arg Thr Val Glu		
	225	230 235 240
Ala Leu Tyr Lys Phe Val Val Pro Lys Pro Arg Ser Glu Cys Ser Lys		
	245	250 255
Pro Glu Gln Leu Val Val Thr Phe Val Ala Gly Tyr Ile Ala Gly Val		
	260	265 270
Phe Cys Ala Ile Val Ser His Pro Ala Asp Ser Val Val Ser Val Leu		
	275	280 285
Asn Lys Glu Lys Gly Ser Ser Ala Ser Leu Val Leu Lys Arg Leu Gly		
	290	295 300
Phe Lys Gly Val Trp Lys Gly Leu Phe Ala Arg Ile Ile Met Ile Gly		
	305	310 315 320
Thr Leu Thr Ala Leu Gln Trp Phe Ile Tyr Asp Ser Val Lys Val Tyr		
	325	330 335
Phe Arg Leu Pro Arg Pro Pro Pro Pro Glu Met Pro Glu Ser Leu Lys		
	340	345 350
Lys Lys Leu Gly Leu Thr Gln		
	355	

<210> 1128

<211> 399.

<212> PRT

<213> Homo sapiens

1131

<220>

<221> SITE

<222> (208)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (349)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1128

Leu Glu Pro Pro Ala Glu Pro Leu Gln Tyr Leu Ala Cys Tyr Arg Phe
 1 5 10 15

His Cys Ser His Gln Leu Gly Asp Asn Met Trp Phe Leu Thr Thr Leu
 20 25 30

Leu Leu Trp Val Pro Val Asp Gly Gln Val Asp Thr Thr Lys Ala Val
 35 40 45

Ile Thr Leu Gln Pro Pro Trp Val Ser Val Phe Gln Glu Glu Thr Val
 50 55 60

Thr Leu His Cys Glu Val Leu His Leu Pro Gly Ser Ser Ser Thr Gln
 65 70 75 80

Trp Phe Leu Asn Gly Thr Ala Thr Gln Thr Ser Thr Pro Ser Tyr Arg
 85 90 95

Ile Thr Ser Ala Ser Val Asn Asp Ser Gly Glu Tyr Arg Cys Gln Arg
 100 105 110

Gly Leu Ser Gly Arg Ser Asp Pro Ile Gln Leu Glu Ile His Arg Gly
 115 120 125

Trp Leu Leu Leu Gln Val Ser Ser Arg Val Phe Thr Glu Gly Glu Pro
 130 135 140

Leu Ala Leu Arg Cys His Ala Trp Lys Asp Lys Leu Val Tyr Asn Val
 145 150 155 160

Leu Tyr Tyr Arg Asn Gly Lys Ala Phe Lys Phe Phe His Trp Asn Ser
 165 170 175

Asn Leu Thr Ile Leu Lys Thr Asn Ile Ser His Asn Gly Thr Tyr His
 180 185 190

Cys Ser Gly Met Gly Lys His Arg Tyr Thr Ser Ala Gly Ile Ser Xaa
 195 200 205

Thr Val Lys Glu Leu Phe Pro Ala Pro Val Leu Asn Ala Ser Val Thr

1132

210	215	220
Ser Pro Leu Leu Glu Gly Asn Leu Val Thr Leu Ser Cys Glu Thr Lys		
225	230	235 240
Leu Leu Leu Gln Arg Pro Gly Leu Gln Leu Tyr Phe Ser Phe Tyr Met		
	245	250 255
Gly Ser Lys Thr Leu Arg Gly Arg Asn Thr Ser Ser Glu Tyr Gln Ile		
	260	265 270
Leu Thr Ala Arg Arg Glu Asp Ser Gly Leu Tyr Trp Cys Glu Ala Ala		
	275	280 285
Thr Glu Asp Gly Asn Val Leu Lys Arg Ser Pro Glu Leu Glu Leu Gln		
	290	295 300
Val Leu Gly Leu Gln Leu Pro Thr Pro Val Trp Phe His Val Leu Phe		
	305	310 315 320
Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val Leu Trp Val		
	325	330 335
Thr Ile Arg Lys Glu Leu Lys Arg Lys Lys Lys Trp Xaa Leu Glu Ile		
	340	345 350
Ser Leu Asp Ser Gly His Glu Lys Lys Val Ile Ser Ser Leu Gln Glu		
	355	360 365
Asp Arg His Leu Glu Glu Glu Leu Lys Cys Gln Glu Gln Lys Glu Glu		
	370	375 380
Gln Leu Gln Glu Gly Val His Arg Lys Glu Pro Gln Gly Ala Thr		
	385	390 395

<210> 1129

<211> 147

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

1133

<400> 1129

Glu Ile Leu Phe Ile Phe Xaa Xaa Phe Phe Lys Gly Leu Ser Asn Ser
 1 5 10 15

Ala Ala Ala Met Ala Pro Val Lys Lys Leu Val Val Lys Gly Gly Lys
 20 25 30

Lys Lys Lys Gln Val Leu Lys Phe Thr Leu Asp Cys Thr His Pro Val
 35 40 45

Glu Asp Gly Ile Met Asp Ala Ala Asn Phe Glu Gln Phe Leu Gln Glu
 50 55 60

Arg Ile Lys Val Asn Gly Lys Ala Gly Asn Leu Gly Gly Gly Val Val
 65 70 75 80

Thr Ile Glu Arg Ser Lys Ser Lys Ile Thr Val Thr Ser Glu Val Pro
 85 90 95

Phe Ser Lys Arg Tyr Leu Lys Tyr Leu Thr Lys Lys Tyr Leu Lys Lys
 100 105 110

Asn Asn Leu Arg Asp Trp Leu Arg Val Val Ala Asn Ser Lys Glu Ser
 115 120 125

Tyr Glu Leu Arg Tyr Phe Gln Ile Asn Gln Asp Glu Glu Glu Glu Glu
 130 135 140

Asp Glu Asp
 145

<210> 1130

<211> 91

<212> PRT

<213> Homo sapiens

<400> 1130

Asn Cys Ser Pro Ala Phe Tyr Gly Ser Ser Leu Pro Cys Pro Gln Thr
 1 5 10 15

Gln Gln Lys Arg Arg Gly Arg Ile Arg Gly Leu Ser Arg Pro Ala Pro
 20 25 30

Leu Pro Thr Cys His Thr Arg Cys Glu Phe Glu His Ser Pro Glu Met
 35 40 45

Glu Thr Ser His Pro Gln Leu Asn Asn Gly Pro Phe Met Pro Thr Leu
 50 55 60

1134

Pro Thr Arg Arg Gly Gln Arg Cys Thr Arg Arg Pro Ser Ser Ser Pro
 65 70 75 80

Ser Ser Ala Pro Ser His Tyr Ser Trp Phe Tyr
 85 90

<210> 1131

<211> 510

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (228)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (352)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1131

Thr Ser Glu Glu Ser Arg Pro Arg Leu Ser Gln Leu Ser Val Thr Asp
 1 5 10 15

Val Thr Thr Ser Ser Leu Arg Leu Asn Trp Glu Ala Pro Pro Gly Ala
 20 25 30

Phe Asp Ser Phe Leu Leu Arg Phe Gly Val Pro Ser Pro Ser Thr Leu
 35 40 45

Glu Pro His Pro Arg Pro Leu Gln Arg Glu Leu Met Val Pro Gly
 50 55 60

Thr Arg His Ser Ala Val Leu Arg Asp Leu Arg Ser Gly Thr Leu Tyr
 65 70 75 80

Ser Leu Thr Leu Tyr Gly Leu Arg Gly Pro His Lys Ala Asp Ser Ile
 85 90 95

Gln Gly Thr Ala Arg Thr Leu Ser Pro Val Leu Glu Ser Pro Arg Asp
 100 105 110

Leu Gln Phe Ser Glu Ile Arg Glu Thr Ser Ala Lys Val Asn Trp Met
 115 120 125

Pro Pro Pro Ser Arg Ala Asp Ser Phe Lys Val Ser Tyr Gln Leu Ala
 130 135 140

1135

Asp Gly Gly Glu Pro Gln Ser Val Gln Val Asp Gly Gln Ala Arg Thr
 145 150 155 160
 Gln Lys Leu Gln Gly Leu Ile Pro Gly Ala Arg Tyr Glu Val Thr Val
 165 170 175
 Val Ser Val Arg Gly Phe Glu Glu Ser Glu Pro Leu Thr Gly Phe Leu
 180 185 190
 Thr Thr Val Pro Asp Gly Pro Thr Gln Leu Arg Ala Leu Asn Leu Thr
 195 200 205
 Glu Gly Phe Ala Val Leu His Trp Lys Pro Pro Gln Asn Pro Val Asp
 210 215 220
 Thr Tyr Asp Xaa Gln Val Thr Ala Pro Gly Ala Pro Pro Leu Gln Ala
 225 230 235 240
 Glu Thr Pro Gly Ser Ala Val Asp Tyr Pro Leu His Asp Leu Val Leu
 245 250 255
 His Thr Asn Tyr Thr Ala Thr Val Arg Gly Leu Arg Gly Pro Asn Leu
 260 265 270
 Thr Ser Pro Ala Ser Ile Thr Phe Thr Thr Gly Leu Glu Ala Pro Arg
 275 280 285
 Asp Leu Glu Ala Lys Glu Val Thr Pro Arg Thr Ala Leu Leu Thr Trp
 290 295 300
 Thr Glu Pro Pro Val Arg Pro Ala Gly Tyr Leu Leu Ser Phe His Thr
 305 310 315 320
 Pro Gly Gly Gln Thr Gln Glu Ile Leu Leu Pro Gly Gly Ile Thr Ser
 325 330 335
 His Gln Leu Leu Gly Leu Phe Pro Ser Thr Ser Tyr Asn Ala Arg Xaa
 340 345 350
 Gln Ala Met Trp Gly Gln Ser Leu Leu Pro Pro Val Ser Thr Ser Phe
 355 360 365
 Thr Thr Gly Gly Leu Arg Ile Pro Phe Pro Arg Asp Cys Gly Glu Glu
 370 375 380
 Met Gln Asn Gly Ala Gly Ala Ser Arg Thr Ser Thr Ile Phe Leu Asn
 385 390 395 400
 Gly Asn Arg Glu Arg Pro Leu Asn Val Phe Cys Asp Met Glu Thr Asp
 405 410 415

1136

Gly Gly Gly Trp Leu Val Phe Gln Arg Arg Met Asp Gly Gln Thr Asp
420 425 430

Phe Trp Arg Asp Trp Glu Asp Tyr Ala His Gly Phe Gly Asn Ile Ser
435 440 445

Gly Glu Phe Trp Leu Gly Asn Glu Ala Leu His Ser Leu Thr Gln Ala
450 455 460

Gly Asp Tyr Ser Met Arg Val Asp Leu Arg Ala Gly Asp Glu Ala Val
465 470 475 480

Phe Ala Gln Tyr Asp Ser Phe His Val Asp Ser Ala Ala Glu Tyr Tyr
485 490 495

Arg Leu His Leu Glu Gly Tyr His Gly Thr Ala Gly Thr Pro
500 505 510

<210> 1132

<211> 430

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (182)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (216)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (408)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (410)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (414)

<223> Xaa equals any of the naturally occurring L-amino acids

1137

<220>

<221> SITE

<222> (420)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (428)

<223> Xaa equals any of the naturally occurring L-amino acids .

<400> 1132

Arg	Thr	Ala	Asp	Gln	Thr	Val	Thr	Ala	Ala	Leu	Thr	Lys	Arg	Ser	Trp
1				5						10				15	

Asn	Ser	Ser	Ser	Ser	Pro	Gln	Arg	Arg	Thr	Glu	Gln	Thr	Ala	Glu	Thr
			20					25					30		

Met	Glu	Ser	Pro	Ser	Ala	Pro	Pro	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
		35						40				45			

Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
	50						55				60				

Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
	65				70					75					80

Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
			85						90					95	

Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
		100						105					110		

Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
		115					120					125			

Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
	130						135					140			

Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
	145				150					155					160

Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
			165					170						175	

Pro	Lys	Pro	Ser	Ile	Xaa	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys
			180					185					190		

Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
		195						200				205			

Leu	Trp	Trp	Val	Asn	Asn	Gln	Xaa	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

210

220

Gly Met Met Xaa Asp Pro Met Asn Val Glu Ser Xaa Thr Asn
420 425 430

<222> (1)

1139

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (140)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (186)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (194)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (308)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (534)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (535)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1133

Xaa His Ala Ser Ala Ala Xaa Pro Thr Val Thr Ala Ala Leu Thr Arg
1 5 10 15

Ala Phe Leu Glu Leu Lys Leu Ser Thr Lys Arg Trp Thr Glu Lys Thr
20 25 30

Ala Glu Thr Met Gly Pro Pro Ser Ala Pro Pro Cys Arg Leu His Val
35 40 45

Pro Trp Lys Glu Val Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn
50 55 60

Pro Pro Thr Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val

1140

65		70		75		80									
Ala	Glu	Gly	Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Leu	Pro	Gln	Asn
				85					90					95	
Arg	Ile	Gly	Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Ser
			100					105					110		
Leu	Ile	Val	Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro
		115						120					125		
Ala	Tyr	Ser	Gly	Arg	Glu	Thr	Ile	Tyr	Pro	Asn	Xaa	Ser	Leu	Leu	Ile
	130							135					140		
Gln	Asn	Val	Thr	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	Gln	Val	Ile
145					150					155					160
Lys	Ser	Asp	Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	His	Val	Tyr
			165						170					175	
Pro	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Xaa	Asn	Asn	Ser	Asn	Pro	Val
			180					185					190		
Glu	Xaa	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Val	Gln	Asn
		195						200					205		
Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser	Pro
	210							215				220			
Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Met	Thr	Leu	Thr	Leu	Leu	Ser	Val
225					230					235					240
Lys	Arg	Asn	Asp	Ala	Gly	Ser	Tyr	Glu	Cys	Glu	Ile	Gln	Asn	Pro	Ala
			245						250					255	
Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro
			260					265					270		
Asp	Gly	Pro	Thr	Ile	Ser	Pro	Ser	Lys	Ala	Asn	Tyr	Arg	Pro	Gly	Glu
		275						280				285			
Asn	Leu	Asn	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr
		290						295				300			
Ser	Trp	Phe	Xaa	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe
305					310					315					320
Ile	Pro	Asn	Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala
				325					330					335	
His	Asn	Ser	Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr

1141

340	345	350
Val Tyr Ala Glu Pro Pro Lys	Pro Phe Ile Thr Ser	Asn Asn Ser Asn
355	360	365
Pro Val Glu Asp Glu Asp Ala Val	Ala Leu Thr Cys Glu Pro Glu Ile	
370	375	380
Gln Asn Thr Thr Tyr Leu Trp Trp	Val Asn Asn Gln Ser Leu Pro Val	
385	390	395 400
Ser Pro Arg Leu Gln Leu Ser Asn	Asp Asn Arg Thr Leu Thr Leu Leu	
405	410	415
Ser Val Thr Arg Asn Asp Val Gly	Pro Tyr Glu Cys Gly Ile Gln Asn	
420	425	430
Glu Leu Ser Val Asp His Ser Asp	Pro Val Ile Leu Asn Val Leu Tyr	
435	440	445
Gly Pro Asp Asp Pro Thr Ile Ser	Pro Ser Tyr Thr Tyr Tyr Arg Pro	
450	455	460
Gly Val Asn Leu Ser Leu Ser Cys	His Ala Ala Ser Asn Pro Pro Ala	
465	470	475 480
Gln Tyr Ser Trp Leu Ile Asp Gly	Asn Ile Gln Gln His Thr Gln Glu	
485	490	495
Leu Phe Ile Ser Asn Ile Thr Glu	Lys Asn Ser Gly Leu Tyr Thr Cys	
500	505	510
Gln Ala Asn Asn Ser Ala Ser Gly	His Ser Arg Thr Thr Val Lys Thr	
515	520	525
Ile Thr Val Ser Ala Xaa Xaa Pro	Lys Pro Ser Ile Ser Ser Asn Asn	
530	535	540
Ser Lys Pro Val Glu Asp Lys Asp	Ala Val Ala Phe Thr Cys Glu Pro	
545	550	555 560
Glu Ala Gln Asn Thr Thr Tyr Leu	Trp Trp Val Asn Gly Gln Ser Leu	
565	570	575
Pro Val Ser Pro Arg Leu Gln Leu	Ser Asn Gly Asn Arg Thr Leu Thr	
580	585	590
Leu Phe Asn Val Thr Arg Asn Asp	Ala Arg Ala Tyr Val Cys Gly Ile	
595	600	605
Gln Asn Ser Val Ser Ala Asn Arg	Ser Asp Pro Val Thr Leu Asp Val	

1142

610 615 620
 Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr
 625 630 635 640
 Leu Ser Gly Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro
 645 650 655
 Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr
 660 665 670
 Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr
 675 680 685
 Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val
 690 695 700
 Lys Ser Ile Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala
 705 710 715 720
 Gly Ala Thr Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu
 725 730 735
 Ile

<210> 1134

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1134

Phe Gly Thr Xaa Arg Ser Val Val Leu Leu Leu Val Ala Val Arg Leu
 1 5 10 15

His Thr Leu Leu Ser Cys Pro Leu Glu Gln Pro Ala Gly Thr Glu Trp
 20 25 30

Ile Leu Glu Glu Gly Val Thr Thr Gly Pro Pro Arg Lys Pro Arg Ala
 35 40 45

Asp Ile Tyr Asn Leu Arg Ser Pro Asp Glu Phe Ile Val Gly Gln Asn
 50 55 60

1143

Gln Ala Leu Ile Glu Pro Gly
65 70

<210> 1135

<211> 244

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (101)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1135

Gly Leu Arg Arg Leu Asp Ser Ala Ser Gly Thr Val Tyr Thr Ala Met
1 5 10 15

Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
20 25 30

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
35 40 45

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
50 55 60

Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
65 70 75 80

Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
85 90 95

Val Cys Arg Glu Xaa Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
100 105 110

Ile Thr Pro Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr
115 120 125

Trp Met Ala Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val
130 135 140

Asp Ile Trp Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu
145 150 155 160

Pro Pro Tyr Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala
165 170 175

Thr Asn Gly Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile
180 185 190

1144

Phe Arg Asp Phe Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg
 195 200 205

Gly Ser Ala Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys
 210 215 220

Pro Leu Ser Ser Leu Thr Pro Leu Ile Ala Ala Ala Lys Glu Ala Thr
 225 230 235 240

Lys Asn Asn His

<210> 1136

<211> 166

<212> PRT

<213> Homo sapiens

<400> 1136

Arg Ala Glu Phe Gly Thr Ser Pro Arg Ala Arg Arg His Glu Cys Cys
 1 5 10 15

Arg Phe Leu Asp Asp Asn Gln Ile Ile Thr Ser Ser Gly Asp Thr Thr
 20 25 30

Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln Thr Val Gly Phe Ala
 35 40 45

Gly His Ser Gly Asp Val Met Ser Leu Ser Leu Ala Pro Asp Gly Arg
 50 55 60

Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ile Lys Leu Trp Asp Val
 65 70 75 80

Arg Asp Ser Met Cys Arg Gln Thr Phe Ile Gly His Glu Ser Asp Ile
 85 90 95

Asn Ala Val Ala Phe Phe Pro Asn Gly Tyr Ala Phe Thr Thr Gly Ser
 100 105 110

Asp Asp Ala Thr Cys Arg Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu
 115 120 125

Leu Met Tyr Ser His Asp Asn Ile Ile Cys Gly Ile Thr Ser Val Ala
 130 135 140

Phe Ser Arg Ser Asp Gly Cys Cys Ser Leu Ala Thr Thr Thr Ser Thr
 145 150 155 160

1145

Ala Thr Ser Gly Met Pro
165

<210> 1137

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1137

Thr Asn Asn Lys Ser Leu Val Gln Leu Lys His Ile Ser Asn Asp Phe
1 5 10 15

Ser Lys Phe Lys Val Asp His Asp Arg Ile Ile Lys Asp Arg Lys Asp
20 25 30

Leu Ser Asn Leu Val Met Thr Ile Ile Ser Ile Phe Ala Glu Leu Lys
35 40 45

Ile Phe Asn Phe Ile Asn Met Leu Leu Gln Leu Pro Asp Leu Lys Lys
50 55 60

Lys Ser Phe Pro His Ser Gln Leu Lys Val Arg Thr Leu His Phe
65 70 75

<210> 1138

<211> 397

<212> PRT

<213> Homo sapiens

<400> 1138

Pro Thr Arg Pro Ser Ser Val Ser Arg Arg Asp Lys Ser Lys Gln Val
1 5 10 15

Trp Glu Ala Val Leu Leu Pro Leu Ser Leu Leu Ser Met Met Asp Leu
20 25 30

Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile Glu Asp Tyr Leu
35 40 45

Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His Ala Ile Asp Ile
50 55 60

Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly Ser Ser Tyr Pro
65 70 75 80

Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser Gly Lys Gly Thr
85 90 95

1146

Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val Phe Leu Ser Pro
100 105 110

Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly Glu Phe Ile Gln
115 120 125

Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu Arg Ala Phe Ser
130 135 140

Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn Pro Arg Ala Leu
145 150 155 160

Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly Val Glu Phe Asp
165 170 175

Val Leu Pro Ala Phe Asp Ala Leu Asp Phe Ala Arg Thr Gly Gln Leu
180 185 190

Thr Gly Gly Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu
195 200 205

Glu Cys Thr Asp Leu Gln Lys Glu Gly Glu Phe Ser Thr Cys Phe Thr
210 215 220

Glu Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser
225 230 235 240

Leu Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu
245 250 255

Gly Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala
260 265 270

Trp Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe
275 280 285

Arg Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr
290 295 300

Trp Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu
305 310 315 320

Arg Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp
325 330 335

Pro Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu
340 345 350

Ala Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp
355 360 365

1147

Asp Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Val Arg Pro Pro Ala
 370 375 380

Ser Ser Leu Pro Phe Ile Pro Ala Pro Leu His Glu Ala
 385 390 395

<210> 1139

<211> 180

<212> PRT

<213> Homo sapiens

<400> 1139

Phe Leu Leu Ser Asn Ala Arg Trp Ser Asn Arg Pro Asp Thr Ala Thr
 1 5 10 15

Ala Leu Ala Gly Gly Ala Val Met Pro Glu Leu Ile Leu Ser Pro Ala
 20 25 30

Thr Ala Pro His Pro Leu Lys Met Phe Ala Cys Ser Lys Phe Val Ser
 35 40 45

Thr Pro Ser Leu Val Lys Ser Thr Ser Gln Leu Leu Ser Arg Pro Leu
 50 55 60

Ser Ala Val Val Leu Lys Arg Pro Glu Ile Leu Thr Asp Glu Ser Leu
 65 70 75 80

Ser Ser Leu Ala Val Ser Cys Pro Leu Thr Ser Leu Val Ser Ser Arg
 85 90 95

Ser Phe Gln Thr Ser Ala Ile Ser Arg Asp Ile Asp Thr Ala Ala Lys
 100 105 110

Phe Ile Gly Ala Gly Ala Ala Thr Val Gly Val Ala Gly Ser Gly Ala
 115 120 125

Gly Ile Gly Thr Val Phe Gly Ser Leu Ile Ile Gly Tyr Ala Arg Asn
 130 135 140

Pro Ser Leu Lys Gln Gln Leu Phe Ser Tyr Ala Ile Leu Gly Phe Ala
 145 150 155 160

Leu Ser Glu Ala Met Gly Leu Phe Cys Leu Met Val Ala Phe Leu Ile
 165 170 175

Leu Phe Ala Met
 180

1148

<210> 1140

<211> 484

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (25)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1140

Trp Leu Leu Arg Ser Pro Gly Lys Leu Thr Ala Arg Glu Arg Ile Ser
1 5 10 15

Leu Leu Leu Asp Pro Gly Ser Phe Xaa Glu Ser Asp Met Phe Val Glu
20 25 30

His Arg Cys Ala Asp Phe Gly Met Ala Ala Asp Lys Asn Lys Phe Pro
35 40 45

Gly Asp Ser Val Val Thr Gly Arg Gly Arg Ile Asn Gly Arg Leu Val
50 55 60

Tyr Val Phe Ser Gln Asp Phe Thr Val Phe Gly Gly Ser Leu Ser Gly
65 70 75 80

Ala His Ala Gln Lys Ile Cys Lys Ile Met Asp Gln Ala Ile Thr Val
85 90 95

Gly Ala Pro Val Ile Gly Leu Asn Asp Ser Gly Gly Ala Arg Ile Gln
100 105 110

Glu Gly Val Glu Ser Leu Ala Gly Tyr Ala Asp Ile Phe Leu Arg Asn
115 120 125

Val Thr Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Pro
130 135 140

Cys Ala Gly Gly Ala Val Tyr Ser Pro Ala Leu Thr Asp Phe Thr Phe
145 150 155 160

Met Val Lys Asp Thr Ser Tyr Leu Phe Ile Thr Gly Pro Asp Val Val
165 170 175

Lys Ser Val Thr Asn Glu Asp Val Thr Gln Glu Glu Leu Gly Gly Ala
180 185 190

Lys Thr His Thr Thr Met Ser Gly Val Ala His Arg Ala Phe Glu Asn
195 200 205

1149

Asp Val Asp Ala Leu Cys Asn Leu Arg Asp Phe Phe Asn Tyr Leu Pro
210 215 220

Leu Ser Ser Gln Asp Pro Ala Pro Val Arg Glu Cys His Asp Pro Ser
225 230 235 240

Asp Arg Leu Val Pro Glu Leu Asp Thr Ile Val Pro Leu Glu Ser Thr
245 250 255

Lys Ala Tyr Asn Met Val Asp Ile Ile His Ser Val Val Asp Glu Arg
260 265 270

Glu Phe Phe Glu Ile Met Pro Asn Tyr Ala Lys Asn Ile Ile Val Gly
275 280 285

Phe Ala Arg Met Asn Gly Arg Thr Val Gly Ile Val Gly Asn Gln Pro
290 295 300

Lys Val Ala Ser Gly Cys Leu Asp Ile Asn Ser Ser Val Lys Gly Ala
305 310 315 320

Arg Phe Val Arg Phe Cys Asp Ala Phe Asn Ile Pro Leu Ile Thr Phe
325 330 335

Val Asp Val Pro Gly Phe Leu Pro Gly Thr Ala Gln Glu Tyr Gly Gly
340 345 350

Ile Ile Arg His Gly Ala Lys Leu Leu Tyr Ala Phe Ala Glu Ala Thr
355 360 365

Val Pro Lys Val Thr Val Ile Thr Arg Lys Ala Tyr Gly Gly Ala Tyr
370 375 380

Asp Val Met Ser Ser Lys His Leu Cys Gly Asp Thr Asn Tyr Ala Trp
385 390 395 400

Pro Thr Ala Glu Ile Ala Val Met Gly Ala Lys Gly Ala Val Glu Ile
405 410 415

Ile Phe Lys Gly His Glu Asn Val Glu Ala Ala Gln Ala Glu Tyr Ile
420 425 430

Glu Lys Phe Ala Asn Pro Phe Pro Ala Ala Val Arg Gly Phe Val Asp
435 440 445

Asp Ile Ile Gln Pro Ser Ser Thr Arg Ala Arg Ile Cys Cys Asp Leu
450 455 460

Asp Val Leu Ala Ser Lys Lys Val Gln Arg Pro Trp Arg Lys His Ala
465 470 475 480

1150

Asn Ile Pro Leu

<210> 1141

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (53)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (54)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1141

Leu	Xaa	Glu	Leu	Glu	Arg	Tyr	Val	Thr	Ser	Cys	Leu	Arg	Lys	Lys	Arg
1				5					10					15	

Lys	Pro	Gln	Ala	Glu	Lys	Val	Asp	Val	Ile	Ala	Gly	Ser	Ser	Lys	Met
		20					25							30	

Lys	Gly	Phe	Ser	Ser	Ser	Glu	Ser	Glu	Ser	Ser	Ser	Glu	Ser	Ser	Ser
		35					40					45			

Ser	Asp	Ser	Glu	Xaa	Xaa	Glu	Thr	Gly	Pro	Ala
	50					55				

<210> 1142

<211> 199

<212> PRT

<213> Homo sapiens

<400> 1142

Ser	Gly	Tyr	Lys	Thr	Ile	Ser	Ala	Met	Gln	Thr	Ile	Lys	Cys	Val	Val
1					5					10				15	

Val	Gly	Asp	Gly	Ala	Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1151

20	25	30
Thr Asn Lys Phe Pro Ser Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr		
35	40	45
Ala Val Thr Val Met Ile Gly Gly Glu Pro Tyr Thr Leu Gly Leu Phe		
50	55	60
Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr		
65	70	75
Pro Gln Thr Asp Val Phe Leu Val Cys Phe Ser Val Val Ser Pro Ser		
85	90	95
Ser Phe Glu Asn Val Lys Glu Lys Trp Val Pro Glu Ile Thr His His		
100	105	110
Cys Pro Lys Thr Pro Phe Leu Leu Val Gly Thr Gln Ile Asp Leu Arg		
115	120	125
Asp Asp Pro Ser Thr Ile Glu Lys Leu Ala Lys Asn Lys Gln Lys Pro		
130	135	140
Ile Thr Pro Glu Thr Ala Glu Lys Leu Ala Arg Asp Leu Lys Ala Val		
145	150	155
Lys Tyr Val Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys Asn Val		
165	170	175
Phe Asp Glu Ala Ile Leu Ala Ala Leu Glu Pro Pro Glu Pro Lys Lys		
180	185	190
Ser Arg Arg Cys Val Leu Leu		
195		

<210> 1143

<211> 171

<212> PRT

<213> Homo sapiens

<400> 1143

Gly Asp Leu Asp Cys Pro Asp Trp Val Leu Ala Glu Ile Ser Thr Leu
1 5 10 15
Ala Lys Met Tyr Glu Lys Ile Leu Lys Leu Thr Ala Asp Ala Lys Phe
20 25 30
Glu Ser Gly Asp Val Lys Ala Thr Val Ala Val Leu Ser Phe Ile Leu
35 40 45

1152

Ser Ser Ala Ala Lys His Ser Val Asp Gly Glu Ser Leu Ser Ser Glu
 50 55 60
 Leu Gln Gln Leu Gly Leu Pro Lys Glu His Ala Ala Ser Leu Cys Arg
 65 70 75 80
 Cys Tyr Glu Glu Lys Gln Ser Pro Leu Gln Lys His Leu Arg Val Cys
 85 90 95
 Ser Leu Arg Met Asn Arg Leu Ala Gly Val Gly Trp Arg Val Asp Tyr
 100 105 110
 Thr Leu Ser Ser Ser Leu Leu Gln Ser Val Glu Glu Pro Met Val His
 115 120 125
 Leu Arg Leu Glu Val Ala Ala Ala Pro Gly Thr Pro Ala Gln Pro Val
 130 135 140
 Ala Met Ser Leu Ser Ala Asp Lys Phe Gln Val Leu Leu Ala Glu Leu
 145 150 155 160
 Lys Gln Ala Gln Thr Leu Met Ser Ser Leu Gly
 165 170

<210> 1144

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (22)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (38)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (40)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1144

Gln Trp Arg Gln Gly Val Gln Gly Arg Ser Ala Ser Gly Thr Ser Thr
 1 5 10 15

1153

Cys Arg Val Ala Arg Xaa Gly Gln Asp Trp Pro Ala Ala Ser Pro Gly
 20 25 30
 Val Asn Leu Arg Asn Xaa Phe Xaa Pro Pro Leu Leu Leu Ala Pro Val
 35 40 45
 Pro Thr Pro Val Ala Pro Ser Leu Gly Ser Pro Leu Leu Leu Ser His
 50 55 60
 Pro Glu Arg Gln Ser Gly Pro Val Thr Gly Gly Ala Gly Glu Gly His
 65 70 75 80
 Arg Cys Ala Ser Pro Gln Thr Val Cys Gln Val Ser Glu Leu Val Thr
 85 90 95
 Arg Pro Ala Ala Gln Pro Ser Ala Ala Ala Gln Pro Ala Ala Pro Ala
 100 105 110
 Gly Gly Arg Thr Pro Gly Arg Ala Gly Pro His Leu Pro Ile Tyr Lys
 115 120 125
 Ile Gly Gln Gly Asn Met Lys Ala Asp Leu Gln Ala Ala Ala Thr Ala
 130 135 140
 Lys Pro Gly Lys Ser Gln Gln
 145 150

<210> 1145

<211> 70

<212> PRT

<213> Homo sapiens

<400> 1145

Ala Asp Ile Ala Gly Val Leu Ala Ile Arg Pro Asp Glu Leu Arg Phe
 1 5 10 15
 Arg Tyr Ser Met Val Ala Tyr Trp Arg Gln Ala Gly Leu Ser Tyr Ile
 20 25 30
 Arg Tyr Ser Gln Ile Cys Ala Lys Ala Val Arg Asp Ala Leu Lys Thr
 35 40 45
 Glu Phe Lys Ala Asn Ala Glu Lys Thr Ser Gly Ser Asn Val Lys Ile
 50 55 60
 Val Lys Val Lys Lys Glu
 65 70

1154

<210> 1146

<211> 166

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (56)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1146

Leu His Ala Asn Gln Val Ile His Arg Asp Ile Lys Ser Asp Asn Val
 1 5 10 15

Leu Leu Gly Met Glu Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys
 20 25 30

Ala Gln Ile Thr Pro Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr
 35 40 45

Pro Tyr Trp Met Ala Pro Glu Xaa Val Thr Arg Lys Ala Tyr Gly Pro
 50 55 60

Lys Val Asp Ile Trp Ser Leu Gly Ile Met Ala Ile Glu Met Val Glu
 65 70 75 80

Gly Glu Pro Pro Tyr Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu
 85 90 95

Ile Ala Thr Asn Gly Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser
 100 105 110

Pro Ile Phe Arg Asp Phe Leu Asn Arg Cys Leu Glu Met Asp Val Glu
 115 120 125

Lys Arg Gly Ser Ala Lys Glu Leu Leu Gln His Pro Phe Leu Lys Leu
 130 135 140

Ala Lys Pro Leu Ser Ser Leu Thr Pro Leu Ile Met Ala Ala Lys Glu
 145 150 155 160

Ala Met Lys Ser Asn Arg
 165

<210> 1147

<211> 420

<212> PRT

<213> Homo sapiens

1155

<220>

<221> SITE

<222> (203)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1147

Cys Pro Pro Phe Ser Val Arg Val Pro Pro Trp Ala Gly Leu Ala Leu
 1 5 10 15
 Leu Pro Ser Pro Ser Leu Met Ala Leu Leu Arg Arg Pro Thr Val Ser
 20 25 30
 Ser Asp Leu Glu Asn Ile Asp Thr Gly Val Asn Ser Lys Val Lys Ser
 35 40 45
 His Val Thr Ile Arg Arg Thr Val Leu Glu Glu Ile Gly Asn Arg Val
 50 55 60
 Thr Thr Arg Ala Ala Gln Val Ala Lys Lys Ala Gln Asn Thr Lys Val
 65 70 75 80
 Pro Val Gln Pro Thr Lys Thr Thr Asn Val Asn Lys Gln Leu Lys Pro
 85 90 95
 Thr Ala Ser Val Lys Pro Val Gln Met Glu Lys Leu Ala Pro Lys Gly
 100 105 110
 Pro Ser Pro Thr Pro Glu Asp Val Ser Met Lys Glu Glu Asn Leu Cys
 115 120 125
 Gln Ala Phe Ser Asp Ala Leu Leu Cys Lys Ile Glu Asp Ile Asp Asn
 130 135 140
 Glu Asp Trp Glu Asn Pro Gln Leu Cys Ser Asp Tyr Val Lys Asp Ile
 145 150 155 160
 Tyr Gln Tyr Leu Arg Gln Leu Glu Val Leu Gln Ser Ile Asn Pro His
 165 170 175
 Phe Leu Asp Gly Arg Asp Ile Asn Gly Arg Met Arg Ala Ile Leu Val
 180 185 190
 Asp Trp Leu Val Gln Val His Ser Lys Phe Xaa Leu Leu Gln Glu Thr
 195 200 205
 Leu Tyr Met Cys Val Gly Ile Met Asp Arg Phe Leu Gln Val Gln Pro
 210 215 220
 Val Ser Arg Lys Lys Leu Gln Leu Val Gly Ile Thr Ala Leu Leu Leu
 225 230 235 240

1156

Ala Ser Lys Tyr Glu Glu Met Phe Ser Pro Asn Ile Glu Asp Phe Val
 245 250 255
 Tyr Ile Thr Asp Asn Ala Tyr Thr Ser Ser Gln Ile Arg Glu Met Glu
 260 265 270
 Thr Leu Ile Leu Lys Glu Leu Lys Phe Glu Leu Gly Arg Pro Leu Pro
 275 280 285
 Leu His Phe Leu Arg Arg Ala Ser Lys Ala Gly Glu Val Asp Val Glu
 290 295 300
 Gln His Thr Leu Ala Lys Tyr Leu Met Glu Leu Thr Leu Ile Asp Tyr
 305 310 315 320
 Asp Met Val His Tyr His Pro Ser Lys Val Ala Ala Ala Ala Ser Cys
 325 330 335
 Leu Ser Gln Lys Val Leu Gly Gln Gly Lys Trp Asn Leu Lys Gln Gln
 340 345 350
 Tyr Tyr Thr Gly Tyr Thr Glu Asn Glu Val Leu Glu Val Met Gln His
 355 360 365
 Met Ala Lys Asn Val Val Lys Val Asn Glu Asn Leu Thr Lys Phe Ile
 370 375 380
 Ala Ile Lys Asn Lys Tyr Ala Ser Ser Lys Leu Leu Lys Ile Ser Met
 385 390 395 400
 Ile Pro Gln Leu Asn Ser Lys Ala Val Lys Asp Leu Ala Ser Pro Leu
 405 410 415
 Ile Gly Arg Ser
 420

<210> 1148

<211> 249

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (244)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1148

Gln Ser Asn Ala Val Trp Leu Leu Gly His Leu His Leu Ser Thr Leu

1157

1	5	10	15
Ser Ser Ser Gln Ser Arg Ala Ser Val Pro Thr Asp Tyr Ser Tyr Leu	20	25	30
Pro Glu Ser Ser Phe Ile Gly Ala Ala Ile Gly Phe Phe Ile Thr Gly	35	40	45
Gly Lys Lys Gly Pro Glu Ser Val Pro Pro Ser Leu Leu Lys Val Val	50	55	60
Met Lys Pro Ile Ala Thr Val Gly Glu Ser Tyr Gln Tyr Pro Pro Val	65	70	75
Asn Trp Ala Ala Leu Leu Ser Pro Leu Met Arg Leu Asn Phe Gly Glu	85	90	95
Glu Ile Gln Gln Leu Cys Leu Glu Ile Met Val Thr Gln Ala Gln Ser	100	105	110
Ser Gln Asn Ala Ala Ala Leu Leu Gly Leu Trp Val Thr Pro Pro Leu	115	120	125
Ile His Ser Leu Ser Leu Asn Thr Lys Arg Tyr Leu Leu Ile Ser Ala	130	135	140
Pro Leu Trp Ile Lys His Ile Ser Asp Glu Gln Ile Leu Gly Phe Val	145	150	155
Glu Asn Leu Met Val Ala Val Phe Lys Ala Ala Ser Pro Leu Gly Ser	165	170	175
Pro Glu Leu Cys Pro Ser Ala Leu His Gly Leu Ser Gln Ala Met Lys	180	185	190
Leu Pro Ser Pro Ala His His Leu Trp Ser Leu Leu Ser Glu Ala Thr	195	200	205
Gly Lys Ile Phe Asp Leu Leu Pro Asn Lys Ile Arg Arg Lys Asp Leu	210	215	220
Glu Leu Tyr Ile Ser Ile Ala Lys Cys Leu Leu Glu Met Thr Asp Asp	225	230	235
Asp Ala Asn Xaa Asp Arg Pro Gly Tyr	245		

<210> 1149

<211> 239

1158

<212> PRT

<213> Homo sapiens

<400> 1149

Arg Asp Pro Pro Arg Pro Val Gln Ser Gly Leu Gly Ala Ala Gly Thr
1 5 10 15

Leu Ser Trp Leu Pro Pro Pro Glu Gln Pro Val Leu Val Pro Arg Leu
20 25 30

Pro Ala Pro Arg Pro Val Met Thr Leu Arg Pro Ser Leu Leu Pro Leu
35 40 45

His Leu Leu Leu Leu Leu Leu Leu Ser Ala Ala Val Cys Arg Ala Glu
50 55 60

Ala Gly Leu Glu Thr Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr
65 70 75 80

Leu Val Glu Pro Pro Glu Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp
85 90 95

Thr Leu His Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile
100 105 110

Asp Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys
115 120 125

Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp Met Cys Val Gly
130 135 140

Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala Tyr Gly Lys Arg
145 150 155 160

Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val Gln Tyr Asp Val
165 170 175

Glu Leu Ile Ala Leu Ile Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys
180 185 190

Gly Ile Leu Pro Leu Val Gly Met Ala Met Val Pro Ala Leu Leu Gly
195 200 205

Leu Ile Gly Tyr His Leu Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser
210 215 220

Lys Lys Lys Leu Lys Glu Glu Lys Arg Asn Lys Ser Lys Lys Lys
225 230 235

1159

<210> 1150

<211> 394

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1150

Ala Glu Xaa Gly Lys Thr Glu Trp Leu Phe Gly Met Asp Glu Gly Arg
 1 5 10 15

Lys Gln Leu Ala Ala Ser Ala Gly Phe Arg Arg Leu Ile Thr Val Ala
 20 25 30

Leu His Arg Gly Gln Gln Tyr Glu Ser Met Asp His Ile Gln Ala Glu
 35 40 45

Leu Ser Ala Arg Val Met Glu Leu Ala Pro Ala Gly Met Pro Thr Gln
 50 55 60

Gln Gln Val Pro Phe Leu Ser Val Gly Gly Asp Ile Gly Val Arg Thr
 65 70 75 80

Val Gln His Gln Asp Cys Ser Pro Leu Ser Gly Asp Tyr Val Ile Glu
 85 90 95

Asp Val Gln Gly Asp Asp Lys Arg Tyr Phe Arg Arg Leu Ile Phe Leu
 100 105 110

Ser Asn Arg Asn Val Val Gln Ser Glu Ala Arg Leu Leu Lys Asp Val
 115 120 125

Ser His Lys Ala Gln Lys Lys Arg Lys Lys Asp Arg Lys Lys Gln Arg
 130 135 140

Pro Ala Asp Ala Glu Asp Leu Pro Ala Ala Pro Gly Gln Ser Ile Asp
 145 150 155 160

Lys Ser Tyr Leu Cys Cys Glu His His Lys Ala Met Ile Ala Gly Leu
 165 170 175

Ala Leu Leu Arg Asn Pro Glu Leu Leu Leu Glu Ile Pro Leu Ala Leu
 180 185 190

Leu Val Val Gly Leu Gly Gly Gly Ser Leu Pro Leu Phe Val His Asp
 195 200 205

His Phe Pro Lys Ser Cys Ile Asp Ala Val Glu Ile Asp Pro Ser Met

1160

210	215	220
Leu Glu Val Ala Thr Gln Trp Phe Gly Phe Ser Gln Ser Asp Arg Met		
225	230	235 240
Lys Val His Ile Ala Asp Gly Leu Asp Tyr Ile Ala Ser Leu Ala Gly		
245	250	255
Gly Gly Glu Ala Arg Pro Cys Tyr Asp Val Ile Met Phe Asp Val Asp		
260	265	270
Ser Lys Asp Pro Thr Leu Gly Met Ser Cys Pro Pro Pro Ala Phe Val		
275	280	285
Glu Gln Ser Phe Leu Gln Lys Val Lys Ser Ile Leu Thr Pro Glu Gly		
290	295	300
Val Phe Ile Leu Asn Leu Val Cys Arg Asp Leu Gly Leu Lys Asp Ser		
305	310	315 320
Val Leu Ala Gly Leu Lys Ala Val Phe Pro Leu Leu Tyr Val Arg Arg		
325	330	335
Ile Glu Gly Glu Val Asn Glu Ile Leu Phe Cys Gln Leu His Pro Glu		
340	345	350
Gln Lys Leu Ala Thr Pro Glu Leu Leu Glu Thr Ala Gln Ala Leu Glu		
355	360	365
Arg Thr Leu Arg Lys Pro Gly Arg Gly Trp Asp Asp Thr Tyr Val Leu		
370	375	380
Ser Asp Met Leu Lys Thr Val Lys Ile Val		
385	390	

<210> 1151

<211> 111

<212> PRT

<213> Homo sapiens

<400> 1151

Val Asn Val Asn Asn Pro Ser Leu Cys His Ser Ser His Leu Val Asp
1 5 10 15
Leu Gly Ser Gly Ser Val Glu Phe Cys Ala Trp Glu Trp Ser Trp Arg
20 25 30
Glu Trp Gly Leu Cys Thr Ala Ala Thr Ser Pro Arg Ser Ser His Leu
35 40 45

1161

Pro Ala Pro Arg Pro Gly Cys Met Ala Ala Pro Val Cys Val Gln Arg
 50 55 60

Ser Val Ser His Pro Leu His Leu Leu Ser Gly Gly Leu Gly Ser Pro
 65 70 75 80

Thr Cys Cys Gln Asp Leu Gly Ala Ile Lys Tyr Ser Gly Phe Val Lys
 85 90 95

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 100 105 110

<210> 1152

<211> 172

<212> PRT

<213> Homo sapiens

<400> 1152

Leu Gly Asp Thr Ile Glu Gly Arg Leu Gln Val Pro Val Arg Asn Ser
 1 5 10 15

Arg Val Asp Pro Arg Val Arg Ala Arg Gly Ala Asp Arg Met Gly Lys
 20 25 30

Cys Arg Gly Leu Arg Thr Ala Arg Lys Leu Arg Ser His Arg Arg Asp
 35 40 45

Gln Lys Trp His Asp Lys Gln Tyr Lys Lys Ala His Leu Gly Thr Ala
 50 55 60

Leu Lys Ala Asn Pro Phe Gly Gly Ala Ser His Ala Lys Gly Ile Val
 65 70 75 80

Leu Glu Lys Val Gly Val Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg
 85 90 95

Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly Lys Lys Ile Thr Ala
 100 105 110

Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Ile Glu Glu Asn Asp Glu
 115 120 125

Val Leu Val Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile
 130 135 140

Pro Gly Val Arg Phe Lys Val Val Lys Val Ala Asn Val Ser Leu Leu
 145 150 155 160

1162

Ala Leu Tyr Lys Gly Lys Lys Glu Arg Pro Arg Ser
 165 170

<210> 1153
 <211> 197
 <212> PRT
 <213> Homo sapiens

<400> 1153

Tyr Trp Cys Glu Gln Cys Asp Val Gln Phe Ser Ser Ser Ser Glu Leu
 1 5 10 15

Tyr Leu His Phe Gln Glu His Ser Cys Asp Glu Gln Tyr Leu Cys Gln
 20 25 30

Phe Cys Glu His Glu Thr Asn Asp Pro Glu Asp Leu His Ser His Val
 35 40 45

Val Asn Glu His Ala Cys Lys Leu Ile Glu Leu Ser Asp Lys Tyr Asn
 50 55 60

Asn Gly Glu His Gly Gln Tyr Ser Leu Leu Ser Lys Ile Thr Phe Asp
 65 70 75 80

Lys Cys Lys Asn Phe Phe Val Cys Gln Val Cys Gly Phe Arg Ser Arg
 85 90 95

Leu His Thr Asn Val Asn Arg His Val Ala Ile Glu His Thr Lys Ile
 100 105 110

Phe Pro His Val Cys Asp Asp Cys Gly Lys Gly Phe Ser Ser Met Leu
 115 120 125

Glu Tyr Cys Lys His Leu Asn Ser His Leu Ser Glu Gly Ile Tyr Leu
 130 135 140

Cys Gln Tyr Cys Glu Tyr Ser Thr Gly Gln Ile Glu Asp Leu Lys Ile
 145 150 155 160

His Leu Asp Phe Lys His Ser Ala Asp Leu Pro His Lys Cys Ser Asp
 165 170 175

Cys Leu Met Arg Phe Gly Asn Glu Arg Glu Leu Ile Ser His Leu Pro
 180 185 190

Val His Glu Thr Thr
 195

1163

<210> 1154

<211> 156

<212> PRT

<213> Homo sapiens

<400> 1154

Pro Ala Lys Glu Arg Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser
1 5 10 15

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly
20 25 30

Ser Ser Ser Ser Asp Ser Glu Gly Ser Ser Leu Pro Val Gln Pro Glu
35 40 45

Val Ala Leu Lys Arg Val Pro Ser Pro Thr Pro Ala Pro Lys Glu Ala
50 55 60

Val Arg Glu Gly Arg Pro Pro Glu Pro Thr Pro Ala Lys Arg Lys Arg
65 70 75 80

Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
85 90 95

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
100 105 110

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Ser Pro Ala Lys
115 120 125

Pro Gly Pro Gln Ala Cys Pro Asn Leu Gln Ala Pro Arg Ser His Pro
130 135 140

Leu Ala Ser Gly Gly Pro Ala Ala Pro Gly Ser Gln
145 150 155

<210> 1155

<211> 125

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (73)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1164

<222> (105)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (122)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1155

Pro Glu Ala Pro Arg Gly Val Val Thr Cys Leu Arg Ala Leu Leu Ser
 1 5 10 15

His Gln His Gln Thr Arg Pro His Arg Val Pro Gly Thr Met Phe Gly
 20 25 30

Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro Ser Asn Phe Glu His
 35 40 45

Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe Thr Gly Leu
 50 55 60

Pro Arg Gln Trp Gln Ser Leu Ile Xaa Glu Ser Ala Arg Arg Pro Lys
 65 70 75 80

Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro Gly Ala Pro
 85 90 95

Lys Thr Ile Val Arg Gly Ser Lys Xaa Ala Lys Asp Gly Ala Leu Thr
 100 105 110

Leu Leu Leu Asp Glu Phe Glu Asn Met Xaa Val Thr Arg
 115 120 125

<210> 1156

<211> 202

<212> PRT

<213> Homo sapiens

<400> 1156

Arg Pro Thr Arg Pro Gln Pro Ser Pro Asp Glu Ala Arg Pro Leu Gln
 1 5 10 15

Ala Leu Leu Asp Gly Arg Gly Leu Cys Val Asn Ala Ser Ala Val Ser
 20 25 30

Arg Leu Arg Ala Tyr Leu Leu Pro Ala Pro Pro Ala Pro Gly Asn Ala
 35 40 45

Ser Glu Ser Glu Glu Asp Arg Ser Ala Gly Ser Val Glu Ser Pro Ser

1165

50		55		60
Val Ser Ser Thr His Arg	Val Ser Asp Pro Lys Phe His Pro Leu His			
65	70	75		80
Ser Lys Ile Ile Ile Ile Lys Lys Gly His Ala Lys Asp Ser Gln Arg				
	85	90		95
Tyr Lys Val Asp Tyr Glu Ser Gln Ser Thr Asp Thr Gln Asn Phe Ser				
	100	105		110
Ser Glu Ser Lys Arg Glu Thr Glu Tyr Gly Pro Cys Arg Arg Glu Met				
	115	120		125
Glu Asp Thr Leu Asn His Leu Lys Phe Leu Asn Val Leu Ser Pro Arg				
	130	135		140
Gly Val His Ile Pro Asn Cys Asp Lys Lys Gly Phe Tyr Lys Lys Lys				
	145	150	155	160
Gln Cys Arg Pro Ser Lys Gly Arg Lys Arg Gly Phe Cys Trp Cys Val				
	165	170		175
Asp Lys Tyr Gly Gln Pro Leu Pro Gly Tyr Thr Thr Lys Gly Lys Glu				
	180	185		190
Asp Val His Cys Tyr Ser Met Gln Ser Lys				
	195	200		

<210> 1157

<211> 269

<212> PRT

<213> Homo sapiens

<400> 1157

Arg Arg Cys Cys His Ser Ala Thr Met Phe Glu Ala Arg Leu Val Gln				
1	5	10		15
Gly Ser Ile Leu Lys Lys Val Leu Glu Ala Leu Lys Asp Leu Ile Asn				
	20	25		30
Glu Ala Cys Trp Asp Ile Ser Ser Ser Gly Val Asn Leu Gln Ser Met				
	35	40		45
Asp Ser Ser His Val Ser Leu Val Gln Leu Thr Leu Arg Ser Glu Gly				
	50	55		60
Phe Asp Thr Tyr Arg Cys Asp Arg Asn Leu Ala Met Gly Val Asn Leu				
	65	70	75	80

1166

Thr Ser Met Ser Lys Ile Leu Lys Cys Ala Gly Asn Glu Asp Ile Ile
 85 90 95
 Thr Leu Arg Ala Glu Asp Asn Ala Asp Thr Leu Ala Leu Val Phe Glu
 100 105 110
 Ala Pro Asn Gln Glu Lys Val Ser Asp Tyr Glu Met Lys Leu Met Asp
 115 120 125
 Leu Asp Val Glu Gln Leu Gly Ile Pro Glu Gln Glu Tyr Ser Cys Val
 130 135 140
 Val Lys Met Pro Ser Gly Glu Phe Ala Arg Ile Cys Arg Asp Leu Ser
 145 150 155 160
 His Ile Gly Asp Ala Val Val Ile Ser Cys Ala Lys Asp Gly Val Lys
 165 170 175
 Phe Ser Ala Ser Gly Glu Leu Gly Asn Gly Asn Ile Lys Leu Ser Gln
 180 185 190
 Thr Ser Asn Val Asp Lys Glu Glu Glu Ala Val Thr Ile Glu Met Asn
 195 200 205
 Glu Pro Val Gln Leu Thr Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr
 210 215 220
 Lys Ala Thr Pro Leu Ser Ser Thr Val Thr Leu Ser Met Ser Ala Asp
 225 230 235 240
 Val Pro Leu Val Val Glu Tyr Lys Ile Ala Asp Met Gly His Leu Lys
 245 250 255
 Tyr Tyr Leu Ala Pro Lys Ile Glu Asp Glu Glu Gly Ser
 260 265

<210> 1158

<211> 639

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (129)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1167

<222> (150)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1158

Met Asp Glu Met Ala Thr Thr Gln Ile Ser Lys Asp Glu Leu Asp Glu
 1 5 10 15

Leu Lys Glu Ala Phe Ala Lys Val Asp Leu Asn Ser Asn Gly Phe Ile
 20 25 30

Cys Asp Tyr Glu Leu His Glu Leu Phe Lys Glu Ala Asn Met Pro Leu
 35 40 45

Pro Gly Tyr Lys Val Arg Glu Ile Ile Gln Lys Leu Met Leu Asp Gly
 50 55 60

Asp Arg Asn Lys Asp Gly Lys Ile Ser Phe Asp Glu Phe Val Tyr Ile
 65 70 75 80

Phe Gln Glu Val Lys Ser Ser Asp Ile Ala Lys Thr Phe Arg Lys Ala
 85 90 95

Ile Asn Arg Lys Glu Gly Ile Cys Ala Leu Gly Gly Thr Ser Glu Leu
 100 105 110

Ser Ser Glu Gly Thr Gln His Ser Tyr Ser Glu Glu Glu Lys Tyr Ala
 115 120 125

Xaa Val Asn Trp Ile Asn Lys Ala Leu Glu Asn Asp Pro Asp Cys Arg
 130 135 140

His Val Ile Pro Met Xaa Pro Asn Thr Asp Asp Leu Phe Lys Ala Val
 145 150 155 160

Gly Asp Gly Ile Val Leu Cys Lys Met Ile Asn Leu Ser Val Pro Asp
 165 170 175

Thr Ile Asp Glu Arg Ala Ile Asn Lys Lys Lys Leu Thr Pro Phe Ile
 180 185 190

Ile Gln Glu Asn Leu Asn Leu Ala Leu Asn Ser Ala Ser Ala Ile Gly
 195 200 205

Cys His Val Val Asn Ile Gly Ala Glu Asp Leu Arg Ala Gly Lys Pro
 210 215 220

His Leu Val Leu Gly Leu Leu Trp Gln Ile Ile Lys Ile Gly Leu Phe
 225 230 235 240

Ala Asp Ile Glu Leu Ser Arg Asn Glu Ala Leu Ala Ala Leu Leu Arg
 245 250 255

1168

Asp Gly Glu Thr Leu Glu Glu Leu Met Lys Leu Ser Pro Glu Glu Leu
260 265 270

Leu Leu Arg Trp Ala Asn Phe His Leu Glu Asn Ser Gly Trp Gln Lys
275 280 285

Ile Asn Asn Phe Ser Ala Asp Ile Lys Leu Ile Asp Phe Ser Asn Ser
290 295 300

Val Lys Asp Ser Lys Ala Tyr Phe His Leu Leu Asn Gln Ile Ala Pro
305 310 315 320

Lys Gly Gln Lys Glu Gly Glu Pro Arg Ile Asp Ile Asn Met Ser Gly
325 330 335

Phe Asn Glu Thr Asp Asp Leu Lys Arg Ala Glu Ser Met Leu Gln Gln
340 345 350

Ala Asp Lys Leu Gly Cys Arg Gln Phe Val Thr Pro Ala Asp Val Val
355 360 365

Ser Gly Asn Pro Lys Leu Asn Leu Ala Phe Val Ala Asn Leu Phe Asn
370 375 380

Lys Tyr Pro Ala Leu Thr Lys Pro Glu Asn Gln Asp Ile Asp Trp Thr
385 390 395 400

Leu Leu Glu Gly Glu Thr Arg Glu Glu Arg Thr Phe Arg Asn Trp Met
405 410 415

Asn Ser Leu Gly Val Asn Pro His Val Asn His Leu Tyr Ala Asp Leu
420 425 430

Gln Asp Ala Leu Val Ile Leu Gln Leu Tyr Glu Arg Ile Lys Val Pro
435 440 445

Val Asp Trp Ser Lys Val Asn Lys Pro Pro Tyr Pro Lys Leu Gly Ala
450 455 460

Asn Met Lys Lys Leu Glu Asn Cys Asn Tyr Ala Val Glu Leu Gly Lys
465 470 475 480

His Pro Ala Lys Phe Ser Leu Val Gly Ile Gly Gly Gln Asp Leu Asn
485 490 495

Asp Gly Asn Gln Thr Leu Thr Leu Ala Leu Val Trp Gln Leu Met Arg
500 505 510

Arg Tyr Thr Leu Asn Val Leu Glu Asp Leu Gly Asp Gly Gln Lys Ala
515 520 525

1169

Asn Asp Asp Ile Ile Val Asn Trp Val Asn Arg Thr Leu Ser Glu Ala
 530 535 540

Gly Lys Ser Thr Ser Ile Gln Ser Phe Lys Asp Lys Thr Ile Ser Ser
 545 550 555 560

Ser Leu Ala Val Val Asp Leu Ile Asp Ala Ile Gln Pro Gly Cys Ile
 565 570 575

Asn Tyr Asp Leu Val Lys Ser Gly Asn Leu Thr Glu Asp Asp Lys His
 580 585 590

Asn Asn Ala Lys Tyr Ala Val Ser Met Ala Arg Arg Ile Gly Ala Arg
 595 600 605

Val Tyr Ala Leu Pro Glu Asp Leu Val Glu Val Lys Pro Lys Met Val
 610 615 620

Met Thr Val Phe Ala Cys Leu Met Gly Arg Gly Met Lys Arg Val
 625 630 635

<210> 1159

<211> 63

<212> PRT

<213> Homo sapiens

<400> 1159

Thr Ile Trp Pro Leu Asn Phe His Arg Lys Asn Asp Pro Thr Phe Leu
 1 5 10 15

Ser Met Ser Tyr Leu Ile Ser Arg Ser Trp Asp Gly Leu Thr Ile Leu
 20 25 30

Val Tyr Ile Leu Asp Thr Glu Arg Cys Tyr Ala Ser Val Ile Ile Pro
 35 40 45

Arg Leu Glu Ile Gly Arg Ala Lys Lys Val Leu Leu Phe Phe Leu
 50 55 60

<210> 1160

<211> 207

<212> PRT

<213> Homo sapiens

<400> 1160

Glu Val Tyr Gly Gly Ser Leu Asp Lys Glu Phe Asp Glu Ser Ser Pro

1170

1	5	10	15
Lys	Gln	Pro	Thr
20	Asn	Pro	Tyr
25	Ala	Ser	Ser
30	Lys	Ala	Ala
	Ala	Glu	Cys
Phe	Val	Gln	Ser
35	Tyr	Trp	Glu
40	Gln	Tyr	Lys
45	Phe	Pro	Val
	Val	Ile	Thr
Arg	Ser	Ser	Asn
50	Val	Tyr	Gly
55	Pro	His	Gln
60	Tyr	Pro	Glu
	Lys	Val	Ile
Pro	Lys	Phe	Ile
65	Ser	Leu	Leu
70	Gln	His	Asn
75	Arg	Lys	Cys
80	Cys	Ile	His
Gly	Ser	Gly	Leu
85	Gln	Thr	Arg
90	Asn	Phe	Leu
95	Tyr	Ala	Thr
	Asp	Val	Val
Glu	Ala	Phe	Leu
100	Thr	Val	Leu
105	Lys	Lys	Gly
110	Lys	Pro	Gly
	Glu	Ile	Tyr
Asn	Ile	Gly	Thr
115	Asn	Phe	Glu
120	Met	Ser	Val
125	Val	Gln	Leu
	Ala	Lys	Glu
Leu	Ile	Gln	Leu
130	Ile	Lys	Glu
135	Thr	Asn	Ser
140	Glu	Ser	Glu
	Met	Glu	Asn
Trp	Val	Asp	Tyr
145	Val	Asn	Asp
150	Arg	Pro	Thr
155	Asn	Asp	Met
160	Arg	Tyr	Pro
Met	Lys	Ser	Glu
165	Lys	Ile	His
170	Gly	Leu	Gly
175	Trp	Arg	Pro
	Lys	Val	Pro
Trp	Lys	Glu	Gly
180	Ile	Lys	Lys
185	Thr	Ile	Glu
190	Trp	Tyr	Arg
	Glu	Asn	Phe
His	Asn	Trp	Lys
195	Asn	Val	Glu
200	Lys	Ala	Leu
205	Glu	Pro	Phe
	Pro	Val	

<210> 1161

<211> 848

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (815)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1171

<221> SITE

<222> (844)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1161

Ala Leu Gly Leu Gly Val Thr Met Ala Thr Glu Glu Phe Ile Ile Arg
 1 5 10 15

Ile Pro Pro Tyr His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val
 20 25 30

Ser Arg Val Glu Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu
 35 40 45

Arg Val Leu Phe Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His
 50 55 60

Tyr Cys Thr Val Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val
 65 70 75 80

Leu Phe Asp Val Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu
 85 90 95

Ile Arg Leu Ala Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu
 100 105 110

Glu Lys Asp Ile Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu
 115 120 125

His Leu Lys Ala Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val
 130 135 140

Val Ala Gly Asp Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro
 145 150 155 160

Arg Lys Glu Val Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg
 165 170 175

Gln Asn Gln Ala Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg
 180 185 190

Asp Gly Lys Glu Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val
 195 200 205

Gly Ala Tyr Leu Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp
 210 215 220

Ala Val Ile Leu Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg
 225 230 235 240

Asn Phe Arg Asp Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp

1172

245	250	255
Leu Val Thr Val Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu		
260	265	270
Glu Val Leu Gly Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr		
275	280	285
Cys Val Ile Leu Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly		
290	295	300
Gln Lys Arg Val Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly		
305	310	315
Glu Gln Leu Glu Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln		
325	330	335
Gln Gly Leu Leu Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp		
340	345	350
Glu Glu Lys Val Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly		
355	360	365
Pro Leu Glu Tyr Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg		
370	375	380
Gln Ala Ile Pro Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val		
385	390	395
Lys Thr Gly Lys Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr		
405	410	415
Gln Asp Glu Val Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu		
420	425	430
Leu Leu Asn Lys Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp		
435	440	445
Thr Ala Lys Ser Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val		
450	455	460
Val Ser Tyr Arg Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr		
465	470	475
Arg Glu Lys Arg Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu		
485	490	495
Gly Pro Glu Glu Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro		
500	505	510
Lys Arg Pro His Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp		

1173

515	520	525
Phe Phe Thr Asp Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu		
530	535	540
Gln Leu Gln Leu Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys		
545	550	555
Asp Pro Gln Glu Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly		
565	570	575
Asp Ala Cys Lys Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser		
580	585	590
Val Thr Phe Asp Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr		
595	600	605
Ala Val Phe Gly Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met		
610	615	620
Ala Leu Pro Arg Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu		
625	630	635
Val Val Ser Ser Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg		
645	650	655
Thr Arg Asp Ala Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr		
660	665	670
Thr Asn Ser Gln Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu		
675	680	685
Gln Glu Ala Arg Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser		
690	695	700
Glu Ala Glu Lys Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser		
705	710	715
Met Ala Val Glu Ser Thr Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg		
725	730	735
Ala Glu Ala Ala Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys		
740	745	750
Leu Lys Ala Gln Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg		
755	760	765
Val Gln Lys Val Arg Glu Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu		
770	775	780
Glu Leu Glu Val Ser Lys Ala Gln Gln Leu Ala Glu Val Glu Val Lys		

1174

785 790 795 800
Lys Phe Lys Gln Met Thr Glu Ala Ile Gly Pro Ser Thr Ile Xaa Asp
 805 810 815
Leu Ala Val Ala Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu
 820 825 830
Gly Leu Lys Ser Thr Leu Ile Thr Asp Gly Phe Xaa Ser Ile Asn Phe
 835 840 845

<210> 1162
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (28)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1162
Phe Xaa Val Gly Ile Val Asn Phe Ser Gln Pro Pro His Ala Ala Gly
1 5 10 15
Glu Cys Gly Cys Ser Ser Ser Glu Met Leu Thr Xaa Lys Arg Glu Val
 20 25 30
Lys Gln Ser Arg Tyr Val Gln Pro Cys Leu Gln Asn Pro Ser Leu Ser
 35 40 45
Ser Leu Ile Arg Ser Phe Leu Val Phe Tyr
50 55

<210> 1163
<211> 565
<212> PRT
<213> Homo sapiens

1175

<400> 1163

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Ile Pro Gly Ser Thr His Ala Ser Ala Gly Asn Leu Asp Ser Pro Glu
 1             5             10             15

Gly Gly Phe Asp Ala Ile Met Gln Val Ala Val Cys Gly Ser Leu Ile
      20             25             30

Gly Trp Arg Asn Val Thr Arg Leu Leu Val Phe Ser Thr Asp Ala Gly
      35             40             45

Phe His Phe Ala Gly Asp Gly Lys Leu Gly Gly Ile Val Leu Pro Asn
 50             55             60

Asp Gly Gln Cys His Leu Glu Asn Asn Met Tyr Thr Met Ser His Tyr
 65             70             75             80

Tyr Asp Tyr Pro Ser Ile Ala His Leu Val Gln Lys Leu Ser Glu Asn
      85             90             95

Asn Ile Gln Thr Ile Phe Ala Val Thr Glu Glu Phe Gln Pro Val Tyr
      100             105             110

Lys Glu Leu Lys Asn Leu Ile Pro Lys Ser Ala Val Gly Thr Leu Ser
      115             120             125

Ala Asn Ser Ser Asn Val Ile Gln Leu Ile Ile Asp Ala Tyr Asn Ser
      130             135             140

Leu Ser Ser Glu Val Ile Leu Glu Asn Gly Lys Leu Ser Glu Gly Val
      145             150             155             160

Thr Ile Ser Tyr Lys Ser Tyr Cys Lys Asn Gly Val Asn Gly Thr Gly
      165             170             175

Glu Asn Gly Arg Lys Cys Ser Asn Ile Ser Ile Gly Asp Glu Val Gln
      180             185             190

Phe Glu Ile Ser Ile Thr Ser Asn Lys Cys Pro Lys Lys Asp Ser Asp
      195             200             205

Ser Phe Lys Ile Arg Pro Leu Gly Phe Thr Glu Glu Val Glu Val Ile
      210             215             220

Leu Gln Tyr Ile Cys Glu Cys Glu Cys Gln Ser Glu Gly Ile Pro Glu
      225             230             235             240

Ser Pro Lys Cys His Glu Gly Asn Gly Thr Phe Glu Cys Gly Ala Cys
      245             250             255

Arg Cys Asn Glu Gly Arg Val Gly Arg His Cys Glu Cys Ser Thr Asp
      260             265             270

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1176

Glu Val Asn Ser Glu Asp Met Asp Ala Tyr Cys Arg Lys Glu Asn Ser
 275 280 285

Ser Glu Ile Cys Ser Asn Asn Gly Glu Cys Val Cys Gly Gln Cys Val
 290 295 300

Cys Arg Lys Arg Asp Asn Thr Asn Glu Ile Tyr Ser Gly Lys Phe Cys
 305 310 315 320

Glu Cys Asp Asn Phe Asn Cys Asp Arg Ser Asn Gly Leu Ile Cys Gly
 325 330 335

Gly Asn Gly Val Cys Lys Cys Arg Val Cys Glu Cys Asn Pro Asn Tyr
 340 345 350

Thr Gly Ser Ala Cys Asp Cys Ser Leu Asp Thr Ser Thr Cys Glu Ala
 355 360 365

Ser Asn Gly Gln Ile Cys Asn Gly Arg Gly Ile Cys Glu Cys Gly Val
 370 375 380

Cys Lys Cys Thr Asp Pro Lys Phe Gln Gly Gln Thr Cys Glu Met Cys
 385 390 395 400

Gln Thr Cys Leu Gly Val Cys Ala Glu His Lys Glu Cys Val Gln Cys
 405 410 415

Arg Ala Phe Asn Lys Gly Glu Lys Lys Asp Thr Cys Thr Gln Glu Cys
 420 425 430

Ser Tyr Phe Asn Ile Thr Lys Val Glu Ser Arg Asp Lys Leu Pro Gln
 435 440 445

Pro Val Gln Pro Asp Pro Val Ser His Cys Lys Glu Lys Asp Val Asp
 450 455 460

Asp Cys Trp Phe Tyr Phe Thr Tyr Ser Val Asn Gly Asn Asn Glu Val
 465 470 475 480

Met Val His Val Val Glu Asn Pro Glu Cys Pro Thr Gly Pro Asp Ile
 485 490 495

Ile Pro Ile Val Ala Gly Val Val Ala Gly Ile Val Leu Ile Gly Leu
 500 505 510

Ala Leu Leu Leu Ile Trp Lys Leu Leu Met Ile Ile His Asp Arg Arg
 515 520 525

Glu Phe Ala Lys Phe Glu Lys Glu Lys Met Asn Ala Lys Trp Asp Thr
 530 535 540

1177

Gly Glu Asn Pro Ile Tyr Lys Ser Ala Val Thr Thr Val Val Asn Pro
 545 550 555 560

Lys Tyr Glu Gly Lys
 565

<210> 1164

<211> 138

<212> PRT

<213> Homo sapiens

<400> 1164

Gly Thr Ala Gly Gly Ala Gly Gly Gln Arg Glu Val Arg Gly Cys Ser
 1 5 10 15

Ala Gln Glu Thr Met Ser Gly Gly Ser Ser Cys Ser Gln Thr Pro Ser
 20 25 30

Arg Ala Ile Pro Ala Thr Arg Arg Val Val Leu Gly Asp Gly Val Gln
 35 40 45

Leu Pro Pro Gly Asp Tyr Ser Thr Thr Pro Gly Gly Thr Leu Phe Ser
 50 55 60

Thr Thr Pro Gly Gly Thr Arg Ile Ile Tyr Asp Arg Lys Phe Leu Met
 65 70 75 80

Glu Cys Arg Asn Ser Pro Val Thr Lys Thr Pro Pro Arg Asp Leu Pro
 85 90 95

Thr Ile Pro Gly Val Thr Ser Pro Ser Ser Asp Glu Pro Pro Met Glu
 100 105 110

Ala Ser Gln Ser His Leu Arg Asn Ser Pro Glu Asp Lys Arg Ala Gly
 115 120 125

Gly Glu Glu Ser Gln Phe Glu Met Asp Ile
 130 135

<210> 1165

<211> 407

<212> PRT

<213> Homo sapiens

<400> 1165

Ala Ala Cys Gln Pro Arg Cys Cys Cys Ser Ser Cys Cys Gly Thr Ala

1178

1	5	10	15
Asp Arg Ala Ala Ala Pro Leu Ser Pro Leu Gln Ala Pro Ile Trp Ala			
20	25	30	
Pro Ala Thr Ser Met Asp Ala Arg Arg Val Pro Gln Lys Asp Leu Arg			
35	40	45	
Val Lys Lys Asn Leu Lys Lys Phe Arg Tyr Val Lys Leu Ile Ser Met			
50	55	60	
Glu Thr Ser Ser Ser Ser Asp Asp Ser Cys Asp Ser Phe Ala Ser Asp			
65	70	75	80
Asn Phe Ala Asn Thr Arg Leu Gln Ser Val Arg Glu Gly Cys Arg Thr			
85	90	95	
Arg Ser Gln Cys Arg His Ser Gly Pro Leu Arg Val Ala Met Lys Phe			
100	105	110	
Pro Ala Arg Ser Thr Arg Gly Ala Thr Asn Lys Lys Ala Glu Ser Arg			
115	120	125	
Gln Pro Ser Glu Asn Ser Val Thr Asp Ser Asn Ser Asp Ser Glu Asp			
130	135	140	
Glu Ser Gly Met Asn Phe Leu Glu Lys Arg Ala Leu Asn Ile Lys Gln			
145	150	155	160
Asn Lys Ala Met Leu Ala Lys Leu Met Ser Glu Leu Glu Ser Phe Pro			
165	170	175	
Gly Ser Phe Arg Gly Arg His Pro Leu Pro Gly Ser Asp Ser Gln Ser			
180	185	190	
Arg Arg Pro Arg Arg Arg Thr Phe Pro Gly Val Ala Ser Arg Arg Asn			
195	200	205	
Pro Glu Arg Arg Ala Arg Pro Leu Thr Arg Ser Arg Ser Arg Ile Leu			
210	215	220	
Gly Ser Leu Asp Ala Leu Pro Met Glu Glu Glu Glu Glu Asp Lys			
225	230	235	240
Tyr Met Leu Val Arg Lys Arg Lys Thr Val Asp Gly Tyr Met Asn Glu			
245	250	255	
Asp Asp Leu Pro Arg Ser Arg Arg Ser Arg Ser Ser Val Thr Leu Pro			
260	265	270	
His Ile Ile Arg Pro Val Glu Glu Ile Thr Glu Glu Glu Leu Glu Asn			

1179

275	280	285
Val Cys Ser Asn Ser Arg Glu Lys Ile Tyr Asn Arg Ser Leu Gly Ser		
290	295	300
Thr Cys His Gln Cys Arg Gln Lys Thr Ile Asp Thr Lys Thr Asn Cys		
305	310	315 320
Arg Asn Pro Asp Cys Trp Gly Val Arg Gly Gln Phe Cys Gly Pro Cys		
	325	330 335
Leu Arg Asn Arg Tyr Gly Glu Glu Val Arg Asp Ala Leu Leu Asp Pro		
	340	345 350
Asn Trp His Cys Pro Pro Cys Arg Gly Ile Cys Asn Cys Ser Phe Cys		
	355	360 365
Arg Gln Arg Asp Gly Arg Cys Ala Thr Gly Val Leu Val Tyr Leu Ala		
	370	375 380
Lys Tyr His Gly Phe Gly Asn Val His Ala Tyr Leu Lys Ser Leu Lys		
	385	390 395 400
Gln Glu Phe Glu Met Gln Ala		
	405	

<210> 1166

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (197)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (201)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (202)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (219)

1180

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1166

Pro Asp Gly Arg Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu
 1 5 10 15

Glu Tyr Ala Gln Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys
 20 25 30

Arg Tyr Ile Glu Leu Phe Arg Ser Thr Ala Ala Glu Val Gln Gln Val
 35 40 45

Leu Asn Arg Phe Ser Ser Ala Pro Leu Ile Pro Leu Pro Thr Pro Pro
 50 55 60

Ile Ile Pro Val Leu Pro Gln Gln Phe Val Pro Pro Thr Asn Val Arg
 65 70 75 80

Asp Cys Ile Arg Leu Arg Gly Leu Pro Tyr Ala Ala Thr Ile Glu Asp
 85 90 95

Ile Leu Asp Phe Leu Gly Glu Phe Ala Thr Asp Ile Arg Thr His Gly
 100 105 110

Val His Met Val Leu Asn His Gln Gly Arg Pro Ser Gly Asp Ala Phe
 115 120 125

Ile Gln Met Lys Ser Ala Asp Arg Ala Phe Met Ala Ala Gln Lys Cys
 130 135 140

His Lys Lys Asn Met Lys Asp Arg Tyr Val Glu Val Phe Gln Cys Ser
 145 150 155 160

Ala Glu Glu Met Asn Phe Val Leu Met Gly Gly Thr Leu Asn Arg Asn
 165 170 175

Gly Leu Ser Pro Pro Pro Cys Leu Ser Pro Pro Ser Tyr Thr Phe Pro
 180 185 190

Ala Pro Ala Ala Xaa Ile Pro Thr Xaa Xaa Ala Ile Tyr Gln Pro Ser
 195 200 205

Val Ile Leu Asn Pro Arg Ala Leu Gln Pro Xaa Thr Ala Tyr Tyr Pro
 210 215 220

Ala Gly Thr Gln Leu Phe Met Asn Tyr Thr Ala Tyr Tyr Pro Ser Val
 225 230 235 240

1181

<210> 1167

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1167

Gly Gly Tyr Ser Val Asp Ser Pro Thr Leu Thr Arg Phe Phe Thr Phe
 1 5 10 15

His Phe Ile Leu Pro Phe Ile Ile Ala Ala Leu Ala Ala Leu His Leu
 20 25 30

Leu Phe Leu His Glu Thr Gly Ser Asn Asn Pro Leu Gly Ile Thr Ser
 35 40 45

His Ser Asp Lys Ile Thr Phe His Pro Tyr Tyr Thr Ile Lys Asp Ala
 50 55 60

Leu Gly Leu Leu Leu Phe Leu Leu Ser Leu Met Thr Leu Thr Leu Phe
 65 70 75 80

Ser Pro Asp Leu Leu Gly Asp Pro Asp Asn Tyr Thr Leu Ala Asn Pro
 85 90 95

Leu Asn Thr Pro Pro His Ile Lys Pro Glu
 100 105

<210> 1168

<211> 210

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (53)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1168

Gln His Val Gln Arg Glu Trp Ser Gly His Gly Glu Asp Arg Gly Asp
 1 5 10 15

Gly Glu Asp Ala Glu Arg Gly Ser Cys Arg Glu Glu Pro Ala His Gly
 20 25 30

Val Glu Gly Ala Gly Asp Gly Ala Ala Ala Ala Gly Pro Gly Gly Gly
 35 40 45

1182

Ala Ala Glu Ala Xaa Gln Val Glu Arg Arg Leu Gln Ser Glu Ser Ala
 50 55 60
 Arg Arg Gln Gln Leu Val Glu Lys Glu Val Lys Met Arg Glu Lys Gln
 65 70 75 80
 Phe Ser Gln Ala Arg Pro Leu Thr Arg Tyr Leu Pro Ile Arg Lys Glu
 85 90 95
 Asp Phe Asp Leu Lys Thr His Ile Glu Ser Ser Gly His Gly Val Asp
 100 105 110
 Thr Cys Leu His Val Val Leu Ser Ser Lys Val Cys Arg Gly Tyr Leu
 115 120 125
 Val Lys Met Gly Gly Lys Ile Lys Ser Trp Lys Lys Arg Trp Phe Val
 130 135 140
 Phe Asp Arg Leu Lys Arg Thr Leu Ser Tyr Tyr Val Asp Lys His Glu
 145 150 155 160
 Thr Lys Leu Lys Gly Val Ile Tyr Phe Gln Ala Ile Glu Gly Ser Val
 165 170 175
 Leu Arg Pro Pro Ala Pro Val Gln Pro Arg Arg Gly Phe Ser Ala Ser
 180 185 190
 Thr Met Val Thr Glu Lys Pro Glu Pro Ser Pro His Leu Leu Arg Lys
 195 200 205
 Asp Pro
 210

<210> 1169
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 1169
 Thr Ser Lys Met Arg Ser Leu Glu Thr Leu Gly Arg Pro Lys Pro Glu
 1 5 10 15
 Cys Glu Gly Tyr Asp Pro Asn Ala Leu Tyr Cys Ile Cys Arg Gln Pro
 20 25 30
 His Asn Asn Arg Phe Met Ile Cys Cys Asp Arg Cys Glu Glu Trp Phe
 35 40 45
 His Gly Asp Cys Val Gly Ile Ser Glu Ala Arg Gly Arg Leu Leu Glu

1183

50	55	60
Arg Asn Gly Glu Asp Tyr Ile Cys Pro Asn Cys Thr Ile Leu Gln Val		
65	70	75 80
Gln Asp Glu Thr His Ser Glu Thr Ala Asp Gln Gln Glu Ala Lys Trp		
	85	90 95
Arg Pro Gly Asp Ala Asp Gly Thr Asp Cys Thr Ser Ile Gly Thr Ile		
100	105	110
Glu Gln Lys Ser Ser Glu Asp Gln Gly Ile Lys Gly Arg Ile Glu Lys		
115	120	125
Ala Ala Asn Pro Ser Gly Lys Lys Lys Leu Lys Ile Phe Gln Pro Val		
130	135	140
Ile Glu Ala Pro Gly Ala Ser Lys Cys Ile Gly Pro Gly Cys Cys His		
145	150	155 160
Val Ala His Pro Thr Arg Cys Thr Ala Val Met Thr Val Ser Ser Asn		
	165	170 175
Thr Pro Gln Arg Gln		
180		

<210> 1170

<211> 166

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (18)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (131)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1170

Ala Gln Xaa Leu Ser Ser Pro Val Arg Gly Ile Ser Gly Glu Gln Ser

1

5

10

15

1184

Thr Xaa Gly Ser Phe Pro Leu Arg Tyr Val Gln Asp Gln Val Ala Ala
 20 25 30

Pro Phe Gln Leu Ser Asn His Thr Gly Arg Ile Lys Val Val Phe Thr
 35 40 45

Pro Ser Ile Cys Lys Val Thr Cys Thr Lys Gly Ser Cys Gln Asn Ser
 50 55 60

Cys Glu Lys Gly Asn Thr Thr Thr Leu Ile Ser Glu Asn Gly His Ala
 65 70 75 80

Ala Asp Thr Leu Thr Ala Thr Asn Phe Arg Val Val Ile Cys His Leu
 85 90 95

Pro Cys Met Asn Gly Gly Gln Cys Ser Ser Arg Asp Lys Cys Gln Cys
 100 105 110

Pro Pro Asn Phe Thr Gly Lys Leu Cys Gln Ile Pro Val His Gly Ala
 115 120 125

Ser Val Xaa Lys Leu Tyr Gln His Ser Gln Gln Pro Gly Lys Ala Leu
 130 135 140

Gly Thr His Val Ile His Ser Thr His Thr Leu Pro Leu Thr Val Thr
 145 150 155 160

Ser Gln Gln Glu Ser Lys
 165

<210> 1171

<211> 37

<212> PRT

<213> Homo sapiens

<400> 1171

Asp Leu Ser Val Asn Phe Trp Glu Pro Asn Gly Phe Gly His Asp Phe
 1 5 10 15

Pro Ala His Tyr Ile Leu Thr Gln Asn Phe Phe Arg Met Ala Phe Thr
 20 25 30

Ser Thr Pro Glu Ile
 35

<210> 1172

1185

<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (70)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (115)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (116)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (163)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (167)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1172
Arg Gly Ala Met Val Ser Cys Arg Pro Gly Cys Cys Cys Pro Trp Thr
1 5 10 15
Pro Ala Val Leu Arg Xaa Ser Val Arg Gly Thr Phe Tyr Ser Pro Pro
20 25 30
Glu Ser Phe Ala Gly Ser Asp Asn Glu Ser Asp Glu Glu Val Ala Gly
35 40 45
Lys Lys Ser Phe Ser Ala Gln Glu Arg Glu Tyr Ile Arg Gln Gly Lys
50 55 60
Glu Ala Thr Ala Val Xaa Asp Gln Ile Leu Ala Gln Glu Glu Asn Trp
65 70 75 80
Lys Phe Glu Lys Asn Asn Glu Tyr Gly Asp Thr Val Tyr Thr Ile Glu

1186

	85		90		95										
Val	Pro	Phe	His	Gly	Lys	Thr	Phe	Ile	Leu	Lys	Thr	Phe	Leu	Pro	Cys
	100							105					110		
Pro	Ala	Xaa	Xaa	Val	Tyr	Gln	Glu	Val	Ile	Leu	Gln	Pro	Glu	Arg	Met
	115						120					125			
Val	Leu	Trp	Asn	Lys	Thr	Val	Thr	Ala	Cys	Gln	Ile	Leu	Gln	Arg	Val
	130					135					140				
Glu	Asp	Asn	Thr	Leu	Ile	Ser	Tyr	Asp	Val	Ser	Ala	Arg	Gly	Cys	Gly
145				150						155				160	
Arg	Arg	Xaa	Leu	Pro	Gln	Xaa	Thr	Ser							
			165												

<210> 1173

<211> 180

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (171)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1173

Glu	Tyr	Gly	Asp	Thr	Val	Tyr	Thr	Ile	Glu	Val	Pro	Phe	His	Gly	Lys
1				5					10					15	
Thr	Phe	Ile	Leu	Lys	Thr	Phe	Leu	Pro	Cys	Pro	Ala	Glu	Leu	Val	Tyr
			20					25					30		
Gln	Glu	Val	Ile	Leu	Gln	Pro	Glu	Arg	Met	Val	Leu	Trp	Asn	Lys	Thr
	35					40					45				
Val	Thr	Ala	Cys	Gln	Ile	Leu	Gln	Arg	Val	Glu	Asp	Asn	Thr	Leu	Ile
	50				55					60					
Ser	Tyr	Asp	Val	Ser	Ala	Gly	Ala	Ala	Gly	Gly	Val	Val	Ser	Pro	Arg
65				70					75					80	
Asp	Phe	Val	Asn	Val	Arg	Arg	Ile	Glu	Arg	Arg	Arg	Asp	Arg	Tyr	Leu
			85					90					95		
Ser	Ser	Gly	Ile	Ala	Thr	Ser	His	Ser	Ala	Lys	Pro	Pro	Thr	His	Lys
		100						105					110		

1187

Tyr Val Arg Gly Glu Asn Gly Pro Gly Gly Phe Ile Val Leu Lys Ser
 115 120 125

Ala Ser Asn Pro Arg Val Cys Thr Phe Val Trp Ile Leu Asn Thr Asp
 130 135 140

Leu Lys Gly Arg Leu Pro Arg Tyr Leu Ile His Gln Ser Leu Ala Ala
 145 150 155 160

Thr Met Phe Glu Phe Ala Phe His Leu Arg Xaa Arg Ile Ser Glu Leu
 165 170 175

Gly Ala Arg Ala
 180

<210> 1174

<211> 436

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (14)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (426)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1174

Arg His Gln Arg Arg Arg Ser Val Trp Arg Ser Arg Gly Xaa Cys Cys
 1 5 10 15

Arg Cys Cys Cys Thr Asn Arg Arg Ser Pro Gln Pro Cys Ala Ser Ser
 20 25 30

Leu Pro Pro Arg Thr Gly Glu Lys Gln Pro Arg Asn Phe Met Asn Lys
 35 40 45

His Gln Lys Pro Val Leu Thr Gly Gln Arg Phe Lys Thr Arg Lys Arg
 50 55 60

Asp Glu Lys Glu Lys Phe Glu Pro Thr Val Phe Arg Asp Thr Leu Val
 65 70 75 80

Gln Gly Leu Asn Glu Ala Gly Asp Asp Leu Glu Ala Val Ala Lys Phe
 85 90 95

1188

Leu Asp Ser Thr Gly Ser Arg Leu Asp Tyr Arg Arg Tyr Ala Asp Thr
100 105 110

Leu Phe Asp Ile Leu Val Ala Gly Ser Met Leu Ala Pro Gly Gly Thr
115 120 125

Arg Ile Asp Asp Gly Asp Lys Thr Lys Met Thr Asn His Cys Val Phe
130 135 140

Ser Ala Asn Glu Asp His Glu Thr Ile Arg Asn Tyr Ala Gln Val Phe
145 150 155 160

Asn Lys Leu Ile Arg Arg Tyr Lys Tyr Leu Glu Lys Ala Phe Glu Asp
165 170 175

Glu Met Lys Lys Leu Leu Leu Phe Leu Lys Ala Phe Ser Glu Thr Glu
180 185 190

Gln Thr Lys Leu Ala Met Leu Ser Gly Ile Leu Leu Gly Asn Gly Thr
195 200 205

Leu Pro Ala Thr Ile Leu Thr Ser Leu Phe Thr Asp Ser Leu Val Lys
210 215 220

Glu Gly Ile Ala Ala Ser Phe Ala Val Lys Leu Phe Lys Ala Trp Met
225 230 235 240

Ala Glu Lys Asp Ala Asn Ser Val Thr Ser Ser Leu Arg Lys Ala Asn
245 250 255

Leu Asp Lys Arg Leu Leu Glu Leu Phe Pro Val Asn Arg Gln Ser Val
260 265 270

Asp His Phe Ala Lys Tyr Phe Thr Asp Ala Gly Leu Lys Glu Leu Ser
275 280 285

Asp Phe Leu Arg Val Gln Gln Ser Leu Gly Thr Arg Lys Glu Leu Gln
290 295 300

Lys Glu Leu Gln Glu Arg Leu Ser Gln Glu Cys Pro Ile Lys Glu Val
305 310 315 320

Val Leu Tyr Val Lys Glu Glu Met Lys Arg Asn Asp Leu Pro Glu Thr
325 330 335

Ala Val Ile Gly Leu Leu Trp Thr Cys Ile Met Asn Ala Val Glu Trp
340 345 350

Asn Lys Lys Glu Glu Leu Val Ala Glu Gln Ala Leu Lys His Leu Lys
355 360 365

1189

Gln Tyr Ala Pro Leu Leu Ala Val Phe Ser Ser Gln Gly Gln Ser Glu
 370 375 380

Leu Ile Leu Leu Gln Lys Val Gln Glu Tyr Cys Tyr Asp Asn Ile His
 385 390 395 400

Phe Met Lys Ala Phe Gln Lys Ile Val Leu Pro Tyr Thr Ile Ser Val
 405 410 415

Leu Leu Leu Arg Ser Glu His Gln Leu Xaa Ser Cys Arg Phe Gly Thr
 420 425 430

Ser Gly Thr Ser
 435

<210> 1175
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 1175
 Thr Glu Pro Val Gly Tyr Thr Lys Ala Glu Glu Pro Ile Ala Met Arg
 1 5 10 15

Ser Leu Gly Ala Leu Leu Leu Leu Ser Ala Cys Leu Ala Val Ser
 20 25 30

Ala Gly Pro Val Pro Thr Pro Pro Asp Asn Ile Gln Val Gln Glu Asn
 35 40 45

Phe Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala Ile Gly
 50 55 60

Ser Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr Val Ser
 65 70 75 80

Thr Leu Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser Met Thr
 85 90 95

Ser Thr Arg Trp Arg Lys Gly Val Cys Glu Glu Thr Ser Gly Ala Tyr
 100 105 110

Glu Lys Thr Asp Thr Asp Gly Lys Phe Leu Tyr His Lys Ser Lys Trp
 115 120 125

Asn Ile Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp Glu Tyr
 130 135 140

Ala Ile Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro Thr Ile

1190

145 150 155 160
Thr Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr Leu Leu
 165 170 175
Gln Asp Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu Asp Ser
 180 185 190
Ile Phe Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu Gln Glu
 195 200 205
Pro Glu Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Val Leu Pro Gln
 210 215 220
Glu Glu Glu Gly Ser Gly Gly Gly Gln Leu Val Thr Glu Val Thr Lys
225 230 235 240
Lys Glu Asp Ser Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys Met Gly
 245 250 255
Met Thr Ser Arg Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys Glu Thr
 260 265 270
Phe Gln Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Val Thr Glu
 275 280 285
Lys Glu Cys Leu Gln Thr Cys Arg Thr Val Ala Ala Cys Asn Leu Pro
 290 295 300
Ile Val Arg Gly Pro Cys Arg Ala Phe Ile Gln Leu Trp Ala Phe Asp
305 310 315 320
Ala Val Lys Gly Lys Cys Val Leu Phe Pro Tyr Gly Gly Cys Gln Gly
 325 330 335
Asn Gly Asn Lys Phe Tyr Ser Glu Lys Glu Cys Arg Glu Tyr Cys Gly
 340 345 350
Val Pro Gly Asp Gly Asp Glu Glu Leu Leu Arg Phe Ser Asn
 355 360 365

<210> 1176

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (105)

1191

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (120)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (126)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1176

Met	Pro	Arg	Ser	Ser	His	His	Pro	Pro	Arg	Arg	His	Tyr	His	His	His
1				5					10					15	

His	Tyr	His	Gln	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Ser	Pro	Pro	Leu	Thr
			20					25						30	

Ser	Pro	Ser	Pro	Leu	Ser	Trp	Ile	Leu	Trp	Thr	Cys	Trp	Pro	Ser	Thr
		35					40					45			

Ala	Ala	Thr	Arg	Pro	Gly	Arg	Arg	Lys	Trp	Gly	Cys	Arg	Leu	Cys	Pro
		50				55					60				

Arg	His	Ser	Ser	Pro	Leu	Leu	Leu	Leu	His	Leu	Asn	Leu	Leu	Ala	Trp
65					70					75					80

Ala	Pro	Tyr	Pro	His	Pro	Ala	Thr	Thr	Arg	Gly	Asp	Arg	Lys	Gln	Lys
				85					90					95	

Lys	Arg	Asp	Gln	Asn	Lys	Ser	Ala	Xaa	Leu	Arg	Tyr	Arg	Gln	Arg	Lys
			100					105					110		

Gly	Ala	Gly	Gly	Val	Glu	Gly	Xaa	Gly	Lys	Gly	Lys	Leu	Xaa	Gly	Gly
		115					120					125			

Trp	Glu	Gly	Lys	Gly
				130

<210> 1177

<211> 583

<212> PRT

<213> Homo sapiens

<400> 1177

Thr	Ala	Gln	Arg	Pro	Arg	Ser	Pro	Glu	Asn	Cys	Arg	Pro	Ser	Thr	Met
1					5				10					15	

1192

Trp Leu Arg Ala Phe Ile Leu Ala Thr Leu Ser Ala Ser Ala Ala Trp
 20 25 30
 Ala Gly His Pro Ser Ser Pro Pro Val Val Asp Thr Val His Gly Lys
 35 40 45
 Val Leu Gly Lys Phe Val Ser Leu Glu Gly Phe Ala Gln Pro Val Ala
 50 55 60
 Ile Phe Leu Gly Ile Pro Phe Ala Lys Pro Pro Leu Gly Pro Leu Arg
 65 70 75 80
 Phe Thr Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Ala
 85 90 95
 Thr Ser Tyr Pro Pro Met Cys Thr Gln Asp Pro Lys Ala Gly Gln Leu
 100 105 110
 Leu Ser Glu Leu Phe Thr Asn Arg Lys Glu Asn Ile Pro Leu Lys Leu
 115 120 125
 Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr
 130 135 140
 Lys Lys Asn Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu
 145 150 155 160
 Met Val Gly Ala Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His
 165 170 175
 Glu Asn Val Val Val Val Thr Ile Gln Tyr Arg Leu Gly Ile Trp Gly
 180 185 190
 Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu
 195 200 205
 Asp Gln Val Ala Ala Leu Arg Trp Val Gln Asp Asn Ile Ala Ser Phe
 210 215 220
 Gly Gly Asn Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly
 225 230 235 240
 Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe
 245 250 255
 His Arg Ala Ile Ser Glu Ser Gly Val Ala Leu Thr Ser Val Leu Val
 260 265 270
 Lys Lys Gly Asp Val Lys Pro Leu Ala Glu Gln Ile Ala Ile Thr Ala
 275 280 285

1193

Gly Cys Lys Thr Thr Thr Ser Ala Val Met Val His Cys Leu Arg Gln
 290 295 300
 Lys Thr Glu Glu Glu Leu Leu Glu Thr Thr Leu Lys Met Lys Phe Leu
 305 310 315 320
 Ser Leu Asp Leu Gln Gly Asp Pro Arg Glu Ser Gln Pro Leu Leu Gly
 325 330 335
 Thr Val Ile Asp Gly Met Leu Leu Leu Lys Thr Pro Glu Glu Leu Gln
 340 345 350
 Ala Glu Arg Asn Phe His Thr Val Pro Tyr Met Val Gly Ile Asn Lys
 355 360 365
 Gln Glu Phe Gly Trp Leu Ile Pro Met Gln Leu Met Ser Tyr Pro Leu
 370 375 380
 Ser Glu Gly Gln Leu Asp Gln Lys Thr Ala Met Ser Leu Leu Trp Lys
 385 390 395 400
 Ser Tyr Pro Leu Val Cys Ile Ala Lys Glu Leu Ile Pro Glu Ala Thr
 405 410 415
 Glu Lys Tyr Leu Gly Gly Thr Asp Asp Thr Val Lys Lys Lys Asp Leu
 420 425 430
 Phe Leu Asp Leu Ile Ala Asp Val Met Phe Gly Val Pro Ser Val Ile
 435 440 445
 Val Ala Arg Asn His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu
 450 455 460
 Phe Gln Tyr Arg Pro Ser Phe Ser Ser Asp Met Lys Pro Lys Thr Val
 465 470 475 480
 Ile Gly Asp His Gly Asp Glu Leu Phe Ser Val Phe Gly Ala Pro Phe
 485 490 495
 Leu Lys Glu Gly Ala Ser Glu Glu Glu Ile Arg Leu Ser Lys Met Val
 500 505 510
 Met Lys Phe Trp Ala Asn Phe Ala Arg Asn Gly Asn Pro Asn Gly Glu
 515 520 525
 Gly Leu Pro His Trp Pro Glu Tyr Asn Gln Lys Glu Gly Tyr Leu Gln
 530 535 540
 Ile Gly Ala Asn Thr Gln Ala Ala Gln Lys Leu Lys Asp Lys Glu Val
 545 550 555 560

1194

Ala Phe Trp Thr Asn Leu Phe Ala Lys Lys Ala Val Glu Lys Pro Pro
565 570 575

Gln Thr Glu His Ile Glu Leu
580

<210> 1178

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1178

Pro Gly Arg Xaa Gln Leu Arg Ala Lys Phe Ser Cys Pro Pro Ala Asp
1 5 10 15

Arg Val Asn Val Thr Val Arg Pro Gly Leu Ala Met Ala Leu Ser Gly
20 25 30

Ser Thr Glu Pro Cys Ala Gln Leu Ser Ile Ser Ser Ile Gly Val Val
35 40 45

Gly Thr Ala Glu Asp Asn Arg Ser His Ser Ala His Phe Phe Glu Phe
50 55 60

Leu Thr Lys Glu Leu Ala Leu Gly Gln Asp Arg Ile Leu Ile Arg Phe
65 70 75 80

Phe Pro Leu Glu Ser Trp Gln Ile Gly Lys Ile Gly Thr Val Met Thr
85 90 95

Phe Leu

<210> 1179

<211> 127

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

1195

<220>

<221> SITE

<222> (50)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (67)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1179

Phe Arg Pro Ala Val Ser Xaa Gly Ser Leu Cys Leu Pro Ala Arg Thr
 1 5 10 15

Ala His Ser Pro Ala Ser Ser Ala Ala Cys Arg Thr Met Ala Gln Gly
 20 25 30

Gln Arg Lys Phe Gln Ala His Lys Pro Ala Lys Ser Lys Thr Ala Ala
 35 40 45

Ala Xaa Ser Glu Lys Asn Arg Gly Pro Arg Lys Gly Gly Arg Val Ile
 50 55 60

Ala Pro Xaa Lys Ala Arg Val Val Gln Gln Gln Lys Leu Lys Lys Asn
 65 70 75 80

Leu Glu Val Gly Ile Arg Lys Lys Ile Glu His Asp Val Val Met Lys
 85 90 95

Ala Ser Ser Ser Leu Pro Lys Lys Leu Ala Leu Leu Lys Ala Pro Ala
 100 105 110

Lys Lys Lys Gly Ala Ala Ala Ala Thr Ser Ser Lys Thr Pro Ser
 115 120 125

<210> 1180

<211> 94

<212> PRT

<213> Homo sapiens

<400> 1180

Ser Ser Tyr Arg Ser Lys Ala Tyr Thr His Thr Lys Ile Thr Val Pro
 1 5 10 15

Arg Glu Arg Val Cys Val Ser Val Arg Val Ser Val Cys Ala Arg Ala
 20 25 30

Arg Ser Trp Pro Asn Val Arg Thr Leu His Lys Gly Gly Arg Ser Ser

1196

35 40 45
 Tyr Arg Leu Phe Asn Val Arg Glu Thr Ile Phe Leu Leu Phe Gln Leu
 50 55 60
 Tyr Gln Ile Leu Val Pro Gln His Arg Asn Asp Ser Glu Ser Gln Thr
 65 70 75 80
 Lys Cys Ile Ile Cys Ser Ile Leu Ile Leu Leu His Ser
 85 90

<210> 1181
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 1181
 Gly Ser Leu Asp Leu Trp Arg Gly Ala Glu Leu Ser Pro Gly His Ser
 1 5 10 15
 Thr Leu Phe Thr Leu Cys Ala Cys Ala Lys Gly Ala Met Ala Ala Ser
 20 25 30
 Cys Val Leu Leu His Thr Gly Gln Lys Met Pro Leu Ile Gly Leu Gly
 35 40 45
 Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala Val Lys Tyr Ala
 50 55 60
 Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ala Ile Tyr Gly Asn
 65 70 75 80
 Glu Pro Glu Ile Gly Glu Ala Leu Lys Glu Asp Val Gly Pro Gly Lys
 85 90 95
 Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys Leu Trp Asn Thr
 100 105 110
 Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg Lys Thr Leu Ala
 115 120 125
 Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met His Trp Pro Tyr
 130 135 140
 Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn Ala Asp Gly Thr
 145 150 155 160
 Ile Cys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp Lys Ala Leu Glu
 165 170 175

1197

Ala Leu Val Ala Lys Gly Leu Val Gln Ala Leu Gly Leu Ser Asn Phe
 180 185 190

Asn Ser Arg Gln Ile Asp Asp Ile Leu Ser Val Ala Ser Val Arg Pro
 195 200 205

Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala Gln Asn Glu Leu
 210 215 220

Ile Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr Ala Tyr Ser Pro
 225 230 235 240

Leu Gly Ser Ser Asp Arg Ala Trp Arg Asp Pro Asp Glu Pro Val Leu
 245 250 255

Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys Tyr Gly Arg Ser
 260 265 270

Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg Lys Val Ile Cys
 275 280 285

Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln Asn Ile Lys Val
 290 295 300

Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln Leu Asn Ala Leu
 305 310 315 320

Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Leu Thr Val Asp Gly Lys
 325 330 335

Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro Phe Asn Asp Pro
 340 345 350

Tyr

<210> 1182
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 1182
 Ala Arg Asp Ser Leu Gln Leu Ser Met Ala Gln Thr Ser Ser Tyr Phe
 1 5 10 15

Met Leu Ile Ser Cys Leu Met Phe Leu Ser Gln Ser Gln Gly Gln Glu
 20 25 30

1198

Ala Gln Thr Glu Leu Pro Gln Ala Arg Ile Ser Cys Pro Glu Gly Thr
 35 40 45
 Asn Ala Tyr Arg Ser Tyr Cys Tyr Tyr Phe Asn Glu Asp Arg Glu Thr
 50 55 60
 Trp Val Asp Ala Asp Leu Tyr Cys Gln Asn Met Asn Ser Gly Asn Leu
 65 70 75 80
 Val Ser Val Leu Thr Gln Ala Glu Gly Ala Phe Val Ala Ser Leu Ile
 85 90 95
 Lys Glu Ser Gly Thr Asp Asp Phe Asn Val Trp Ile Gly Leu His Asp
 100 105 110
 Pro Lys Lys Asn Arg Arg Trp His Trp Ser Ser Gly Ser Leu Val Ser
 115 120 125
 Tyr Lys Ser Trp Gly Ile Gly Ala Pro Ser Ser Val Asn Pro Gly Tyr
 130 135 140
 Cys Val Ser Leu Thr Ser Ser Thr Gly Phe Gln Lys Trp Lys Asp Val
 145 150 155 160
 Pro Cys Glu Asp Lys Phe Ser Phe Val Cys Lys Phe Lys Asn
 165 170

<210> 1183

<211> 342

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (169)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (171)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (187)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1199

<222> (302)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (308)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1183

Ser Ile Phe Ser Tyr Ile Arg Leu Glu Leu Pro Ser Met Trp Leu Leu
 1 5 10 15

Val Ser Val Ile Leu Ile Ser Arg Ile Ser Ser Val Gly Gly Glu Ala
 20 25 30

Thr Phe Cys Asp Phe Pro Lys Ile Asn His Gly Ile Leu Tyr Asp Glu
 35 40 45

Glu Lys Tyr Lys Pro Phe Ser Gln Val Pro Thr Gly Glu Val Phe Tyr
 50 55 60

Tyr Ser Cys Glu Tyr Asn Phe Val Ser Pro Ser Lys Ser Phe Trp Thr
 65 70 75 80

Arg Ile Thr Cys Thr Glu Glu Gly Trp Ser Pro Thr Pro Lys Cys Leu
 85 90 95

Arg Leu Cys Phe Phe Pro Phe Val Glu Asn Gly His Ser Glu Ser Ser
 100 105 110

Gly Gln Thr His Leu Glu Gly Asp Thr Val Gln Ile Ile Cys Asn Thr
 115 120 125

Gly Tyr Arg Leu Gln Asn Asn Glu Asn Asn Ile Ser Cys Val Glu Arg
 130 135 140

Gly Trp Ser Thr Pro Pro Lys Cys Arg Ser Thr Asp Thr Ser Cys Val
 145 150 155 160

Asn Pro Pro Thr Val Gln Asn Ala Xaa Ile Xaa Ser Arg Gln Met Ser
 165 170 175

Lys Tyr Pro Ser Gly Glu Arg Val Arg Tyr Xaa Cys Arg Ser Pro Tyr
 180 185 190

Glu Met Phe Gly Asp Glu Glu Val Met Cys Leu Asn Gly Asn Trp Thr
 195 200 205

Glu Pro Pro Gln Cys Lys Asp Ser Thr Gly Lys Cys Gly Pro Pro Pro
 210 215 220

1200

Pro Ile Asp Asn Gly Asp Ile Thr Ser Phe Pro Leu Ser Val Tyr Ala
225 230 235 240

Pro Ala Ser Ser Val Glu Tyr Gln Cys Gln Asn Leu Tyr Gln Leu Glu
245 250 255

Gly Asn Lys Arg Ile Thr Cys Arg Asn Gly Gln Trp Ser Glu Pro Pro
260 265 270

Lys Cys Leu His Pro Cys Val Ile Ser Arg Glu Ile Met Glu Asn Tyr
275 280 285

Asn Ile Ala Leu Arg Trp Thr Ala Lys Gln Lys Leu Tyr Xaa Arg Thr
290 295 300

Gly Glu Ser Xaa Glu Phe Val Cys Lys Arg Gly Tyr Arg Leu Ser Ser
305 310 315 320

Arg Ser His Thr Leu Arg Thr Thr Cys Trp Asp Gly Lys Leu Glu Tyr
325 330 335

Pro Thr Cys Ala Lys Arg
340

<210> 1184

<211> 198

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (161)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1184

Pro Xaa Arg Pro Arg Gly Ala Ala Ala Ala Ala Ala Ala Gly Ala
1 5 10 15

Ala Met Pro Lys Gly Gly Arg Lys Gly Gly His Lys Gly Arg Ala Arg
20 25 30

Gln Tyr Thr Ser Pro Glu Glu Ile Asp Ala Gln Leu Gln Ala Glu Lys
35 40 45

1201

Gln Lys Ala Arg Glu Glu Glu Glu Gln Lys Glu Gly Gly Asp Gly Ala
 50 55 60
 Ala Gly Asp Pro Lys Lys Glu Lys Lys Ser Leu Asp Ser Asp Glu Ser
 65 70 75 80
 Glu Asp Glu Glu Asp Asp Tyr Gln Gln Lys Arg Lys Gly Val Glu Gly
 85 90 95
 Leu Ile Asp Ile Glu Asn Pro Asn Arg Val Ala Gln Thr Thr Lys Lys
 100 105 110
 Val Thr Gln Leu Asp Leu Asp Gly Pro Lys Glu Leu Ser Arg Arg Glu
 115 120 125
 Arg Glu Glu Ile Glu Lys Gln Lys Ala Lys Glu Arg Tyr Met Lys Met
 130 135 140
 His Leu Ala Gly Lys Thr Glu Gln Ala Lys Ala Asp Leu Ala Arg Leu
 145 150 155 160
 Xaa Ile Ile Arg Lys Gln Arg Glu Glu Ala Ala Arg Lys Lys Glu Glu
 165 170 175
 Glu Arg Lys Ala Lys Asp Asp Ala Thr Leu Ser Gly Lys Arg Met Gln
 180 185 190
 Ser Leu Ser Leu Asn Lys
 195

<210> 1185

<211> 210

<212> PRT

<213> Homo sapiens

<400> 1185

Ala His Ala Ser Ala His Ala Ser Gly Met Asp Leu Ser Leu Leu Trp
 1 5 10 15
 Val Leu Leu Pro Leu Val Thr Met Ala Trp Gly Gln Tyr Gly Asp Tyr
 20 25 30
 Gly Tyr Pro Tyr Gln Gln Tyr His Asp Tyr Ser Asp Asp Gly Trp Val
 35 40 45
 Asn Leu Asn Arg Gln Gly Phe Ser Tyr Gln Cys Pro Gln Gly Gln Val
 50 55 60
 Ile Val Ala Val Arg Ser Ile Phe Ser Lys Lys Glu Gly Ser Asp Arg

1202

65 70 75 80
 Gln Trp Asn Tyr Ala Cys Met Pro Thr Pro Gln Ser Leu Gly Glu Pro
 85 90 95
 Thr Glu Cys Trp Trp Glu Glu Ile Asn Arg Ala Gly Met Glu Trp Tyr
 100 105 110
 Gln Thr Cys Ser Asn Asn Gly Leu Val Ala Gly Phe Gln Ser Arg Tyr
 115 120 125
 Phe Glu Ser Val Leu Asp Arg Glu Trp Gln Phe Tyr Cys Cys Arg Tyr
 130 135 140
 Ser Lys Arg Cys Pro Tyr Ser Cys Trp Leu Thr Thr Glu Tyr Pro Gly
 145 150 155 160
 His Tyr Gly Glu Glu Met Asp Met Ile Ser Tyr Asn Tyr Asp Tyr Tyr
 165 170 175
 Ile Arg Gly Ala Thr Thr Thr Phe Ser Ala Val Glu Arg Asp Arg Gln
 180 185 190
 Trp Lys Phe Ile Met Cys Arg Met Thr Glu Tyr Asp Cys Glu Phe Ala
 195 200 205
 Asn Val
 210

<210> 1186
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 1186
 Arg Ala Ile Tyr Phe Leu Arg Val His Arg Leu Trp Ser Ser Ile Ser
 1 5 10 15
 Leu Leu Phe Phe Pro Ser Ala Lys Met Ala Leu Glu Thr Val Pro Lys
 20 25 30
 Asp Leu Arg His Leu Arg Ala Cys Leu Leu Cys Ser Leu Val Lys Thr
 35 40 45
 Ile Asp Gln Phe Glu Tyr Asp Gly Cys Asp Asn Cys Asp Ala Tyr Leu
 50 55 60
 Gln Met Lys Gly Asn Arg Glu Met Val Tyr Asp Cys Thr Ser Ser Ser
 65 70 75 80

1203

Phe Asp Gly Ile Ile Ala Met Met Ser Pro Glu Asp Ser Trp Val Ser
85 90 95

Lys Trp Gln Arg Val Ser Asn Phe Lys Pro Gly Val Tyr Ala Val Ser
100 105 110

Val Thr Gly Arg Leu Pro Gln Gly Ile Val Arg Glu Leu Lys Ser Arg
115 120 125

Gly Val Ala Tyr Lys Ser Arg Asp Thr Ala Ile Lys Thr
130 135 140

<210> 1187

<211> 76

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (66)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (74)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1187

Leu Leu Gly Ser Cys Leu Gln Glu Ala Met Thr Leu Asn Ser Glu Pro
1 5 10 15

Tyr Ser Val Leu Thr Ser Gly Ser His Val Phe Leu Cys Gln Val Ile
20 25 30

Lys Tyr Leu Val Leu Val Phe Cys Leu Xaa Pro Lys Leu Pro Leu Trp
35 40 45

Val His Arg Arg Leu Gly Ser Ile Val Arg Met Ala Ile Arg Glu Tyr
50 55 60

Lys Xaa Gly Phe Ser Lys Gly Leu Gly Xaa Asp Ser
65 70 75

1204

<210> 1188

<211> 516

<212> PRT

<213> Homo sapiens

<400> 1188

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Ile Arg Ile Ala Ala Leu Asp Asp Phe Arg Thr Ser Leu Thr Met Ser
 1             5             10             15

Ser Thr Arg Ser Gln Asn Pro His Gly Leu Lys Gln Ile Gly Leu Asp
      20             25             30

Gln Ile Trp Asp Asp Leu Arg Ala Gly Ile Gln Gln Val Tyr Thr Arg
      35             40             45

Gln Ser Met Ala Lys Ser Arg Tyr Met Glu Leu Tyr Thr His Val Tyr
      50             55             60

Asn Tyr Cys Thr Ser Val His Gln Ser Asn Gln Ala Arg Gly Ala Gly
      65             70             75             80

Val Pro Pro Ser Lys Ser Lys Lys Gly Gln Thr Pro Gly Gly Ala Gln
      85             90             95

Phe Val Gly Leu Glu Leu Tyr Lys Arg Leu Lys Glu Phe Leu Lys Asn
      100            105            110

Tyr Leu Thr Asn Leu Leu Lys Asp Gly Glu Asp Leu Met Asp Glu Ser
      115            120            125

Val Leu Lys Phe Tyr Thr Gln Gln Trp Glu Asp Tyr Arg Phe Ser Ser
      130            135            140

Lys Val Leu Asn Gly Ile Cys Ala Tyr Leu Asn Arg His Trp Val Arg
      145            150            155            160

Arg Glu Cys Asp Glu Gly Arg Lys Gly Ile Tyr Glu Ile Tyr Ser Leu
      165            170            175

Ala Leu Val Thr Trp Arg Asp Cys Leu Phe Arg Pro Leu Asn Lys Gln
      180            185            190

Val Thr Asn Ala Val Leu Lys Leu Ile Glu Lys Glu Arg Asn Gly Glu
      195            200            205

Thr Ile Asn Thr Arg Leu Ile Ser Gly Val Val Gln Ser Tyr Val Glu
      210            215            220

Leu Gly Leu Asn Glu Asp Asp Ala Phe Ala Lys Gly Pro Thr Leu Thr

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1205

225 230 235 240
 Val Tyr Lys Glu Ser Phe Glu Ser Gln Phe Leu Ala Asp Thr Glu Arg
 245 250 255
 Phe Tyr Thr Arg Glu Ser Thr Glu Phe Leu Gln Gln Asn Pro Val Thr
 260 265 270
 Glu Tyr Met Lys Lys Ala Glu Ala Arg Leu Leu Glu Glu Gln Arg Arg
 275 280 285
 Val Gln Val Tyr Leu His Glu Ser Thr Gln Asp Glu Leu Ala Arg Lys
 290 295 300
 Cys Glu Gln Val Leu Ile Glu Lys His Leu Glu Ile Phe His Thr Glu
 305 310 315 320
 Phe Gln Asn Leu Leu Asp Ala Asp Lys Asn Glu Asp Leu Gly Arg Met
 325 330 335
 Tyr Asn Leu Val Ser Arg Ile Gln Asp Gly Leu Gly Glu Leu Lys Lys
 340 345 350
 Leu Leu Glu Thr His Ile His Asn Gln Gly Leu Ala Ala Ile Glu Lys
 355 360 365
 Cys Gly Glu Ala Ala Leu Asn Asp Pro Lys Met Tyr Val Gln Thr Val
 370 375 380
 Leu Asp Val His Lys Lys Tyr Asn Ala Leu Val Met Ser Ala Phe Asn
 385 390 395 400
 Asn Asp Ala Gly Phe Val Ala Ala Leu Asp Lys Ala Cys Gly Arg Phe
 405 410 415
 Ile Asn Asn Asn Ala Val Thr Lys Met Ala Gln Ser Ser Ser Lys Ser
 420 425 430
 Pro Glu Leu Leu Ala Arg Tyr Cys Asp Ser Leu Leu Lys Lys Ser Ser
 435 440 445
 Lys Asn Pro Glu Glu Ala Glu Leu Glu Asp Thr Leu Asn Gln Val Met
 450 455 460
 Val Val Phe Lys Tyr Ile Glu Asp Lys Asp Val Phe Gln Lys Phe Tyr
 465 470 475 480
 Ala Lys Met Leu Ala Lys Arg Leu Val His Gln Asn Ser Ala Ser Asp
 485 490 495
 Asp Ala Glu Ala Ser Met Ile Ser Lys Leu Lys Gln Ala Cys Gly Phe

1206

500

505

510

Glu Tyr Thr Ser
515

<210> 1189

<211> 287

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (20)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (24)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (27)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (55)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (172)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (254)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (271)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (274)

<223> Xaa equals any of the naturally occurring L-amino acids

1207

<220>

<221> SITE

<222> (275)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (280)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1189

Met Ser Tyr Cys Asp Glu Ser Arg Leu Ser Asn Leu Leu Arg Arg Ile
 1 5 10 15

Thr Arg Glu Xaa Asp Arg Asp Xaa Arg Leu Xaa Thr Val Lys Gln Leu
 20 25 30

Lys Glu Phe Ile Gln Gln Pro Glu Asn Lys Leu Val Leu Val Lys Gln
 35 40 45

Leu Asp Ile Leu Ala Ala Xaa His Asp Val Leu Asn Glu Ser Ser Lys
 50 55 60

Leu Leu Gln Glu Leu Arg Gln Glu Gly Ala Cys Cys Leu Gly Leu Leu
 65 70 75 80

Cys Ala Ser Leu Ser Tyr Glu Ala Glu Lys Ile Phe Lys Trp Ile Phe
 85 90 95

Ser Lys Phe Ser Ser Ser Ala Lys Asp Glu Val Lys Leu Leu Tyr Leu
 100 105 110

Cys Ala Thr Tyr Lys Ala Leu Glu Thr Val Gly Glu Lys Lys Ala Phe
 115 120 125

Ser Ser Val Met Gln Leu Val Met Thr Ser Leu Gln Ser Ile Leu Glu
 130 135 140

Asn Val Asp Thr Pro Glu Leu Leu Cys Lys Cys Val Lys Cys Ile Leu
 145 150 155 160

Leu Val Ala Arg Cys Tyr Pro His Ile Phe Ser Xaa Asn Phe Arg Asp
 165 170 175

Thr Val Asp Ile Leu Val Gly Trp His Arg Asp His Thr Gln Lys Pro
 180 185 190

Ser Leu Thr Gln Gln Val Ser Gly Trp Leu Gln Ser Leu Glu Pro Phe
 195 200 205

1208

Trp Val Ala Asp Leu Ala Phe Pro Thr Thr Leu Leu Gly Gln Phe Leu
210 215 220

Glu Asp Met Glu Ala Tyr Ala Glu Asp Leu Ser His Val Ala Ser Gly
225 230 235 240

Glu Ser Val Asp Glu Asp Val Pro Pro Pro Ser Val Ser Xaa Pro Lys
245 250 255

Leu Ala Ala Leu Leu Arg Val Phe Ser Thr Val Val Arg Ser Xaa Gly
260 265 270

Glu Xaa Xaa Ser Pro Ile Arg Xaa Leu Gln Leu Leu Arg His Thr
275 280 285

<210> 1190
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1190
Arg Pro Pro Ser Arg Trp Ser Trp Trp Gln Gly Lys Pro Thr Gly Gly
1 5 10 15

Val Cys Val Ala Ala Ala Arg Ser Ser Pro Ser Val Thr Ala Pro Thr
20 25 30

Ser Ser Asn Ala Leu Ala Tyr Leu His Ser Ser Ser Arg Pro Lys Arg
35 40 45

Pro Ala Trp Trp His Ser Val Pro Ala Arg Pro Leu Arg Gly Pro Arg
50 55 60

Thr Ala Met Ala Pro Thr Gly Val Ser Ala Cys Arg Arg Gln Lys Trp
65 70 75 80

Ala Pro His Ser Glu Gly Ala Ala Ala Val Gln Pro Gln Val Ala Leu
85 90 95

Ala Pro Gly Leu
100

<210> 1191
<211> 115
<212> PRT
<213> Homo sapiens

1209

<400> 1191

Asn Asp Val Ile His Gln Tyr Val Tyr Met Tyr Phe Tyr Ile Asp Leu
 1 5 10 15

Glu Asn Thr Ala Lys Thr Phe Met Thr Ser Cys Ile Thr Ala Phe Val
 20 25 30

Tyr Ile Phe Leu Thr Val Ile Ile Pro Thr Gly Thr Leu Thr Val Ala
 35 40 45

Leu Leu Asn Val Gln Asn Leu Tyr Phe Arg Asn Asn Lys Lys Lys Asp
 50 55 60

Thr Tyr Met Phe Pro Lys Gln Trp Cys Gly Glu Cys Val Arg Lys Thr
 65 70 75 80

Asn Leu Ile Gly Ser Thr Asn Thr Lys Cys Ile Thr Asn Ala Pro Val
 85 90 95

His Val Phe Val Leu Lys Arg Val Asn Glu Asp Leu Tyr Ile Ser Ile
 100 105 110

Asn Asp Ile
 115

<210> 1192

<211> 415

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (11)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (13)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1192

Arg Ile Pro Pro Glu Ser Leu Ala Arg Glu Xaa Arg Xaa Thr Lys Ser
 1 5 10 15

Phe Ser Asn Pro Arg Arg Pro Asp Arg Gly Thr Trp Ser Leu Ser Glu
 20 25 30

Lys Phe Asn Leu Arg Asp Lys Met Gln Trp Thr Ser Leu Leu Leu
 35 40 45

1210

Ala Gly Leu Phe Ser Leu Ser Gln Ala Gln Tyr Glu Asp Asp Pro His
 50 55 60

Trp Trp Phe His Tyr Leu Arg Ser Gln Gln Ser Thr Tyr Tyr Asp Pro
 65 70 75 80

Tyr Asp Pro Tyr Pro Tyr Glu Thr Tyr Glu Pro Tyr Pro Tyr Gly Val
 85 90 95

Asp Glu Gly Pro Ala Tyr Thr Tyr Gly Ser Pro Ser Pro Pro Asp Pro
 100 105 110

Arg Asp Cys Pro Gln Glu Cys Asp Cys Pro Pro Asn Phe Pro Thr Ala
 115 120 125

Met Tyr Cys Asp Asn Arg Asn Leu Lys Tyr Leu Pro Phe Val Pro Ser
 130 135 140

Arg Met Lys Tyr Val Tyr Phe Gln Asn Asn Gln Ile Thr Ser Ile Gln
 145 150 155 160

Glu Gly Val Phe Asp Asn Ala Thr Gly Leu Leu Trp Ile Ala Leu His
 165 170 175

Gly Asn Gln Ile Thr Ser Asp Lys Val Gly Arg Lys Val Phe Ser Lys
 180 185 190

Leu Arg His Leu Glu Arg Leu Tyr Leu Asp His Asn Asn Leu Thr Arg
 195 200 205

Met Pro Gly Pro Leu Pro Arg Ser Leu Arg Glu Leu His Leu Asp His
 210 215 220

Asn Gln Ile Ser Arg Val Pro Asn Asn Ala Leu Glu Gly Leu Glu Asn
 225 230 235 240

Leu Thr Ala Leu Tyr Leu Gln His Asn Glu Ile Gln Glu Val Gly Ser
 245 250 255

Ser Met Arg Gly Leu Arg Ser Leu Ile Leu Leu Asp Leu Ser Tyr Asn
 260 265 270

His Leu Arg Lys Val Pro Asp Gly Leu Pro Ser Ala Leu Glu Gln Leu
 275 280 285

Tyr Met Glu His Asn Asn Val Tyr Thr Val Pro Asp Ser Tyr Phe Arg
 290 295 300

Gly Ala Pro Lys Leu Leu Tyr Val Arg Leu Ser His Asn Ser Leu Thr
 305 310 315 320

1211

Asn Asn Gly Leu Ala Ser Asn Thr Phe Asn Ser Ser Ser Leu Leu Glu
 325 330 335

Leu Asp Leu Ser Tyr Asn Gln Leu Gln Lys Ile Pro Pro Val Asn Thr
 340 345 350

Asn Leu Glu Asn Leu Tyr Leu Gln Gly Asn Arg Ile Asn Glu Phe Ser
 355 360 365

Ile Ser Ser Phe Cys Thr Val Val Asp Val Val Asn Phe Ser Lys Leu
 370 375 380

Gln Val Leu Arg Leu Asp Gly Asn Glu Ile Lys Arg Ser Ala Met Pro
 385 390 395 400

Ala Asp Ala Pro Leu Cys Leu Arg Leu Ala Ser Leu Ile Glu Ile
 405 410 415

<210> 1193

<211> 620

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (375)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (501)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (532)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (546)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1193

Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp
 1 5 10 15

Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val

1212

20	25	30
Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu		
35	40	45
Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys		
50	55	60
Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala		
65	70	75 80
Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser		
85	90	95
Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala		
100	105	110
Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys		
115	120	125
Asp Glu Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro		
130	135	140
Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser		
145	150	155 160
Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu		
165	170	175
Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe		
180	185	190
Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln		
195	200	205
Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile		
210	215	220
Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val		
225	230	235 240
Arg Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr		
245	250	255
Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu		
260	265	270
Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg		
275	280	285
Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr		

1213

290	295	300
Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg		
305	310	315 320
Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp		
	325	330 335
Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His		
	340	345 350
Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys		
	355	360 365
Asp Ser Val Asn Asp Cys Xaa Asp Asn Ser Asp Glu Gln Gly Cys Ser		
	370	375 380
Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys		
	385	390 395 400
Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu		
	405	410 415
Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr		
	420	425 430
Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp		
	435	440 445
Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys		
	450	455 460
Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp		
	465	470 475 480
Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly		
	485	490 495
Gln Gly Thr Ser Xaa Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val		
	500	505 510
Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp		
	515	520 525
Pro Thr Gln Xaa Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg		
	530	535 540
Ser Xaa Leu Gly Cys Arg Ser Ala Gly Ser Ser Ala Ser Ser Pro Thr		
	545	550 555 560
Pro Ser Ser Met Thr Ser Pro Ser Thr Met Thr Ser Arg Cys Trp Ser		

1214

565

570

575

Trp Arg Asn Arg Gln Ser Thr Ala Pro Trp Cys Gly Pro Ser Ala Cys
580 585 590

Arg Thr Pro Pro Met Ser Ser Leu Pro Ala Arg Pro Ser Gly Ser Arg
595 600 605

Ala Gly Asp Thr Pro Ser Met Glu Ala Leu Ala Arg
610 615 620

<210> 1194

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1194

Arg Thr Leu Cys His Leu Thr Thr Leu Asp Glu Leu Ser Cys Gln Arg
1 5 10 15

Glu Asn Leu Met Phe Lys Glu His Phe Pro Leu Ala Asp Val Thr Ala
20 25 30

Gly Phe Val Phe His Met Cys Phe Ser Tyr Thr His Leu Asn Ala Phe
35 40 45

Lys His Leu
50

<210> 1195

<211> 269

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (245)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (246)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (257)

1215

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (266)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1195

Pro Ala Glu Asp Ala Ala Ser Leu Thr Trp Gly Val Ala Ile Arg Ala
1 5 10 15

Gly Arg Ser Trp Phe Ser Gly Pro Ala Ala Pro Ala Ala Ala Met Ser
20 25 30

Phe Phe Pro Glu Leu Tyr Phe Asn Val Asp Asn Gly Tyr Leu Glu Gly
35 40 45

Leu Val Arg Gly Leu Lys Ala Gly Val Leu Ser Gln Ala Asp Tyr Leu
50 55 60

Asn Leu Val Gln Cys Glu Thr Leu Glu Asp Leu Lys Leu His Leu Gln
65 70 75 80

Ser Thr Asp Tyr Gly Asn Phe Leu Ala Asn Glu Ala Ser Pro Leu Thr
85 90 95

Val Ser Val Ile Asp Asp Arg Leu Lys Glu Lys Met Val Val Glu Phe
100 105 110

Arg His Met Arg Asn His Ala Tyr Glu Pro Leu Ala Ser Phe Leu Asp
115 120 125

Phe Ile Thr Tyr Ser Tyr Met Ile Asp Asn Val Ile Leu Leu Ile Thr
130 135 140

Gly Thr Leu His Gln Arg Ser Ile Ala Glu Leu Val Pro Lys Cys His
145 150 155 160

Pro Leu Gly Ser Phe Glu Gln Met Glu Ala Val Asn Ile Ala Gln Thr
165 170 175

Pro Ala Glu Leu Tyr Asn Ala Ile Leu Val Asp Thr Pro Leu Ala Ala
180 185 190

Phe Phe Gln Asp Cys Ile Ser Glu Gln Asp Leu Asp Glu Met Asn Ile
195 200 205

Glu Ile Ile Arg Asn Thr Leu Tyr Lys Ala Tyr Leu Glu Ser Phe Tyr
210 215 220

Lys Phe Cys Thr Leu Leu Gly Gly Thr Thr Ala Asp Ala Met Cys Pro

1216

225 230 235 240
 Ile Leu Glu Phe Xaa Xaa Gln Thr Val Pro Ser Ser Phe His Thr Val
 245 250 255

Xaa Gly Ser Thr Leu Arg Ala Trp Arg Xaa Gly Ser Gly
 260 265

<210> 1196

<211> 301

<212> PRT

<213> Homo sapiens

<400> 1196

Arg His Glu Pro Ala Pro Arg Glu Ala Pro Gly Ser Arg Ala Ser Ala
 1 5 10 15

Phe Leu Leu Pro Ser Phe Leu Pro Gly Pro Arg Leu Val Pro Ala Gly
 20 25 30

His Pro Thr Ala Thr Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp
 35 40 45

Leu Ala Gly Phe Thr Leu Leu Met Pro Ala Val Ser Val Gly Asn Val
 50 55 60

Gly Gln Leu Ala Met Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys
 65 70 75 80

Ile Gly Tyr Phe Tyr Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn
 85 90 95

Pro Tyr Ala Thr Thr Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala
 100 105 110

Glu Val Tyr Ser Leu Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg
 115 120 125

Ser Ile Phe Ile Lys Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu
 130 135 140

Ser Trp Val Lys Ser Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser
 145 150 155 160

Ser His Ser Tyr Gln Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe
 165 170 175

Arg Tyr Leu Leu Thr Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile
 180 185 190

1217

Lys Ser Leu Asn Trp Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu
 195 200 205

Ile Asp Asp Ser Glu Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr
 210 215 220

Lys Thr Leu Tyr Asp Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val
 225 230 235 240

Leu Leu Lys Phe Val Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly
 245 250 255

Leu Val Glu Tyr Leu Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser
 260 265 270

Asp Asp Pro Thr Val Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp
 275 280 285

Arg Leu Leu Phe Gly Ser Gly Leu Pro Pro Ala Leu Phe
 290 295 300

<210> 1197

<211> 246

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (49)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (65)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (230)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1197

Gly Thr Arg Asp Leu Leu Ala Ala Ala Ala Thr Gly Lys Leu
 1 5 10 15

Lys Ser Phe Ala Arg Lys Phe Ile Asn Leu Asn Glu Phe Thr Thr Tyr
 20 25 30

1218

Gly Ser Glu Glu Ser Thr Lys Pro Ala Ser Val Arg Ala Leu Leu Phe
35 40 45

Xaa Ile Ser Phe Leu Met Leu Cys His Val Ala Gln Thr Tyr Gly Ser
50 55 60

Xaa Val Ile Leu Ser Glu Ser Arg Thr Gly Ala Glu Val Pro Phe Phe
65 70 75 80

Glu Thr Trp Met Gln Thr Cys Met Pro Glu Glu Gly Lys Ile Leu Asn
85 90 95

Pro Asp His Pro Cys Phe Arg Pro Asp Ser Thr Lys Val Glu Ser Leu
100 105 110

Val Ala Leu Leu Asn Asn Ser Ser Glu Met Lys Leu Val Gln Met Lys
115 120 125

Trp His Glu Ala Cys Leu Ser Ile Ser Ala Ala Ile Leu Glu Ile Leu
130 135 140

Asn Ala Trp Glu Asn Gly Val Leu Ala Phe Glu Ser Ile Gln Lys Ile
145 150 155 160

Thr Asp Asn Ile Lys Gly Lys Val Cys Ser Leu Ala Val Cys Ala Val
165 170 175

Ala Trp Leu Val Ala His Val Arg Met Leu Gly Leu Asp Glu Arg Glu
180 185 190

Lys Ser Leu Gln Met Ile Arg Gln Leu Ala Gly Pro Leu Phe Ser Glu
195 200 205

Asn Thr Leu Gln Phe Tyr Asn Glu Arg Val Val Ile Met Asn Ser Ile
210 215 220

Leu Gly Ala His Val Xaa Arg Arg Ala Ala Ala Asp Ser His Ala Gly
225 230 235 240

Phe Lys Phe Pro Ser Asn
245

<210> 1198

<211> 465

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

1219

<222> (203)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (460)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (461)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1198

Lys Asn Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu
1 5 10 15

Thr Asn Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu
20 25 30

Gln Ala Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg
35 40 45

Ile Leu Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly
50 55 60

Lys Asn Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val
65 70 75 80

Pro Asp Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile
85 90 95

Glu Thr Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu
100 105 110

Gly Leu Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu
115 120 125

Ser Asp Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp
130 135 140

Phe Asp Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly
145 150 155 160

Ile Ile Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr
165 170 175

Gln Thr Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp
180 185 190

Arg Val Val Leu Ile Gly Gly Lys Pro Asp Xaa Val Val Glu Cys Ile

1220

195	200	205
Lys Ile Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala		
210	215	220
Gln Pro Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly		
225	230	235 240
Phe Thr Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro		
	245	250 255
Met Arg Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly		
	260	265 270
Arg Pro Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg		
	275	280 285
Arg Gly Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser		
	290	295 300
Arg Ala Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Arg Gly Gly		
	305	310 315 320
Asp Leu Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp		
	325	330 335
Gly Met Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp		
	340	345 350
Thr Trp Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly		
	355	360 365
Ser Gly Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp		
	370	375 380
Leu Gly Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu		
	385	390 395 400
Ala Gly Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg		
	405	410 415
His Glu Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser		
	420	425 430
Glu Asp Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn		
	435	440 445
Ala Gln Tyr Leu Leu Gln Asn Ser Val Ser Ser Xaa Xaa Leu Ala Leu		
	450	455 460

Cys

1221

465

<210> 1199

<211> 446

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (87)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (88)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1199

Tyr	Pro	Ala	Ala	Cys	Xaa	Thr	Gly	Pro	Glu	Phe	Pro	Gly	Arg	Pro	Thr
1				5					10					15	

Arg	Pro	His	Glu	Met	Asp	Gln	Tyr	Trp	Gly	Ile	Gly	Ser	Leu	Ala	Ser
		20					25						30		

Gly	Ile	Asn	Leu	Phe	Thr	Asn	Ser	Phe	Glu	Gly	Pro	Val	Leu	Asp	His
		35				40						45			

Arg	Tyr	Tyr	Ala	Gly	Gly	Cys	Ser	Pro	His	Tyr	Ile	Leu	Asn	Thr	Arg
	50					55						60			

Phe	Arg	Lys	Pro	Tyr	Asn	Val	Glu	Ser	Tyr	Thr	Pro	Gln	Thr	Gln	Gly
65					70					75					80

Lys	Tyr	Glu	Phe	Ile	Leu	Xaa	Xaa	Tyr	Glu	Ser	Tyr	Ser	Asp	Phe	Glu
			85						90						95

Arg	Asn	Val	Thr	Glu	Lys	Met	Ala	Ser	Lys	Ser	Gly	Phe	Ser	Phe	Gly
		100							105					110	

Phe	Lys	Ile	Pro	Gly	Ile	Phe	Glu	Leu	Gly	Ile	Ser	Ser	Gln	Ser	Asp
		115					120						125		

Arg	Gly	Lys	His	Tyr	Ile	Arg	Arg	Thr	Lys	Arg	Phe	Ser	His	Thr	Lys
		130					135								140

1222

Ser Val Phe Leu His Ala Arg Ser Asp Leu Glu Val Ala His Tyr Lys
 145 150 155 160
 Leu Lys Pro Arg Ser Leu Met Leu His Tyr Glu Phe Leu Gln Arg Val
 165 170 175
 Lys Arg Leu Pro Leu Glu Tyr Ser Tyr Gly Glu Tyr Arg Asp Leu Phe
 180 185 190
 Arg Asp Phe Gly Thr His Tyr Ile Thr Glu Ala Val Leu Gly Gly Ile
 195 200 205
 Tyr Glu Tyr Thr Leu Val Met Asn Lys Glu Ala Met Glu Arg Gly Asp
 210 215 220
 Tyr Thr Leu Asn Asn Val His Ala Cys Ala Lys Asn Asp Phe Lys Ile
 225 230 235 240
 Gly Gly Ala Ile Glu Glu Val Tyr Val Ser Leu Gly Val Ser Val Gly
 245 250 255
 Lys Cys Arg Gly Ile Leu Asn Glu Ile Lys Asp Arg Asn Lys Arg Asp
 260 265 270
 Thr Met Val Glu Asp Leu Val Val Leu Val Arg Gly Gly Ala Ser Glu
 275 280 285
 His Ile Thr Thr Leu Ala Tyr Gln Glu Leu Pro Thr Ala Asp Leu Met
 290 295 300
 Gln Glu Trp Gly Asp Ala Val Gln Tyr Asn Pro Ala Ile Ile Lys Val
 305 310 315 320
 Lys Val Glu Pro Leu Tyr Glu Leu Val Thr Ala Thr Asp Phe Ala Tyr
 325 330 335
 Ser Ser Thr Val Arg Gln Asn Met Lys Gln Ala Leu Glu Glu Phe Gln
 340 345 350
 Lys Glu Val Ser Ser Cys His Cys Ala Pro Cys Gln Gly Asn Gly Val
 355 360 365
 Pro Val Leu Lys Gly Ser Arg Cys Asp Cys Ile Cys Pro Val Gly Ser
 370 375 380
 Gln Gly Leu Ala Cys Glu Val Ser Tyr Arg Lys Asn Thr Pro Ile Asp
 385 390 395 400
 Gly Lys Trp Asn Cys Trp Ser Asn Trp Ser Ser Cys Ser Gly Arg Arg
 405 410 415

1223

Lys Thr Arg Gln Arg Gln Cys Asn Asn Pro Pro Pro Gln Asn Gly Gly
 420 425 430

Ser Pro Cys Ser Gly Pro Ala Ser Glu Thr Leu Asp Cys Ser
 435 440 445

<210> 1200

<211> 437

<212> PRT

<213> Homo sapiens

<400> 1200

Leu Gly Ser Ser Asp Ser Tyr Ala Ser Pro Gly Arg Ala Ala Ala Pro
 1 5 10 15

Pro Ala Ala Ala Gly Pro Gly Asp Thr Ser Ala Cys Tyr Lys Ser Ser
 20 25 30

Gly Pro Arg Cys Leu Leu Pro Asp Leu Ala Pro Ser Ser Glu Pro Gly
 35 40 45

Ala Cys Leu Gly Gly Leu Ser Val Phe Thr Met Glu Gln Leu Ser Ser
 50 55 60

Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe Leu Ala Leu Ser Glu Asn
 65 70 75 80

Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro Phe Ser Ile Ser Ser Ala
 85 90 95

Met Ala Met Val Phe Leu Gly Thr Arg Gly Asn Thr Ala Ala Gln Leu
 100 105 110

Ser Lys Thr Phe His Phe Asn Thr Val Glu Glu Val His Ser Arg Phe
 115 120 125

Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg Gly Ala Ser Tyr Ile Leu
 130 135 140

Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys Thr Tyr Asn Phe Leu Pro
 145 150 155 160

Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr Gly Ala Asp Leu Ala Ser
 165 170 175

Val Asp Phe Gln His Ala Ser Glu Asp Ala Arg Lys Thr Ile Asn Gln
 180 185 190

1224

Trp Val Lys Gly Gln Thr Glu Gly Lys Ile Pro Glu Leu Leu Ala Ser
195 200 205

Gly Met Val Asp Asn Met Thr Lys Leu Val Leu Val Asn Ala Ile Tyr
210 215 220

Phe Lys Gly Asn Trp Lys Asp Lys Phe Met Lys Glu Ala Thr Thr Asn
225 230 235 240

Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg Lys Thr Val Lys Met Met
245 250 255

Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr Ile Glu Asp Leu Lys Cys
260 265 270

Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu Glu Leu Ser Met Val Ile
275 280 285

Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser Thr Gly Leu Lys Lys Ile
290 295 300

Glu Glu Gln Leu Thr Leu Glu Lys Leu His Glu Trp Thr Lys Pro Glu
305 310 315 320

Asn Leu Asp Phe Ile Glu Val Asn Val Ser Leu Pro Arg Phe Lys Leu
325 330 335

Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu Ala Arg Leu Gly Val Gln
340 345 350

Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu Ser Gly Met Ser Gly Ala
355 360 365

Arg Asp Ile Phe Ile Ser Lys Ile Val His Lys Ser Phe Val Glu Val
370 375 380

Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Ala Gly Ile Ala Thr
385 390 395 400

Phe Cys Met Leu Met Pro Glu Glu Asn Phe Thr Ala Asp His Pro Phe
405 410 415

Leu Phe Phe Ile Arg His Asn Ser Ser Gly Ser Ile Leu Phe Leu Gly
420 425 430

Arg Phe Ser Ser Pro
435

<210> 1201

1225

<211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (82)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1201

Gln Leu Gly Pro Val Val Gly Gly Trp Tyr Lys Val Leu Asp Arg Phe
 1 5 10 15

Ile Pro Gly Thr Thr Lys Val Asp Ala Leu Lys Lys Met Leu Leu Asp
 20 25 30

Gln Gly Gly Phe Ala Pro Cys Phe Leu Gly Cys Phe Leu Pro Leu Val
 35 40 45

Gly Ala Leu Asn Gly Leu Ser Ala Gln Asp Asn Trp Pro Asn Tyr Ser
 50 55 60

Gly Ile Ile Leu Met Pro Leu Ser Pro Thr Thr Ile Tyr Gly Leu Leu
 65 70 75 80

Cys Xaa

<210> 1202
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 1202

Ile Ser Arg Ser Ser Ala Arg Arg Gln Pro Phe Arg His Gly Arg Leu
 1 5 10 15

Trp Arg Ala Ala Ala Met Ala Leu Arg Tyr Pro Met Ala Val Gly Leu
 20 25 30

Asn Lys Gly His Lys Val Thr Lys Asn Val Ser Lys Pro Arg His Ser
 35 40 45

Arg Arg Arg Gly Arg Leu Thr Lys His Thr Lys Phe Val Arg Asp Met
 50 55 60

Ile Arg Glu Val Cys Gly Phe Ala Pro Tyr Glu Arg Arg Ala Met Glu
 65 70 75 80

1226

Leu Leu Lys Val Ser Lys Asp Lys Arg Ala Leu Lys Phe Ile Lys Lys
85 90 95

Arg Val Gly Thr His Ile Arg Ala Lys Arg Lys Arg Glu Glu Leu Ser
100 105 110

Asn Val Leu Ala Ala Met Arg Lys Ala Ala Ala Lys Lys Asp
115 120 125

<210> 1203

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (27)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1203

Asp Trp Asn Pro Asp Leu Gln Ala Ser Ala Val Cys Ile Lys Arg Val
1 5 10 15

Gly Glu Ser Gly Pro Leu Ala Gln Glu Pro Xaa Leu Leu Lys Glu Gly
20 25 30

Phe Lys Ala Lys Trp Val Cys Gln Arg Cys Cys Leu Pro Phe Leu Glu
35 40 45

Met Leu Ile Ser Leu Ser Lys Thr Glu Lys Ser Arg Cys Tyr Arg Asn
50 55 60

Asn Leu Val Cys Cys Ile Asn Cys Ser Trp Ala Trp Ser Ser Ile Pro
65 70 75 80

Thr Leu Arg Phe Pro Ala Ser Leu Cys Cys Pro Gly Ser His Ser Cys
85 90 95

Arg Arg Pro Asn Pro Leu Ala Val Phe Cys Leu Lys Ile Trp Gly Ala
100 105 110

Pro Ser Leu Ser Ser Pro Gly Asn Ser Leu Ala Glu Gly Gly Asp Pro
115 120 125

Pro Gln
130

1227

<210> 1204
 <211> 228
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (189)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (196)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (199)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (225)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (228)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1204
 Trp Ala Ala Phe Glu Pro Ala Thr Leu Ala Trp Lys Phe Pro Phe Gln
 1 5 10 15
 Ser Gly Phe Cys Leu Leu Leu Pro Ser Pro Ser Pro Arg Tyr Leu Phe
 20 25 30
 Thr Ser His Leu Ile Ser Leu Cys Ser Ser Val Ser Pro Thr His Ile
 35 40 45
 Ile Gly Asp Ser Gly Gly Ser Leu Thr Ser Leu Leu Ser Asn Ala Arg
 50 55 60
 Pro Ser Gly Leu Ala Ser Val Ala Ser His Ile Asp Val Thr Leu Glu
 65 70 75 80
 Leu Leu Pro Gln Arg Gly Arg Arg Asp Arg Leu Ser Pro His Leu Pro
 85 90 95
 Pro Tyr Ser Pro Leu Tyr Ser Arg Phe Asp His Leu Ser Pro Ser Ala
 100 105 110

1228

Ala Pro Ser His Phe Gly Gln Ser Gln Ala Pro Ile Arg Leu Pro Pro
 115 120 125

Pro Pro Gly Ala Pro Ser Ile Ser Leu Ser Pro Leu Pro Gln Asn Leu
 130 135 140

Cys Lys Gly Tyr Glu Arg Asp Pro Leu Pro Ser Arg Pro Pro Leu Arg
 145 150 155 160

Ala Val Arg Ser Lys Lys Gln Lys Leu Val Gly Gly Trp Leu Gly Leu
 165 170 175

Cys Pro Val Pro Arg Trp Asp Lys Leu Ala Phe Ser Xaa Ile Pro Ser
 180 185 190

Trp Val Pro Xaa Ser Phe Xaa Ala Pro Gly Ala Arg Thr His Cys Ala
 195 200 205

Val Phe Leu Phe Ser Phe Val Gly Lys Gly Thr Lys Val Phe Ala Lys
 210 215 220

Xaa Pro Val Xaa
 225

<210> 1205

<211> 270

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (128)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1205

Leu Pro Gly Ala Val Ala Ala Ser Ser Gly Ser Pro Pro Gly Ser Ala
 1 5 10 15

Leu Ala Ala Val Ala Ser Gly Gly Asp Leu Phe Pro Gly Gln Pro Val
 20 25 30

Ser Glu Leu Ile Ala Gln Leu Leu Arg Ala Glu Pro Tyr Pro Ala Ala
 35 40 45

Ala Gly Arg Phe Gly Ala Gly Gly Gly Ala Ala Gly Ala Val Leu Gly
 50 55 60

Ile Asp Asn Val Cys Glu Leu Ala Ala Arg Leu Leu Phe Ser Thr Val

1229

65 70 75 80
 Glu Trp Ala Arg His Ala Pro Phe Phe Pro Glu Leu Pro Val Ala Asp
 85 90 95
 Gln Val Ala Leu Leu Arg Leu Ser Trp Ser Glu Leu Phe Val Leu Asn
 100 105 110
 Ala Ala Gln Ala Ala Leu Pro Leu His Thr Ala Pro Leu Leu Ala Xaa
 115 120 125
 Ala Gly Leu His Ala Ala Pro Met Ala Ala Glu Arg Ala Val Ala Phe
 130 135 140
 Met Asp Gln Val Arg Ala Phe Gln Glu Gln Val Asp Lys Leu Gly Arg
 145 150 155 160
 Leu Gln Val Asp Ser Ala Glu Tyr Gly Cys Leu Lys Ala Ile Ala Leu
 165 170 175
 Phe Thr Pro Asp Ala Cys Gly Leu Ser Asp Pro Ala His Val Glu Ser
 180 185 190
 Leu Gln Glu Lys Ala Gln Val Ala Leu Thr Glu Tyr Val Arg Ala Gln
 195 200 205
 Tyr Pro Ser Gln Pro Gln Arg Phe Gly Arg Leu Leu Leu Arg Leu Pro
 210 215 220
 Ala Leu Arg Ala Val Pro Ala Ser Leu Ile Ser Gln Leu Phe Phe Met
 225 230 235 240
 Arg Leu Val Gly Lys Thr Pro Ile Glu Thr Leu Ile Arg Asp Met Leu
 245 250 255
 Leu Ser Gly Ser Thr Phe Asn Trp Pro Tyr Gly Ser Gly Gln
 260 265 270

<210> 1206

<211> 89

<212> PRT

<213> Homo sapiens

<400> 1206

Met Phe His Cys Ser Asp Lys Tyr Phe Thr Phe Phe Ser Val His Gln
 1 5 10 15

Arg Glu Arg Asp Pro Pro Thr Ala Val Thr Ser Lys Cys Ser Cys Ser
 20 25 30

1230

Ile Asn Gly Val Thr Asp Thr Glu Val His Ser Trp Phe Leu Ser Arg
 35 40 45

Val Val Ile Leu Val Ser Trp Ser Leu Gly His Trp Gly Cys Thr Leu
 50 55 60

Lys Ser Pro Asn Arg Leu Ala Ile Lys Ile Asn Lys Ala Ala Ala Pro
 65 70 75 80

Phe Gln Phe Thr Phe His Leu Thr Gln
 85

<210> 1207

<211> 145

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (137)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1207

Cys Val Gly Lys Ala Gly Val Glu Leu Gly Cys Ser Gly Glu Gly Val
 1 5 10 15

Val Lys Lys Ala Ser Ser Arg Gly His Lys Ala Arg Phe Pro Leu Arg
 20 25 30

Ser His Lys Val Leu Ser Pro Ala Pro Gly Ala Gly Gly Val His Gly
 35 40 45

Pro Gly Phe Thr Ser Thr His Pro Ala His Pro Arg Gly Glu Gly Pro
 50 55 60

Arg Ala Pro Gly Pro Ala Ala Asp Arg Ile Leu Cys Lys Leu Cys Ser
 65 70 75 80

Val His Cys Lys Thr Pro Ala Gln Leu Ala Gly His Met Gln Thr His
 85 90 95

Leu Gly Gly Ala Ala Pro Leu Ser Arg Glu Thr Pro Pro Ser His Ser
 100 105 110

Pro Pro Ala Glu Gly Asp Pro Arg Thr His Gln Val Leu Val Arg Phe
 115 120 125

Val Gln Trp Arg Arg Gln Arg Gln Xaa Arg Gln Arg Gln Arg Gln

1231

130

135

140

Gln
145

<210> 1208

<211> 378

<212> PRT

<213> Homo sapiens

<400> 1208

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Ser Ala Ser Arg Ala Thr Ala Met Ser Ser Arg Gly Gly Lys Lys Lys
 1              5              10              15

Ser Thr Lys Thr Ser Arg Ser Ala Lys Ala Gly Val Ile Phe Pro Val
      20              25              30

Gly Arg Met Leu Arg Tyr Ile Lys Lys Gly His Pro Lys Tyr Arg Ile
      35              40              45

Gly Val Gly Ala Pro Val Tyr Met Ala Ala Val Leu Glu Tyr Leu Thr
      50              55              60

Ala Glu Ile Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys
      65              70              75              80

Gly Arg Val Thr Pro Arg His Ile Leu Leu Ala Val Ala Asn Asp Glu
      85              90              95

Glu Leu Asn Gln Leu Leu Lys Gly Val Thr Ile Ala Ser Gly Gly Val
      100             105             110

Leu Pro Asn Ile His Pro Glu Leu Leu Ala Lys Lys Arg Gly Ser Lys
      115             120             125

Gly Lys Leu Glu Ala Ile Ile Thr Pro Pro Pro Ala Lys Lys Ala Lys
      130             135             140

Ser Pro Ser Gln Lys Lys Pro Val Ser Lys Lys Ala Gly Gly Lys Lys
      145             150             155             160

Gly Ala Arg Lys Ser Lys Lys Gln Gly Glu Val Ser Lys Ala Ala Ser
      165             170             175

Ala Asp Ser Thr Thr Glu Gly Thr Pro Ala Asp Gly Phe Thr Val Leu
      180             185             190

Ser Thr Lys Ser Leu Phe Leu Gly Gln Lys Leu Asn Leu Ile His Ser
      195             200             205

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1232

Glu Ile Ser Asn Leu Ala Gly Phe Glu Val Glu Ala Ile Ile Asn Pro
210 215 220

Thr Asn Ala Asp Ile Asp Leu Lys Asp Asp Leu Gly Asn Thr Leu Glu
225 230 235 240

Lys Lys Gly Gly Lys Glu Phe Val Glu Ala Val Leu Glu Leu Arg Lys
245 250 255

Lys Asn Gly Pro Leu Glu Val Ala Gly Ala Ala Val Ser Ala Gly His
260 265 270

Gly Leu Pro Ala Lys Phe Val Ile His Cys Asn Ser Pro Val Trp Gly
275 280 285

Ala Asp Lys Cys Glu Glu Leu Leu Glu Lys Thr Val Lys Asn Cys Leu
290 295 300

Ala Leu Ala Asp Asp Lys Lys Leu Lys Ser Ile Ala Phe Pro Ser Ile
305 310 315 320

Gly Ser Gly Arg Asn Gly Phe Pro Lys Gln Thr Ala Ala Gln Leu Ile
325 330 335

Leu Lys Ala Ile Ser Ser Tyr Phe Val Ser Thr Met Ser Ser Ser Ile
340 345 350

Lys Thr Val Tyr Phe Val Leu Phe Asp Ser Glu Ser Ile Gly Ile Tyr
355 360 365

Val Gln Glu Met Ala Lys Leu Asp Ala Asn
370 375

<210> 1209

<211> 220

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

1233

<220>

<221> SITE

<222> (27)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1209

Arg	Gly	Gly	Lys	Ile	Xaa	Asp	Thr	Phe	Xaa	Arg	Tyr	Ala	Arg	Arg	Tyr
1				5					10					15	

Arg	Ser	Gly	Ile	Pro	Gly	Ser	Thr	His	Ala	Xaa	Ala	Pro	Gly	Ala	Met
			20					25						30	

Arg	Leu	Ser	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Trp	Ala	Ile	
	35					40					45				

Pro	Gly	Gly	Leu	Gly	Asp	Arg	Ala	Pro	Leu	Thr	Ala	Thr	Ala	Pro	Gln
	50					55					60				

Leu	Asp	Asp	Glu	Glu	Met	Tyr	Ser	Ala	His	Met	Pro	Ala	His	Leu	Arg
65					70					75				80	

Cys	Asp	Ala	Cys	Arg	Ala	Val	Ala	Tyr	Gln	Met	Trp	Gln	Asn	Leu	Ala
				85					90					95	

Lys	Ala	Glu	Thr	Lys	Leu	His	Thr	Ser	Asn	Ser	Gly	Gly	Arg	Arg	Glu
		100						105					110		

Leu	Ser	Glu	Leu	Val	Tyr	Thr	Asp	Val	Leu	Asp	Arg	Ser	Cys	Ser	Arg
	115						120					125			

Asn	Trp	Gln	Asp	Tyr	Gly	Val	Arg	Glu	Val	Asp	Gln	Val	Lys	Arg	Leu
	130					135					140				

Thr	Gly	Pro	Gly	Leu	Ser	Glu	Gly	Pro	Glu	Pro	Ser	Ile	Ser	Val	Met
145				150					155					160	

Val	Thr	Gly	Gly	Pro	Trp	Pro	Thr	Arg	Leu	Ser	Arg	Thr	Cys	Leu	His
			165					170						175	

Tyr	Leu	Gly	Glu	Phe	Gly	Glu	Asp	Gln	Ile	Tyr	Glu	Ala	His	Gln	Gln
		180					185						190		

Gly	Arg	Gly	Ala	Leu	Glu	Ala	Leu	Leu	Cys	Gly	Gly	Pro	Gln	Gly	Ala
	195						200						205		

Cys	Ser	Glu	Lys	Val	Ser	Ala	Thr	Arg	Glu	Glu	Leu				
	210					215					220				

<210> 1210

1234

<211> 231

<212> PRT

<213> Homo sapiens

<400> 1210

Ala Leu Ser Pro Ala Met Val Val Pro Glu Asp Gln Leu Thr Arg Trp
 1 5 10 15

His Pro Arg Phe Asn Val Asp Glu Val Pro Asp Ile Glu Pro Ala Ala
 20 25 30

Leu Pro Gln Pro Pro Ala Thr Glu Lys Leu Thr Thr Ala Gln Glu Val
 35 40 45

Leu Ala Arg Ala Arg Asn Leu Ile Ser Pro Arg Met Glu Lys Ala Leu
 50 55 60

Ser Gln Leu Ala Leu Arg Ser Ala Ala Pro Ser Ser Pro Gly Ser Pro
 65 70 75 80

Arg Pro Ala Leu Pro Ala Thr Pro Pro Ala Thr Pro Pro Ala Ala Ser
 85 90 95

Pro Ser Ala Leu Lys Gly Val Ser Gln Asp Leu Leu Glu Arg Ile Arg
 100 105 110

Ala Lys Glu Ala Gln Lys Gln Leu Ala Gln Met Thr Arg Cys Pro Glu
 115 120 125

Gln Glu Gln Arg Leu Gln Arg Leu Glu Arg Leu Pro Glu Leu Ala Arg
 130 135 140

Val Leu Arg Ser Val Phe Val Ser Glu Arg Lys Pro Ala Leu Ser Met
 145 150 155 160

Glu Val Ala Cys Ala Arg Met Val Gly Ser Cys Cys Thr Ile Met Ser
 165 170 175

Pro Gly Glu Met Glu Lys His Leu Leu Leu Ser Glu Leu Leu Pro
 180 185 190

Asp Trp Leu Ser Leu His Arg Ile Arg Thr Asp Thr Tyr Val Lys Leu
 195 200 205

Asp Lys Ala Ala Asp Leu Ala His Ile Thr Ala Arg Leu Ala His Gln
 210 215 220

Thr Arg Ala Glu Glu Gly Leu
 225 230

1235

<210> 1211

<211> 346

<212> PRT

<213> Homo sapiens

<400> 1211

Asn Cys Thr Thr Ile Ser Leu Val Tyr Leu His Phe Val Phe Tyr Asn
 1 5 10 15

Ser Tyr Ser Leu Phe Pro Ser Lys Glu Asn Cys Val Tyr Glu Thr Val
 20 25 30

Val Leu Pro Leu Asp Glu Arg Ala Phe Glu Lys Thr Leu Thr Pro Ile
 35 40 45

Ile Gln Glu Tyr Phe Glu His Gly Asp Thr Asn Glu Val Ala Glu Met
 50 55 60

Leu Arg Asp Leu Asn Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu
 65 70 75 80

Ala Val Ser Leu Ala Leu Glu Gly Lys Ala Ser His Arg Glu Met Thr
 85 90 95

Ser Lys Leu Leu Ser Asp Leu Cys Gly Thr Val Met Ser Thr Thr Asp
 100 105 110

Val Glu Lys Ser Phe Asp Lys Leu Leu Lys Asp Leu Pro Glu Leu Ala
 115 120 125

Leu Asp Thr Pro Arg Ala Pro Gln Leu Val Gly Gln Phe Ile Ala Arg
 130 135 140

Ala Val Gly Asp Gly Ile Leu Cys Asn Thr Tyr Ile Asp Ser Tyr Lys
 145 150 155 160

Gly Thr Val Asp Cys Val Gln Ala Arg Ala Ala Leu Asp Lys Ala Thr
 165 170 175

Val Leu Leu Ser Met Ser Lys Gly Gly Lys Arg Lys Asp Ser Val Trp
 180 185 190

Gly Ser Gly Gly Gly Gln Gln Ser Val Asn His Leu Val Lys Glu Ile
 195 200 205

Asp Met Leu Leu Lys Glu Tyr Leu Leu Ser Gly Asp Ile Ser Glu Ala
 210 215 220

Glu His Cys Leu Lys Glu Leu Glu Val Pro His Phe His His Glu Leu
 225 230 235 240

1236

Val Tyr Glu Ala Ile Ile Met Val Leu Glu Ser Thr Gly Glu Ser Thr
 245 250 255

Phe Lys Met Ile Leu Asp Leu Leu Lys Ser Leu Trp Lys Ser Ser Thr
 260 265 270

Ile Thr Val Asp Gln Met Lys Arg Gly Tyr Glu Arg Ile Tyr Asn Glu
 275 280 285

Ile Pro Asp Ile Asn Leu Asp Val Pro His Ser Tyr Ser Val Leu Glu
 290 295 300

Arg Phe Val Glu Glu Cys Phe Gln Ala Gly Ile Ile Ser Lys Gln Leu
 305 310 315 320

Arg Asp Leu Cys Pro Ser Arg Gly Arg Lys Arg Phe Val Ser Glu Gly
 325 330 335

Asp Gly Gly Arg Leu Lys Pro Glu Ser Tyr
 340 345

<210> 1212

<211> 175

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (63)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1212

Pro Arg Xaa Ile Val Ser Ala Ala Cys Gly Arg Asn His Thr Leu Ala
 1 5 10 15

Leu Thr Glu Thr Gly Ser Val Phe Ala Phe Gly Glu Asn Lys Met Gly
 20 25 30

Gln Leu Gly Leu Gly Asn Gln Thr Asp Ala Val Pro Ser Pro Ala Gln
 35 40 45

Ile Met Tyr Asn Gly Gln Pro Ile Thr Lys Met Ala Cys Gly Xaa Glu
 50 55 60

1237

Phe Ser Met Ile Met Asp Cys Lys Gly Asn Leu Tyr Ser Phe Gly Cys
65 70 75 80

Pro Glu Tyr Gly Gln Leu Gly His Asn Ser Asp Gly Lys Phe Ile Ala
85 90 95

Arg Ala Gln Arg Ile Glu Tyr Asp Cys Glu Leu Val Pro Arg Arg Val
100 105 110

Ala Ile Phe Ile Glu Lys Thr Lys Asp Gly Gln Ile Leu Pro Val Pro
115 120 125

Asn Val Val Val Arg Asp Val Ala Cys Gly Ala Asn His Thr Leu Val
130 135 140

Leu Asp Ser Gln Lys Arg Val Phe Ser Trp Gly Phe Gly Gly Tyr Gly
145 150 155 160

Arg Leu Gly Thr Gln Ser Arg Arg Met Arg Trp Ser Pro Ala Trp
165 170 175

<210> 1213

<211> 127

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (41)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1213

Cys Phe Ile Cys Val Trp Cys Lys Arg Lys Leu Asp Gln Ile Asn Leu
1 5 10 15

Gln Leu Met Ser Pro Asn Ala Asn Thr Gly Thr His Met His Thr Pro
20 25 30

Ile Asn Thr His Thr Val His Leu Xaa Lys Gly Gln Val Ile Ser His
35 40 45

Pro Asn Phe Thr Ser Thr Asp Pro Leu Ala Pro Thr Pro Ala Ser Thr
50 55 60

Val Thr Ser Lys Ala Arg Ala Thr Cys Ala His Gln Thr Cys Ile Lys
65 70 75 80

Gln Leu Ala Gly Asp Gly Cys Gly Ala Gly Gly Leu Ser Asp Gly Ser

1238

85 90 95
Leu Leu Leu Pro Leu Leu Arg Val Lys Leu Leu Ser Phe Leu Arg Val
100 105 110

Tyr Leu Cys Gln Val Cys Ala Phe Asn Cys Phe Tyr Phe Val Phe
115 120 125

<210> 1214
<211> 146
<212> PRT
<213> Homo sapiens

<400> 1214
Cys Thr Trp Asn Arg Cys Ser Ala Ser Pro Ala Gly Trp Gln Asn Ser
1 5 10 15

Phe Leu Gly His Leu Asn Pro Ser Ser Leu Leu Gln Asn Pro Pro Ala
20 25 30

Asn Arg Ile Gly Met Gly Ala Thr Leu Asp Ile Gln Arg Gln Gln Arg
35 40 45

Met Glu Leu Leu Asp Arg Gln Leu Met Phe Ser Gln Phe Ala Gln Gly
50 55 60

Arg Arg Gln Arg Gln Gln Gln Gly Gly Met Ile Asn Trp Asn Arg Leu
65 70 75 80

Phe Pro Pro Leu Arg Gln Arg Gln Asn Val Asn Tyr Gln Gly Gly Arg
85 90 95

Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu Val Ser Glu Glu Gln Val
100 105 110

Ala Arg Leu Met Glu Met Gly Phe Ser Arg Gly Asp Ala Leu Glu Ala
115 120 125

Leu Arg Ala Ser Asn Asn Asp Leu Asn Val Ala Thr Asn Phe Leu Leu
130 135 140

Gln His
145

<210> 1215
<211> 116
<212> PRT

1239

<213> Homo sapiens

<220>

<221> SITE

<222> (107)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (108)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1215

Leu Lys Asn His Gln Lys Thr His Thr Ser Glu Lys Ser Tyr Lys Cys
1 5 10 15

Asn Glu Cys Arg Lys Ala Phe Ser Tyr Cys Ser Gly Leu Ile Gln Cys
20 25 30

Gln Val Ile His Thr Ile Glu Lys Pro Tyr Glu Tyr Gly Lys Cys Gly
35 40 45

Lys Ala Phe Arg Gln Arg Thr Asp Leu Lys Lys His Gln Lys Met His
50 55 60

Thr Glu Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Ser
65 70 75 80

Gln Ser Thr Tyr Leu Thr Lys His Gln Lys Ile His Ser Glu Glu Lys
85 90 95

Ser Asn Ile His Thr Glu Cys Gly Glu Thr Xaa Xaa Gln Asn Ser Ser
100 105 110

Phe Leu Gln Gln
115

<210> 1216

<211> 201

<212> PRT

<213> Homo sapiens

<400> 1216

Ala Ala Gly Gly Glu Gly Phe Gly Ser Leu His Ala Ser Leu Val Gly
1 5 10 15

Phe Arg Gly Val Val Ala Gly Cys Ala Arg His Phe Arg Ala Ser Arg
20 25 30

1240

Asn Gly Val Ala Asn Gly Leu Gln Ser Asn Met Pro Lys Phe Tyr Cys
 35 40 45
 Asp Tyr Cys Asp Thr Tyr Leu Thr His Asp Ser Pro Ser Val Arg Lys
 50 55 60
 Thr His Cys Ser Gly Arg Lys His Lys Glu Asn Val Lys Asp Tyr Tyr
 65 70 75 80
 Gln Lys Trp Met Glu Glu Gln Ala Gln Ser Leu Ile Asp Lys Thr Thr
 85 90 95
 Ala Ala Phe Gln Gln Gly Lys Ile Pro Pro Thr Pro Phe Ser Ala Pro
 100 105 110
 Pro Pro Ala Gly Ala Met Ile Pro Pro Pro Pro Ser Leu Pro Gly Pro
 115 120 125
 Pro Arg Pro Gly Met Met Pro Ala Pro His Met Gly Gly Pro Pro Met
 130 135 140
 Met Pro Met Met Gly Pro Pro Pro Pro Gly Met Met Pro Val Gly Pro
 145 150 155 160
 Ala Pro Gly Met Arg Pro Pro Met Gly Gly His Met Pro Met Met Pro
 165 170 175
 Gly Pro Pro Met Met Arg Pro Pro Ala Arg Pro Met Met Val Pro Thr
 180 185 190
 Arg Pro Gly Met Thr Arg Pro Asp Arg
 195 200

<210> 1217

<211> 473

<212> PRT

<213> Homo sapiens

<400> 1217

Lys Phe Thr Met Lys Phe Leu Leu Ile Leu Leu Leu Gln Ala Thr Ala
 1 5 10 15
 Ser Gly Ala Leu Pro Leu Asn Ser Ser Thr Ser Leu Glu Lys Asn Asn
 20 25 30
 Val Leu Phe Gly Glu Arg Tyr Leu Glu Lys Phe Tyr Gly Leu Glu Ile
 35 40 45
 Asn Lys Leu Pro Val Thr Lys Met Lys Tyr Ser Gly Asn Leu Met Lys

1241

50	55	60
Glu Lys Ile Gln Glu Met Gln His Phe Leu Gly Leu Lys Val Thr Gly		
65	70	75 80
Gln Leu Asp Thr Ser Thr Leu Glu Met Met His Ala Pro Arg Cys Gly		
	85	90 95
Val Pro Asp Val His His Phe Arg Glu Met Pro Gly Gly Pro Val Trp		
	100	105 110
Arg Lys His Tyr Ile Thr Tyr Arg Ile Asn Asn Tyr Thr Pro Asp Met		
	115	120 125
Asn Arg Glu Asp Val Asp Tyr Ala Ile Arg Lys Ala Phe Gln Val Trp		
	130	135 140
Ser Asn Val Thr Pro Leu Lys Phe Ser Lys Ile Asn Thr Gly Met Ala		
145	150	155 160
Asp Ile Leu Val Val Phe Ala Arg Gly Ala His Gly Asp Phe His Ala		
	165	170 175
Phe Asp Gly Lys Gly Gly Ile Leu Ala His Ala Phe Gly Pro Gly Ser		
	180	185 190
Gly Ile Gly Gly Asp Ala His Phe Asp Glu Asp Glu Phe Trp Thr Thr		
	195	200 205
His Ser Gly Gly Thr Asn Leu Phe Leu Thr Ala Val His Glu Ile Gly		
	210	215 220
His Ser Leu Gly Leu Gly His Ser Ser Asp Pro Lys Ala Val Met Phe		
225	230	235 240
Pro Thr Tyr Lys Tyr Val Asp Ile Asn Thr Phe Arg Leu Ser Ala Asp		
	245	250 255
Asp Ile Arg Gly Ile Gln Ser Leu Tyr Gly Asp Pro Lys Glu Asn Gln		
	260	265 270
Arg Leu Pro Asn Pro Asp Asn Ser Glu Pro Ala Leu Cys Asp Pro Asn		
	275	280 285
Leu Ser Phe Asp Ala Val Thr Thr Val Gly Asn Lys Ile Phe Phe Phe		
	290	295 300
Lys Asp Arg Phe Phe Trp Leu Lys Val Ser Glu Arg Pro Lys Thr Ser		
305	310	315 320
Val Asn Leu Ile Ser Ser Leu Trp Pro Thr Leu Pro Ser Gly Ile Glu		

1242

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<210> 1218
<211> 598
<212> PRT
<213> Homo sapiens
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<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

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<220>  
<221> SITE  
<222> (144)  
<223> Xaa equals any of the naturally occurring L-amino acids
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<400> 1218
Ala Thr Ser Arg Gln Pro Ser Tyr Xaa Arg Thr Trp Cys Arg Arg Cys
1 5 10 15

Cys Leu Pro Leu Ala Leu Asn Pro Val Pro Ala Ala Met Ala Pro Gly

1243

20	25	30
Gln Leu Ala Leu Phe Ser Val Ser Asp Lys Thr Gly Leu Val Glu Phe		
35	40	45
Ala Arg Asn Leu Thr Ala Leu Gly Leu Asn Leu Val Ala Ser Gly Gly		
50	55	60
Thr Ala Lys Ala Leu Arg Asp Ala Gly Leu Ala Val Arg Asp Val Ser		
65	70	75 80
Glu Leu Thr Gly Phe Pro Glu Met Leu Gly Gly Arg Val Lys Thr Leu		
85	90	95
His Pro Ala Val His Ala Gly Ile Leu Ala Arg Asn Ile Pro Glu Asp		
100	105	110
Asn Ala Asp Met Ala Arg Leu Asp Phe Asn Leu Ile Arg Val Val Ala		
115	120	125
Cys Asn Leu Tyr Pro Phe Val Lys Thr Val Ala Ser Pro Gly Val Xaa		
130	135	140
Val Glu Glu Ala Val Glu Gln Ile Asp Ile Gly Gly Val Thr Leu Leu		
145	150	155 160
Arg Ala Ala Ala Lys Asn His Ala Arg Val Thr Val Val Cys Glu Pro		
165	170	175
Glu Asp Tyr Val Val Val Ser Thr Glu Met Gln Ser Ser Glu Ser Lys		
180	185	190
Asp Thr Ser Leu Glu Thr Arg Arg Gln Leu Ala Leu Lys Ala Phe Thr		
195	200	205
His Thr Ala Gln Tyr Asp Glu Ala Ile Ser Asp Tyr Phe Arg Lys Gln		
210	215	220
Tyr Ser Lys Gly Val Ser Gln Met Pro Leu Arg Tyr Gly Met Asn Pro		
225	230	235 240
His Gln Thr Pro Ala Gln Leu Tyr Thr Leu Gln Pro Lys Leu Pro Ile		
245	250	255
Thr Val Leu Asn Gly Ala Pro Gly Phe Ile Asn Leu Cys Asp Ala Leu		
260	265	270
Asn Ala Trp Gln Leu Val Lys Glu Leu Lys Glu Ala Leu Gly Ile Pro		
275	280	285
Ala Ala Ala Ser Phe Lys His Val Ser Pro Ala Gly Ala Ala Val Gly		

1244

290	295	300
Ile Pro Leu Ser Glu Asp Glu Ala Lys Val Cys Met Val Tyr Asp Leu		
305	310	315 320
Tyr Lys Thr Leu Thr Pro Ile Ser Ala Ala Tyr Ala Arg Ala Arg Gly		
	325	330 335
Ala Asp Arg Met Ser Ser Phe Gly Asp Phe Val Ala Leu Ser Asp Val		
	340	345 350
Cys Asp Val Pro Thr Ala Lys Ile Ile Ser Arg Glu Val Ser Asp Gly		
	355	360 365
Ile Ile Ala Pro Gly Tyr Glu Glu Glu Ala Leu Thr Ile Leu Ser Lys		
	370	375 380
Lys Lys Asn Gly Asn Tyr Cys Val Leu Gln Met Asp Gln Ser Tyr Lys		
	385	390 395 400
Pro Asp Glu Asn Glu Val Arg Thr Leu Phe Gly Leu His Leu Ser Gln		
	405	410 415
Lys Arg Asn Asn Gly Val Val Asp Lys Ser Leu Phe Ser Asn Val Val		
	420	425 430
Thr Lys Asn Lys Asp Leu Pro Glu Ser Ala Leu Arg Asp Leu Ile Val		
	435	440 445
Ala Thr Ile Ala Val Lys Tyr Thr Gln Ser Asn Ser Val Cys Tyr Ala		
	450	455 460
Lys Asn Gly Gln Val Ile Gly Ile Gly Ala Gly Gln Gln Ser Arg Ile		
	465	470 475 480
His Cys Thr Arg Leu Ala Gly Asp Lys Ala Asn Tyr Trp Trp Leu Arg		
	485	490 495
His His Pro Gln Val Leu Ser Met Lys Phe Lys Thr Gly Val Lys Arg		
	500	505 510
Ala Glu Ile Ser Asn Ala Ile Asp Gln Tyr Val Thr Gly Thr Ile Gly		
	515	520 525
Glu Asp Glu Asp Leu Ile Lys Trp Lys Ala Leu Phe Glu Glu Val Pro		
	530	535 540
Glu Leu Leu Thr Glu Ala Glu Lys Lys Glu Trp Val Glu Lys Leu Thr		
	545	550 555 560
Glu Val Ser Ile Ser Ser Asp Ala Phe Phe Pro Phe Arg Asp Asn Val		

1245

565

570

575

Asp Arg Ala Lys Arg Ser Gly Val Ala Tyr Ile Ala Ala Pro Pro Val
 580 585 590

Leu Leu Leu Thr Lys Leu
 595

<210> 1219

<211> 209

<212> PRT

<213> Homo sapiens

<400> 1219

Tyr Thr Ala Ile Met Ser Ile Met Ser Tyr Asn Gly Gly Ala Val Met
 1 5 10 15

Ala Met Lys Gly Lys Asn Cys Val Ala Ile Ala Ala Asp Arg Arg Phe
 20 25 30

Gly Ile Gln Ala Gln Met Val Thr Thr Asp Phe Gln Lys Ile Phe Pro
 35 40 45

Met Gly Asp Arg Leu Tyr Ile Gly Leu Ala Gly Leu Ala Thr Asp Val
 50 55 60

Gln Thr Val Ala Gln Arg Leu Lys Phe Arg Leu Asn Leu Tyr Glu Leu
 65 70 75 80

Lys Glu Gly Arg Gln Ile Lys Pro Tyr Thr Leu Met Ser Met Val Ala
 85 90 95

Asn Leu Leu Tyr Glu Lys Arg Phe Gly Pro Tyr Tyr Thr Glu Pro Val
 100 105 110

Ile Ala Gly Leu Asp Pro Lys Thr Phe Lys Pro Phe Ile Cys Ser Leu
 115 120 125

Asp Leu Ile Gly Cys Pro Met Val Thr Asp Asp Phe Val Val Ser Gly
 130 135 140

Thr Cys Ala Glu Gln Met Tyr Gly Met Cys Glu Ser Leu Trp Glu Pro
 145 150 155 160

Asn Met Asp Pro Asp His Leu Phe Glu Thr Ile Ser Gln Ala Met Leu
 165 170 175

Asn Ala Val Asp Arg Asp Ala Val Ser Gly Met Gly Val Ile Val His
 180 185 190

1246

Ile Ile Glu Lys Asp Lys Ile Thr Thr Arg Thr Leu Lys Ala Arg Met
 195 200 205

Asp

<210> 1220

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (51)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (64)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (77)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1220

Ile Ile Ser Ile Ile Ser Thr Ser Asn Lys Ile Lys Met Ser Glu Ala
 1 5 10 15

Pro Arg Phe Phe Val Gly Pro Glu Asp Thr Glu Ile Asn Pro Gly Asn
 20 25 30

Tyr Arg His Phe Phe His His Ala Asp Glu Asp Asp Glu Glu Glu Asp
 35 40 45

Asp Ser Xaa Pro Glu Arg Gln Ile Val Val Gly Ile Cys Ser Met Xaa
 50 55 60

Lys Lys Ser Lys Ser Lys Pro Met Lys Glu Ile Leu Xaa Arg Ile Ser
 65 70 75 80

Leu Phe Lys Tyr Ile Thr Val Val Val Phe Glu Glu Glu Val Ile Leu
 85 90 95

Asn Glu Pro Val Glu Asn Trp Pro Leu Cys Asp Cys Leu Ile Ser Phe
 100 105 110

1247

His Ser Lys Gly Phe Pro Leu Asp Lys Ala Val Ala Tyr Ala Lys Leu
115 120 125

Arg Asn Pro Phe Val Ile Asn Asp Leu Asn Met Gln
130 135 140

<210> 1221

<211> 45

<212> PRT

<213> Homo sapiens

<400> 1221

Gly Leu Met Glu Ile Glu Ile Thr Cys Lys Asp Ile Thr Val Phe Met
1 5 10 15

Ser Tyr Ile Leu Val Leu Glu Ile Val Glu Cys Met Ile Asp Asn Ile
20 25 30

Phe Leu Ile Phe Ile Phe Ser Ser Asn Thr Ser Thr Val
35 40 45

<210> 1222

<211> 70

<212> PRT

<213> Homo sapiens

<400> 1222

Val Ala Tyr Ile Cys Tyr Ser Lys Phe Cys Lys Tyr Ala Asn Gln Leu
1 5 10 15

Tyr Arg Phe Ile Thr Ser Phe Leu Gly Phe Phe Trp Gly Arg Val Ile
20 25 30

Ile Leu Leu Lys Ile Thr Met Asn Thr Leu Thr Val Arg Ile Cys Gly
35 40 45

Lys Val Pro Leu Asn Ile Thr Lys Ile Ile Ser Leu Glu Gly Arg Asn
50 55 60

Asn His Ser Asn Glu Leu
65 70

<210> 1223

<211> 88

<212> PRT

1248

<213> Homo sapiens

<400> 1223

Phe Tyr Pro Ser Thr Tyr Leu Lys Ala Pro Ser Ser Leu Val Cys Gly
 1 5 10 15

Val Leu Glu Pro Val Ser Ser Phe Trp Arg Phe Lys Leu Asn Ser Asn
 20 25 30

Asn Tyr Val Thr Gln Ser Met Trp Arg Lys Ser Glu Thr Ser His Gly
 35 40 45

Asp Ala Gly Pro Arg Ala Arg Pro Ala Val Trp Pro Ala Leu Leu Thr
 50 55 60

Ser Val Ser Arg Ser Phe Pro Ser His Glu Val Pro Ser Gly His Gly
 65 70 75 80

Asp Glu Gly Arg Glu Gly Thr Gly
 85

<210> 1224

<211> 298

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (279)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1224

Ala Thr Arg Arg Arg Ala Ala Glu Ala Gly Met Ala Ala Val Leu Gln
 1 5 10 15

Arg Val Glu Arg Leu Ser Asn Arg Val Val Arg Val Leu Gly Cys Asn
 20 25 30

Pro Gly Pro Met Thr Leu Gln Gly Thr Asn Thr Tyr Leu Val Gly Thr
 35 40 45

Gly Pro Arg Arg Ile Leu Ile Asp Thr Gly Glu Pro Ala Ile Pro Glu
 50 55 60

Tyr Ile Ser Cys Leu Lys Gln Ala Leu Thr Glu Phe Asn Thr Ala Ile
 65 70 75 80

Gln Glu Ile Val Val Thr His Trp His Arg Asp His Ser Gly Gly Ile
 85 90 95

1249

Gly Asp Ile Cys Lys Ser Ile Asn Asn Asp Thr Thr Tyr Cys Ile Lys
 100 105 110
 Lys Leu Pro Arg Asn Pro Gln Arg Glu Glu Ile Ile Gly Asn Gly Glu
 115 120 125
 Gln Gln Tyr Val Tyr Leu Lys Asp Gly Asp Val Ile Lys Thr Glu Gly
 130 135 140
 Ala Thr Leu Arg Val Leu Tyr Thr Pro Gly His Thr Asp Asp His Met
 145 150 155 160
 Ala Leu Leu Leu Glu Glu Glu Asn Ala Ile Phe Ser Gly Asp Cys Ile
 165 170 175
 Leu Gly Glu Gly Thr Thr Val Phe Glu Asp Leu Tyr Asp Tyr Met Asn
 180 185 190
 Ser Leu Lys Glu Leu Leu Lys Ile Lys Ala Asp Ile Ile Tyr Pro Gly
 195 200 205
 His Gly Pro Val Ile His Asn Ala Glu Ala Lys Ile Gln Gln Tyr Ile
 210 215 220
 Ser His Arg Asn Ile Arg Glu Gln Gln Ile Leu Thr Leu Phe Arg Glu
 225 230 235 240
 Asn Phe Glu Lys Ser Phe Thr Val Met Glu Leu Val Lys Ile Ile Tyr
 245 250 255
 Lys Asn Thr Pro Glu Asn Leu His Glu Met Ala Lys His Asn Leu Leu
 260 265 270
 Leu His Leu Lys Lys Leu Xaa Lys Glu Gly Lys Ile Phe Ser Asn Thr
 275 280 285
 Asp Pro Asp Lys Lys Trp Lys Ala His Leu
 290 295

<210> 1225

<211> 27

<212> PRT

<213> Homo sapiens

<400> 1225

Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln Asp Gly Pro
 1 5 10 15

1250

Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Lys Val
 20 25

<210> 1226

<211> 380

<212> PRT

<213> Homo sapiens

<400> 1226

Glu Gln Glu Leu Asp Thr Leu Lys Arg Lys Ser Pro Ser Asp Leu Trp
 1 5 10 15

Lys Glu Asp Leu Ala Thr Phe Ile Glu Glu Leu Glu Ala Val Glu Ala
 20 25 30

Lys Glu Lys Gln Asp Glu Gln Val Gly Leu Pro Gly Lys Val Gly Lys
 35 40 45

Ala Lys Gly Lys Lys Thr Gln Met Ala Glu Val Leu Pro Ser Pro Arg
 50 55 60

Gly Gln Arg Val Ile Pro Arg Ile Thr Ile Glu Met Lys Ala Glu Ala
 65 70 75 80

Glu Lys Lys Asn Lys Lys Lys Ile Lys Asn Glu Asn Thr Glu Gly Ser
 85 90 95

Pro Gln Glu Asp Gly Val Glu Leu Glu Gly Leu Lys Gln Arg Leu Glu
 100 105 110

Lys Lys Gln Lys Arg Glu Pro Gly Thr Lys Thr Lys Lys Gln Thr Thr
 115 120 125

Leu Ala Phe Lys Pro Ile Lys Lys Gly Lys Lys Arg Asn Pro Trp Ser
 130 135 140

Asp Ser Glu Ser Asp Arg Ser Ser Asp Glu Ser Asn Phe Asp Val Pro
 145 150 155 160

Pro Arg Glu Thr Glu Pro Arg Arg Ala Ala Thr Lys Thr Lys Phe Thr
 165 170 175

Met Asp Leu Asp Ser Asp Glu Asp Phe Ser Asp Phe Asp Glu Lys Thr
 180 185 190

Asp Asp Glu Asp Phe Val Pro Ser Asp Ala Ser Pro Pro Lys Thr Lys
 195 200 205

Thr Ser Pro Lys Leu Ser Asn Lys Glu Leu Lys Pro Gln Lys Ser Val

1251

210	215	220
Val Ser Asp Leu Glu Ala Asp Asp Val Lys Gly Ser Val Pro Leu Ser		
225	230	235 240
Ser Ser Pro Pro Ala Thr His Phe Pro Asp Glu Thr Glu Ile Thr Asn		
	245	250 255
Pro Val Pro Lys Lys Asn Val Thr Val Lys Lys Thr Ala Ala Lys Ser		
	260	265 270
Gln Ser Ser Thr Ser Thr Thr Gly Ala Lys Lys Arg Ala Ala Pro Lys		
	275	280 285
Gly Thr Lys Arg Asp Pro Ala Leu Asn Ser Gly Val Ser Gln Lys Pro		
	290	295 300
Asp Pro Ala Lys Thr Lys Asn Arg Arg Lys Arg Lys Pro Ser Thr Ser		
	305	310 315 320
Asp Asp Ser Asp Ser Asn Phe Glu Lys Ile Val Ser Lys Ala Val Thr		
	325	330 335
Ser Lys Lys Ser Lys Gly Glu Ser Asp Asp Phe His Met Asp Phe Asp		
	340	345 350
Ser Ala Val Ala Pro Arg Ala Lys Ser Val Arg Ala Lys Lys Pro Ile		
	355	360 365
Lys Tyr Leu Glu Glu Ser Asp Glu Asp Asp Leu Phe		
	370	375 380

<210> 1227

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (26)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1227

Phe Asn Ser Leu Lys Cys Leu Phe Gly Ile Met Ile Gly Asn Leu Asp
1 5 10 15

Glu Phe Arg Gly Lys Lys Leu Ser Ala Xaa Met Leu Arg Ala His Leu
20 25 30

1252

Ser Pro His Thr Pro Thr Glu Leu Thr Gly Leu Gln Cys Phe Ile Arg
 35 40 45

Lys Phe Pro Ile Pro Leu Ser Cys Val Phe Met Leu Lys Ile Leu Leu
 50 55 60

His Phe Ser Phe Glu Cys Gln Phe Leu Thr Ser Thr Ile Ser
 65 70 75

<210> 1228

<211> 222

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (142)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1228

Ala Asn Glu Lys Val Ala Leu Gln Lys Ala Leu Leu Tyr Tyr Glu Ser
 1 5 10 15

Ile His Gly Arg Pro Val Thr Lys Asn Glu Arg Gln Val Met Lys Pro
 20 25 30

Leu Tyr Asp Arg Tyr Arg Leu Val Lys Gln Ile Leu Ser Arg Ala Asn
 35 40 45

Thr Ile Pro Ile Ile Gly Ser Pro Ser Ser Lys Arg Arg Ser Pro Leu
 50 55 60

Leu Gln Pro Ile Ile Glu Gly Glu Thr Ala Ser Phe Phe Lys Glu Ile
 65 70 75 80

Lys Glu Glu Glu Glu Gly Ser Glu Asp Asp Ser Asn Val Lys Pro Asp
 85 90 95

Phe Met Val Thr Leu Lys Thr Asp Phe Ser Ala Arg Cys Phe Leu Asp
 100 105 110

Gln Phe Glu Asp Asp Ala Asp Gly Phe Ile Ser Pro Met Asp Asp Lys
 115 120 125

Ile Pro Ser Lys Cys Ser Gln Asp Thr Gly Leu Ser Asn Xaa His Ala
 130 135 140

Ala Ser Ile Pro Glu Leu Leu Glu His Leu Gln Glu Met Arg Glu Glu
 145 150 155 160

1253

Lys Lys Arg Ile Arg Lys Lys Leu Arg Asp Phe Glu Asp Asn Phe Phe
 165 170 175

Arg Gln Asn Gly Arg Asn Val Gln Lys Glu Asp Arg Thr Pro Met Ala
 180 185 190

Glu Glu Tyr Ser Glu Tyr Lys His Ile Lys Ala Lys Leu Arg Leu Leu
 195 200 205

Glu Val Leu Ile Ser Lys Arg Asp Thr Asp Ser Lys Ser Met
 210 215 220

<210> 1229

<211> 220

<212> PRT

<213> Homo sapiens

<400> 1229

Lys Gly Ser Thr Leu Gly His Leu Cys Thr Ala Met Ala Gly Met Met
 1 5 10 15

Lys Gly Ile Arg Trp Ser Cys Pro Ala Ile Ala Ser Ile Ser Gln Thr
 20 25 30

Arg Ser Ser Gln Glu Lys Asp Ser Ser Ser Pro Pro Trp Asp Leu Arg
 35 40 45

Arg Ala Ala Thr Glu Gly Glu Ala Pro Asp Ala Leu Cys Gln Ser Gln
 50 55 60

Val Arg Gly Gln Ser Ser Pro Cys His Pro Trp Cys Arg Pro Ala Pro
 65 70 75 80

Ser Ser Phe Met Pro Gly Pro Ala Gly Thr Pro Ala Thr Thr Glu Ser
 85 90 95

Thr Arg Ser Ala Leu Cys Ser Trp Arg Arg His Ser Arg Val Glu Ser
 100 105 110

Cys Pro Ser Leu Ser Leu Gly His Leu Gly Gly Glu Ser Gly Leu Arg
 115 120 125

Ser Glu Leu Asp Pro Gly Asp Leu Gly Ser Phe Phe Leu Ala His Gln
 130 135 140

Pro Cys Arg Pro His Leu Ser Gln Asn Pro Leu Cys Leu Gly Gly Ser
 145 150 155 160

1254

Gly Ser Ala Leu Leu Cys Ser Arg Arg Leu Gly Ser Gly Gln His Gln
165 170 175

Val Gly Lys Trp Ser Pro Pro Ser Cys Phe Cys Arg Ile Leu Thr Val
180 185 190

Gly Leu Glu Glu Lys Ser Ile Asp Leu Ile Ser Pro Thr Thr His Pro
195 200 205

Ser Phe Ser Phe Phe His His Ser Pro Pro Gln Leu
210 215 220

<210> 1230

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (11)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (12)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (30)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1230

Glu Leu Lys Arg Leu Thr Ile Gly Lys Asn Xaa Xaa Arg Leu Thr Gly
1 5 10 15

Asn Arg Xaa Gly Ile Pro Gly Ser Thr His Ala Ser Glu Xaa Glu Val
20 25 30

Glu Glu Glu Gly Asp Val Asp Ser Asp Glu Glu Glu Glu Asp Glu
35 40 45

Glu Ser Ser Ser Glu Gly Leu Glu Ala Glu Asp Trp Ala Gln Gly Val
50 55 60

1255

Val Glu Ala Gly Gly Ser Phe Gly Ala Tyr Gly Ala Gln Glu Glu Ala
65 70 75 80
Gln Cys Pro Thr Leu His Phe Leu Glu Gly Gly Glu Asp Ser Asp Ser
85 90 95
Asp Ser Glu Glu Glu Asp Asp Glu Glu Glu Asp Asp Glu Asp Glu Asp
100 105 110
Asp Asp Asp Asp Glu Glu Asp Gly Asp Glu Val Pro Val Pro Ser Phe
115 120 125
Gly Glu Ala Met Ala Tyr Phe Ala Met Val Lys Arg Tyr Leu Thr Ser
130 135 140
Phe Pro Ile Asp Asp Arg Val Gln Ser His Ile Leu His Leu Glu His
145 150 155 160
Asp Leu Val His Val Thr Arg Lys Asn His Ala Arg Gln Ala Gly Val
165 170 175
Arg Gly Leu Gly His Gln Ser
180

<210> 1231
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1231
Asn Leu Tyr Lys Leu Lys Leu Asn His Glu Leu Gln Lys Lys Ser Ile
1 5 10 15
Leu Pro Lys Leu Asp Val Thr Thr Leu Thr Ser Leu Lys Tyr Glu Val
20 25 30
Asp Cys Leu Lys Asp Ser Ala Tyr Ile Leu Val Cys Thr Phe Arg Asn
35 40 45
Ile Phe Leu Gly Lys Ser Thr Gln His Phe Leu
50 55

<210> 1232
<211> 135
<212> PRT
<213> Homo sapiens

1256

<400> 1232

Gly Ser Thr His Ala Ser Gly Pro Pro Gln Ala Pro Gln Leu Ile Tyr
 1 5 10 15

Gln Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
 20 25 30

Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
 35 40 45

Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
 50 55 60

Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
 65 70 75 80

Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
 85 90 95

Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
 100 105 110

Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
 115 120 125

Leu Gly Leu Asp Val Pro Val
 130 135

<210> 1233

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1233

Arg Gly Glu Thr Arg Glu Met Ala Gly Asn Leu Leu Ser Gly Ala Gly
 1 5 10 15

Arg Arg Leu Trp Asp Trp Val Pro Leu Ala Cys Arg Ser Phe Ser Leu
 20 25 30

Gly Val Pro Arg Leu Ile Gly Ile Arg Leu Thr Leu Pro Pro Pro Lys
 35 40 45

Val Val Asp Arg Trp Asn Glu Lys Arg Ala Met Phe Gly Val Tyr Asp
 50 55 60

Asn Ile Gly Ile Leu Gly Asn Phe Glu Lys His Pro Lys Glu Leu Ile
 65 70 75 80

1257

Arg Gly Pro Ile Trp Leu Arg Gly Trp Lys Gly Asn Glu Leu Gln Arg
 85 90 95

Cys Ile Arg Lys Arg Lys Met Val Gly Ser Arg Met Phe Ala Asp Asp
 100 105 110

Leu His Asn Leu Asn Lys Arg Ile Arg Tyr Leu Tyr Lys His Phe Asn
 115 120 125

Arg His Gly Lys Phe Arg
 130

<210> 1234

<211> 282

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (18)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1234

Thr Gly Pro Glu Phe Pro Gly Xaa Pro Thr Arg Pro Arg Thr Ala Ala
 1 5 10 15

Ala Xaa Ser Ala Arg Thr Arg Thr Arg Gly Ser Pro Arg Met Gly Glu
 20 25 30

Phe Asn Glu Lys Lys Thr Thr Cys Gly Thr Val Cys Leu Lys Tyr Leu
 35 40 45

Leu Phe Thr Tyr Asn Cys Cys Phe Trp Leu Ala Gly Leu Ala Val Met
 50 55 60

Ala Val Gly Ile Trp Thr Leu Ala Leu Lys Ser Asp Tyr Ile Ser Leu
 65 70 75 80

Leu Ala Ser Gly Thr Tyr Leu Ala Thr Ala Tyr Ile Leu Val Val Ala
 85 90 95

Gly Thr Val Val Met Val Thr Gly Val Leu Gly Cys Cys Ala Thr Phe
 100 105 110

1258

Lys Glu Arg Arg Asn Leu Leu Arg Leu Tyr Phe Ile Leu Leu Leu Ile
 115 120 125

Ile Phe Leu Leu Glu Ile Ile Ala Gly Ile Leu Ala Tyr Ala Tyr Tyr
 130 135 140

Gln Gln Leu Asn Thr Glu Leu Lys Glu Asn Leu Lys Asp Thr Met Thr
 145 150 155 160

Lys Arg Tyr His Gln Pro Gly His Glu Ala Val Thr Ser Ala Val Asp
 165 170 175

Gln Leu Gln Gln Glu Phe His Cys Cys Gly Ser Asn Asn Ser Gln Asp
 180 185 190

Trp Arg Asp Ser Glu Trp Ile Arg Ser Gln Glu Ala Gly Gly Arg Val
 195 200 205

Val Pro Asp Ser Cys Cys Lys Thr Val Val Ala Leu Cys Gly Gln Arg
 210 215 220

Asp His Ala Ser Asn Ile Tyr Lys Val Glu Gly Gly Cys Ile Thr Lys
 225 230 235 240

Leu Glu Thr Phe Ile Gln Glu His Leu Arg Val Ile Gly Ala Val Gly
 245 250 255

Ile Gly Ile Ala Cys Val Gln Val Phe Gly Met Ile Phe Thr Cys Cys
 260 265 270

Leu Tyr Arg Ser Leu Lys Leu Glu His Tyr
 275 280

<210> 1235

<211> 66

<212> PRT

<213> Homo sapiens

<400> 1235

Ala Glu Ile Gln Val Phe Gln Val Gly Leu Val Ser Trp Gly Leu Tyr
 1 5 10 15

Asn Pro Cys Leu Gly Ser Ala Asp Lys Asn Ser Arg Lys Arg Ala Pro
 20 25 30

Arg Ser Lys Val Pro Pro Pro Arg Asp Phe His Ile Asn Leu Phe Arg
 35 40 45

1259

Met Gln Pro Trp Leu Arg Gln His Leu Gly Asp Val Leu Asn Phe Leu
 50 55 60

Pro Leu
 65

<210> 1236
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 1236
 Ala Arg Arg Arg Arg Gly Gly Trp Ala Gly Gly Gly Gly Thr Arg
 1 5 10 15

Arg Ala Leu Gly Val Pro Val Ala Arg Arg Arg Met Trp Arg Ala
 20 25 30

Glu Gly Lys Trp Leu Pro Lys Thr Ser Arg Lys Ser Val Ser Gln Ser
 35 40 45

Val Phe Cys Gly Thr Ser Thr Tyr Cys Val Leu Asn Thr Val Pro Pro
 50 55 60

Ile Glu Asp Asp His Gly Asn Ser Asn Ser Ser His Val Lys Ile Phe
 65 70 75 80

Leu Pro Lys Lys Leu Leu Glu Cys Leu Pro Lys Cys Ser Ser Leu Pro
 85 90 95

Lys Glu Arg His Arg Trp Asn Thr Asn Glu Arg Ser
 100 105

<210> 1237
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 1237
 Arg Gly Gly Gly Ser Lys Gly Asn Glu Val Arg Pro Val Ala Gly Ser
 1 5 10 15

Ala Glu Ser Ala Ala Leu Arg Leu Arg Ala Pro Leu Gln Gln Val Gln
 20 25 30

Ala Gln Leu Ser Pro Leu Gln Asn Ile Ser Pro Trp Ile Leu Ala Val
 35 40 45

1260

Leu Thr Leu Gln Ile Gln Ser Leu Ile Ser Cys Trp Ala Phe Trp Thr
 50 55 60
 Thr Trp Thr Gln Ser Cys Ser Ser Asn Ala Leu Pro Gln Ser Leu Pro
 65 70 75 80
 Ala Trp Arg Ser Ser Gln Arg Ser Thr Gln Lys Asp Pro Val Pro Tyr
 85 90 95
 Gln Pro Pro Phe Leu Cys Gln Trp Gly Arg His Gln Pro Ser Trp Lys
 100 105 110
 Pro Leu Met Asn
 115

<210> 1238

<211> 311

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (16)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1238

Val Thr Ser Glu Gly Val Arg Val Arg Ser Ser Arg Gly Arg Ala Xaa
 1 5 10 15
 Gly Val Trp Arg Phe Glu Arg Asp Glu Asp Gly Thr Gly Ala Gly Cys
 20 25 30
 Gly Gln Trp Thr Arg Phe Cys Arg Glu Pro Lys Met Ala Val Asn Val
 35 40 45
 Tyr Ser Thr Ser Val Thr Ser Asp Asn Leu Ser Arg His Asp Met Leu
 50 55 60
 Ala Trp Ile Asn Glu Ser Leu Gln Leu Asn Leu Thr Lys Ile Glu Gln
 65 70 75 80
 Leu Cys Ser Gly Ala Ala Tyr Cys Gln Phe Met Asp Met Leu Phe Pro
 85 90 95
 Gly Ser Ile Ala Leu Lys Lys Val Lys Phe Gln Ala Lys Leu Glu His
 100 105 110
 Glu Tyr Ile Gln Asn Phe Lys Ile Leu Gln Ala Gly Phe Lys Arg Met

1261

115	120	125
Gly Val Asp Lys Ile Ile Pro Val Asp Lys Leu Val Lys Gly Lys Phe		
130	135	140
Gln Asp Asn Phe Glu Phe Val Gln Trp Phe Lys Lys Phe Phe Asp Ala		
145	150	155 160
Asn Tyr Asp Gly Lys Asp Tyr Asp Pro Val Ala Ala Arg Gln Gly Gln		
165	170	175
Glu Thr Ala Val Ala Pro Ser Leu Val Ala Pro Ala Leu Asn Lys Pro		
180	185	190
Lys Lys Pro Leu Thr Ser Ser Ser Ala Ala Pro Gln Arg Pro Ile Ser		
195	200	205
Thr Gln Arg Thr Ala Ala Ala Pro Lys Ala Gly Pro Gly Val Val Arg		
210	215	220
Lys Asn Pro Gly Val Gly Asn Gly Asp Asp Glu Ala Ala Glu Leu Met		
225	230	235 240
Gln Gln Val Asn Val Leu Lys Leu Thr Val Glu Asp Leu Glu Lys Glu		
245	250	255
Arg Asp Phe Tyr Phe Gly Lys Leu Arg Asn Ile Glu Leu Ile Cys Gln		
260	265	270
Glu Asn Glu Gly Glu Asn Asp Pro Val Leu Gln Arg Ile Val Asp Ile		
275	280	285
Leu Tyr Ala Thr Asp Glu Gly Phe Val Ile Pro Asp Glu Gly Gly Pro		
290	295	300
Gln Glu Glu Gln Glu Glu Tyr		
305	310	

<210> 1239

<211> 345

<212> PRT

<213> Homo sapiens

<400> 1239

Ala Ala Arg Leu Ala Val Glu Met Lys Thr Asp Leu Leu Ile Val Leu
1 5 10 15

Ser Asp Val Glu Gly Leu Phe Asp Ser Pro Pro Gly Ser Asp Asp Ala
20 25 30

1262

Lys Leu Ile Asp Ile Phe Tyr Pro Gly Asp Gln Gln Ser Val Thr Phe
 35 40 45
 Gly Thr Lys Ser Arg Val Gly Met Gly Gly Met Glu Ala Lys Val Lys
 50 55 60
 Ala Ala Leu Trp Ala Leu Gln Gly Gly Thr Ser Val Val Ile Ala Asn
 65 70 75 80
 Gly Thr His Pro Lys Val Ser Gly His Val Ile Thr Asp Ile Val Glu
 85 90 95
 Gly Lys Lys Val Gly Thr Phe Phe Ser Glu Val Lys Pro Ala Gly Pro
 100 105 110
 Thr Val Glu Gln Gln Gly Glu Met Ala Arg Ser Gly Gly Arg Met Leu
 115 120 125
 Ala Thr Leu Glu Pro Glu Gln Arg Ala Glu Ile Ile His His Leu Ala
 130 135 140
 Asp Leu Leu Thr Asp Gln Arg Asp Glu Ile Leu Leu Ala Asn Lys Lys
 145 150 155 160
 Asp Leu Glu Glu Ala Glu Gly Arg Leu Ala Ala Pro Leu Leu Lys Arg
 165 170 175
 Leu Ser Leu Ser Thr Ser Lys Leu Asn Ser Leu Ala Ile Gly Leu Arg
 180 185 190
 Gln Ile Ala Ala Ser Ser Gln Asp Ser Val Gly Arg Val Leu Arg Arg
 195 200 205
 Thr Arg Ile Ala Lys Asn Leu Glu Leu Glu Gln Val Thr Val Pro Ile
 210 215 220
 Gly Val Leu Leu Val Ile Phe Glu Ser Arg Pro Asp Cys Leu Pro Gln
 225 230 235 240
 Val Ala Ala Leu Ala Ile Ala Ser Gly Asn Gly Leu Leu Leu Lys Gly
 245 250 255
 Gly Lys Glu Ala Ala His Ser Asn Arg Ile Leu His Leu Leu Thr Gln
 260 265 270
 Glu Ala Leu Ser Ile His Gly Val Lys Glu Ala Val Gln Leu Val Asn
 275 280 285
 Thr Arg Glu Glu Val Glu Asp Leu Cys Arg Leu Asp Lys Met Ile Asp
 290 295 300

1263

Leu Ile Ile Pro Arg Gly Ser Ser Gln Leu Val Arg Asp Ile Gln Lys
305 310 315 320

Ala Ala Lys Gly Ile Pro Val Met Gly His Ser Glu Gly Ile Cys Ala
325 330 335

His Val Cys Gly Phe Arg Gly Gln Cys
340 345

<210> 1240

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1240

Gly Tyr Cys Phe Ile Ser Thr Ser Arg Thr Pro Lys Glu Thr Ile Trp
1 5 10 15

Val Lys Ala Thr Ser Thr Ala Leu Ala Leu His Arg Phe Leu Glu Phe
20 25 30

Leu Ser Phe Thr Phe Ser Leu Thr Gln His Cys Leu Leu Phe Val Phe
35 40 45

Val Ala Trp Phe Val Phe Phe Leu Pro Cys Ser Pro Asn Leu Cys Pro
50 55 60

Asn Ser Phe Gly Leu Met Gln Lys Tyr Leu Cys Gly Arg Glu Glu Leu
65 70 75 80

Phe Ser Trp Arg Ala Phe Arg
85

<210> 1241

<211> 196

<212> PRT

<213> Homo sapiens

<400> 1241

Arg Ala Gly Ser Pro Ala Ser Pro Ala His Val Ala Trp Pro Pro Ala
1 5 10 15

Pro Thr Trp Ser Arg Ala Leu Pro Arg Val Ala Pro Arg Ser Ser Ser
20 25 30

Arg Arg Gly Arg Arg Tyr Pro Glu Arg Ser Gln Arg Arg Arg Glu Val

1264

35 40 45

Ala Ala Thr Ala Met Pro Lys Asn Lys Gly Lys Gly Gly Lys Asn Arg
50 55 60

Arg Arg Gly Lys Asn Glu Asn Glu Ser Glu Lys Arg Glu Leu Val Phe
65 70 75 80

Lys Glu Asp Gly Gln Glu Tyr Ala Gln Val Ile Lys Met Leu Gly Asn
85 90 95

Gly Arg Leu Glu Ala Met Cys Phe Asp Gly Val Lys Arg Leu Cys His
100 105 110

Ile Arg Gly Lys Leu Arg Lys Lys Val Trp Ile Asn Thr Ser Asp Ile
115 120 125

Ile Leu Val Gly Leu Arg Asp Tyr Gln Asp Asn Lys Ala Asp Val Ile
130 135 140

Leu Lys Tyr Asn Ala Asp Glu Ala Arg Ser Leu Lys Ala Tyr Gly Glu
145 150 155 160

Leu Pro Glu His Ala Lys Ile Asn Glu Thr Asp Thr Phe Gly Pro Gly
165 170 175

Asp Asp Asp Glu Ile Gln Phe Asp Asp Ile Gly Asp Asp Asp Glu Asp
180 185 190

Ile Asp Asp Ile
195

<210> 1242

<211> 218

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1242

Ala Val Xaa Phe Lys Asp Xaa Ile Tyr Glu Ile Phe Gln Lys Leu Asn

1265

1	5	10	15
Thr Ser Ile Gln Val Val Leu Leu Ser Ala Thr Met Pro Thr Asp Val			
20	25	30	
Leu Glu Val Thr Lys Lys Phe Met Arg Asp Pro Ile Arg Ile Leu Val			
35	40	45	
Lys Lys Glu Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Tyr Ile Asn			
50	55	60	
Val Glu Arg Glu Glu Trp Lys Leu Asp Thr Leu Cys Asp Leu Tyr Glu			
65	70	75	80
Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Leu Asn Thr Arg Arg Lys			
85	90	95	
Val Asp Trp Leu Thr Glu Lys Met His Ala Arg Asp Phe Thr Val Ser			
100	105	110	
Ala Leu His Gly Asp Met Asp Gln Lys Glu Arg Asp Val Ile Met Arg			
115	120	125	
Glu Phe Arg Ser Gly Ser Ser Arg Val Leu Ile Thr Thr Asp Leu Leu			
130	135	140	
Ala Arg Gly Ile Asp Val Gln Gln Val Ser Leu Val Ile Asn Tyr Asp			
145	150	155	160
Leu Pro Thr Asn Arg Glu Asn Tyr Ile His Arg Ile Gly Arg Gly Gly			
165	170	175	
Arg Phe Gly Arg Lys Gly Val Ala Ile Asn Phe Val Thr Glu Glu Asp			
180	185	190	
Lys Arg Ile Leu Arg Asp Ile Glu Thr Phe Tyr Asn Thr Thr Val Glu			
195	200	205	
Glu Met Pro Met Asn Val Ala Asp Leu Ile			
210	215		

<210> 1243

<211> 173

<212> PRT

<213> Homo sapiens

<400> 1243

Leu Asp Gly Ser Ala Arg Ala Glu Leu Ala Leu Ser Val Ala Val Asn
1 5 10 15

1266

Val Ala Pro Gly Arg Leu Cys Ala Gly Arg Tyr Ser Ser Asp Val Gln
 20 25 30
 Glu Met Ile Leu Ser Ser Ala Thr Ala Asp Arg Ile Pro Ile Ala Val
 35 40 45
 Ser Gly Val Arg Gly Met Gly Phe Leu Met Arg His His Ile Glu Thr
 50 55 60
 Gly Gly Gly Gln Leu Pro Ala Lys Leu Ser Ser Leu Phe Val Lys Cys
 65 70 75 80
 Leu Gln Asn Pro Ser Ser Asp Ile Arg Leu Val Ala Glu Lys Met Ile
 85 90 95
 Trp Trp Ala Asn Lys Asp Pro Leu Pro Pro Leu Asp Pro Gln Ala Ile
 100 105 110
 Lys Pro Ile Leu Lys Ala Leu Leu Asp Asn Thr Lys Asp Lys Asn Thr
 115 120 125
 Val Val Arg Ala Tyr Ser Asp Gln Ala Ile Val Asn Leu Leu Lys Met
 130 135 140
 Arg Gln Gly Glu Glu Val Phe Gln Ser Leu Ser Lys Ile Leu Asp Val
 145 150 155 160
 Ala Ser Leu Glu Val Leu Asn Glu Val Asn Arg Ser Pro
 165 170

<210> 1244

<211> 222

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (72)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1244

Tyr Ile Lys Ile Tyr Gln Gly Glu Glu Leu Pro His Pro Lys Ser Met
 1 5 10 15

1267

Xaa Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Val Ala Thr Ala
 20 25 30

Lys Asp Thr Tyr Asn Lys Lys Met Glu Glu Ile Cys Gly Gly Asp Lys
 35 40 45

Pro Phe Leu Ala Pro Asn Asp Leu Gln Thr Lys His Leu Gln Leu Lys
 50 55 60

Glu Glu Ser Val Lys Leu Phe Xaa Gly Val Lys Lys Met Gly Gly Glu
 65 70 75 80

Glu Phe Ser Arg Arg Tyr Leu Gln Gln Leu Glu Ser Glu Ile Asp Glu
 85 90 95

Leu Tyr Ile Gln Tyr Ile Lys His Asn Asp Ser Lys Asn Ile Phe His
 100 105 110

Ala Ala Arg Thr Pro Ala Thr Leu Phe Val Val Ile Phe Ile Thr Tyr
 115 120 125

Val Ile Ala Gly Val Thr Gly Phe Ile Gly Leu Asp Ile Ile Ala Ser
 130 135 140

Leu Cys Asn Met Ile Met Gly Leu Thr Leu Ile Thr Leu Cys Thr Trp
 145 150 155 160

Ala Tyr Ile Arg Tyr Ser Gly Glu Tyr Arg Glu Leu Gly Ala Val Ile
 165 170 175

Asp Gln Val Ala Ala Ala Leu Trp Asp Gln Ala Leu Tyr Lys Leu Tyr
 180 185 190

Ser Ala Ala Ala Thr His Arg His Leu Tyr His Gln Ala Phe Pro Thr
 195 200 205

Pro Lys Ser Glu Ser Thr Glu Gln Ser Glu Lys Lys Lys Met
 210 215 220

<210> 1245

<211> 278

<212> PRT

<213> Homo sapiens

<400> 1245

Ser Ala Glu Asp Val Glu Phe Gln Lys Glu Val Ala Gln Val Arg Lys
 1 5 10 15

1268

Arg Ile Thr Gln Arg Lys Lys Gln Glu Gln Leu Thr Pro Gly Val Val
20 25 30

Tyr Val Arg His Leu Pro Asn Leu Leu Asp Glu Thr Gln Ile Phe Ser
35 40 45

Tyr Phe Ser Gln Phe Gly Thr Val Thr Arg Phe Arg Leu Ser Arg Ser
50 55 60

Lys Arg Thr Gly Asn Ser Lys Gly Tyr Ala Phe Val Glu Phe Glu Ser
65 70 75 80

Glu Asp Val Ala Lys Ile Val Ala Glu Thr Met Asn Asn Tyr Leu Phe
85 90 95

Gly Glu Arg Leu Leu Glu Cys His Phe Met Pro Pro Glu Lys Val His
100 105 110

Lys Glu Leu Phe Lys Asp Trp Asn Ile Pro Phe Lys Gln Pro Ser Tyr
115 120 125

Pro Ser Val Lys Arg Tyr Asn Arg Asn Arg Thr Leu Thr Gln Lys Leu
130 135 140

Arg Met Glu Glu Arg Phe Lys Lys Lys Glu Arg Leu Leu Arg Lys Lys
145 150 155 160

Leu Ala Lys Lys Gly Ile Asp Tyr Asp Phe Pro Ser Leu Ile Leu Gln
165 170 175

Lys Thr Glu Ser Ile Ser Lys Thr Asn Arg Gln Thr Ser Thr Lys Gly
180 185 190

Gln Val Leu Arg Lys Lys Lys Lys Val Ser Gly Thr Leu Asp Thr
195 200 205

Pro Glu Lys Thr Val Asp Ser Gln Gly Pro Thr Pro Val Cys Thr Pro
210 215 220

Thr Phe Leu Glu Arg Arg Lys Ser Gln Val Ala Glu Leu Asn Asp Asp
225 230 235 240

Asp Lys Asp Asp Glu Ile Val Phe Lys Gln Pro Ile Ser Cys Val Lys
245 250 255

Glu Glu Ile Gln Glu Thr Gln Thr Pro Thr His Ser Arg Lys Lys Arg
260 265 270

Arg Arg Ser Ser Asn Gln
275

1269

<210> 1246

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (100)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1246

Ser Pro Pro Pro Leu Ser Leu Ile Leu Leu Ser Pro Ile Lys Ala Lys
 1 5 10 15

Tyr Gly Leu Thr Thr Ser Pro Lys Ser Val Leu Arg Pro Ser Leu Cys
 20 25 30

Leu Cys Ala Leu Leu Gly Val Ser Gln Arg Ser Gly Gln Asp Cys Ala
 35 40 45

Gly Pro Ala Ser Pro Cys Ala Ser Gln Glu His Arg Gln Gly Val Leu
 50 55 60

Val Ala Val Ala Gly His Leu Ser Pro Ser Ser Leu Leu Asn Val Leu
 65 70 75 80

Thr Ala Arg Gly Asn Gly Val Ser Phe Pro Thr Lys Lys Pro Leu Leu
 85 90 95

Tyr Ile Phe Xaa Leu Gln Ser His Arg Leu Gln Thr Thr Leu Leu Phe
 100 105 110

Phe Met Asp Phe Ser Ala His Phe Arg
 115 120

<210> 1247

<211> 36

<212> PRT

<213> Homo sapiens

<400> 1247

Ile Phe His Arg Val Leu Leu Cys Asp Leu Asn Phe Ser Leu Gly Pro
 1 5 10 15

Ala Ser Asp Ile Val Gly Gly Leu Ser Trp Phe Gln Glu Ile Arg Leu
 20 25 30

1270

Ala Phe Ser Ser
35

<210> 1248
<211> 184
<212> PRT
<213> Homo sapiens

<400> 1248

Trp Ile Pro Arg Ala Cys Arg Glu Phe Gly Thr Arg Phe Gly Gly Val
1 5 10 15

Thr Arg Gly Phe Asn Met Arg Ile Glu Lys Cys Tyr Phe Cys Ser Gly
20 25 30

Pro Ile Tyr Pro Gly His Gly Met Met Phe Val Arg Asn Asp Cys Lys
35 40 45

Val Phe Arg Phe Cys Lys Ser Lys Cys His Lys Asn Phe Lys Lys Lys
50 55 60

Arg Asn Pro Arg Lys Val Arg Trp Thr Lys Ala Phe Arg Lys Ala Ala
65 70 75 80

Gly Lys Glu Leu Thr Val Asp Asn Ser Phe Glu Phe Glu Lys Arg Arg
85 90 95

Asn Glu Pro Ile Lys Tyr Gln Arg Glu Leu Trp Asn Lys Thr Ile Asp
100 105 110

Ala Met Lys Arg Val Glu Glu Ile Lys Gln Lys Arg Gln Ala Lys Phe
115 120 125

Ile Met Asn Arg Leu Lys Lys Asn Lys Glu Leu Gln Lys Val Gln Asp
130 135 140

Ile Lys Glu Val Lys Gln Asn Ile His Leu Ile Arg Ala Pro Leu Ala
145 150 155 160

Gly Lys Gly Lys Gln Leu Glu Glu Lys Met Val Gln Gln Leu Gln Glu
165 170 175

Asp Val Asp Met Glu Asp Ala Pro
180

<210> 1249
<211> 188

1271

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (104)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1249

Gly Cys Pro Ala His Ser Pro Gly Ser Ala Lys Arg Trp Thr Gln Ala
 1 5 10 15

Ala Met Ser Arg Pro Arg Met Arg Leu Val Val Thr Ala Asp Asp Phe
 20 25 30

Gly Tyr Cys Pro Arg Arg Asp Glu Gly Ile Val Glu Ala Phe Leu Ala
 35 40 45

Gly Ala Val Thr Ser Val Ser Leu Leu Val Asn Gly Ala Ala Thr Glu
 50 55 60

Ser Ala Ala Glu Leu Ala Arg Arg His Ser Ile Pro Thr Gly Leu His
 65 70 75 80

Ala Asn Leu Ser Glu Gly Arg Pro Val Gly Pro Ala Arg Arg Gly Ala
 85 90 95

Ser Ser Leu Leu Gly Pro Glu Xaa Phe Phe Leu Gly Lys Met Gly Phe
 100 105 110

Arg Glu Ala Val Ala Ala Gly Asp Val Asp Leu Pro Gln Val Arg Ser
 115 120 125

Arg Ser Tyr Arg Arg Met Leu Ala Arg Thr Pro Arg Ala Pro Pro Gly
 130 135 140

Gly Thr Val Arg Pro Leu Glu Leu Ala Val Asp Asp Phe Arg Ile Gln
 145 150 155 160

Thr Leu Glu Pro Ser His Gly Ser Thr Arg Arg Val Ser Ser Ala Ala
 165 170 175

Thr Pro Gly Arg Ser Arg Cys Leu Ser Leu Ala Leu
 180 185

<210> 1250

<211> 201

<212> PRT

<213> Homo sapiens

1272

<220>

<221> SITE

<222> (36)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (96)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (97)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (101)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1250

Arg	Lys	Asn	Leu	Glu	Ile	Tyr	Glu	Ala	Val	Thr	Ser	Pro	Gln	Gly	Pro
1				5					10					15	

Ala	Met	Thr	Trp	Ser	Met	Phe	Ala	Val	Gly	Trp	Met	Glu	Leu	Lys	Asp
			20					25					30		

Ala	Cys	Gly	Xaa	Arg	Gly	Leu	Leu	Asp	Arg	Ser	Phe	Ala	Asn	Met	Ala
	35					40						45			

Glu	Pro	Phe	Lys	Val	Trp	Thr	Glu	Asn	Ala	Asp	Gly	Ser	Gly	Ala	Val
	50					55					60				

Asn	Phe	Leu	Thr	Gly	Met	Gly	Gly	Phe	Leu	Gln	Ala	Val	Val	Phe	Gly
65					70					75				80	

Cys	Thr	Gly	Phe	Arg	Val	Ser	Val	Ser	Gly	Ile	Phe	Tyr	Gln	Gly	Xaa
				85					90					95	

Xaa	Leu	Asn	Phe	Xaa	Phe	Ser	Glu	Asp	Ser	Val	Thr	Val	Glu	Val	Thr
		100						105					110		

Ala	Arg	Ala	Gly	Pro	Trp	Ala	Pro	His	Leu	Glu	Ala	Glu	Leu	Trp	Pro
	115					120						125			

Ser	Gln	Ser	Arg	Leu	Ser	Leu	Leu	Pro	Gly	His	Lys	Val	Ser	Phe	Pro
	130					135					140				

Arg	Ser	Ala	Gly	Arg	Ile	Gln	Met	Ser	Pro	Pro	Lys	Leu	Pro	Gly	Ser
145					150					155				160	

1273

Ser Ser Ser Glu Phe Pro Gly Arg Thr Phe Ser Asp Val Arg Asp Pro
 165 170 175

Leu Gln Ser Pro Leu Trp Val Thr Leu Gly Ser Ser Ser Pro Thr Glu
 180 185 190

Ser Leu Thr Val Asp Pro Ala Ser Glu
 195 200

<210> 1251

<211> 266

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (16)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1251

Ser Val Gly Ser Val Ala Ala Ala Thr Arg Thr Gly Pro Val Ser Xaa
 1 5 10 15

Lys Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu Ile Ala
 20 25 30

Phe Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp
 35 40 45

Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser
 50 55 60

Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu
 65 70 75 80

Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile
 85 90 95

Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala
 100 105 110

Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser
 115 120 125

Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys
 130 135 140

Asn Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe Ile Ile

1274

145 150 155 160
 Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr Leu Val
 165 170 175
 Tyr Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe Phe Asn
 180 185 190
 Ser Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala Tyr Leu
 195 200 205
 Ile Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val Glu Asp
 210 215 220
 Glu Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu Glu Ala
 225 230 235 240
 Ala Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly His Pro
 245 250 255
 Ile Leu Asn Asn Asn His Arg Lys Asn Asp
 260 265

<210> 1252

<211> 163

<212> PRT

<213> Homo sapiens

<400> 1252

Lys Met Gly Thr Asn Lys Cys Ala Ser Gln Ala Gly Met Thr Ala Tyr
 1 5 10 15
 Gly Thr Arg Arg His Leu Tyr Asp Pro Lys Met Gln Thr Asp Lys Pro
 20 25 30
 Phe Asp Gln Thr Thr Ile Ser Leu Gln Met Gly Thr Asn Lys Gly Ala
 35 40 45
 Ser Gln Ala Gly Met Leu Ala Pro Gly Thr Arg Arg Asp Ile Tyr Asp
 50 55 60
 Gln Lys Leu Thr Leu Gln Pro Val Asp Asn Ser Thr Ile Ser Leu Gln
 65 70 75 80
 Met Gly Thr Asn Lys Val Ala Ser Gln Lys Gly Met Ser Val Tyr Gly
 85 90 95
 Leu Gly Arg Gln Val Tyr Asp Pro Lys Tyr Cys Ala Ala Pro Thr Glu
 100 105 110

1275

Pro Val Ile His Asn Gly Ser Gln Gly Thr Gly Thr Asn Gly Ser Glu
 115 120 125

Ile Ser Asp Ser Asp Tyr Gln Ala Glu Tyr Pro Asp Glu Tyr His Gly
 130 135 140

Glu Tyr Gln Asp Asp Tyr Pro Arg Asp Tyr Gln Tyr Ser Asp Gln Gly
 145 150 155 160

Ile Asp Tyr

<210> 1253

<211> 298

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (109)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1253

Leu Glu Glu Thr Pro Cys Leu Arg Thr Ala Val Ala Cys Glu Gln Arg
 1 5 10 15

Asp Pro Gly Thr Glu Ser Gln Pro Arg Arg Cys Cys Arg Arg Arg Arg
 20 25 30

Pro Glu Thr Ala Glu Pro Val Arg Pro Pro Pro Pro Thr Pro Asp
 35 40 45

Thr Glu His Pro Val Met Asp Lys Asn Glu Leu Val Gln Lys Ala Lys
 50 55 60

Leu Ala Glu Gln Ala Glu Arg Tyr Asp Asp Met Ala Ala Cys Met Lys
 65 70 75 80

Ser Val Thr Glu Gln Gly Ala Glu Leu Ser Asn Glu Glu Arg Asn Leu
 85 90 95

Leu Ser Val Ala Tyr Lys Asn Val Val Gly Ala Arg Xaa Ser Ser Trp
 100 105 110

Arg Val Val Ser Ser Ile Glu Gln Lys Thr Glu Gly Ala Glu Lys Lys
 115 120 125

Gln Gln Met Ala Arg Glu Tyr Arg Glu Lys Ile Glu Thr Glu Leu Arg

1276

130	135	140
Asp Ile Cys Asn Asp Val Leu Ser Leu Leu Glu Lys Phe Leu Ile Pro		
145	150	155 160
Asn Ala Ser Gln Ala Glu Ser Lys Val Phe Tyr Leu Lys Met Lys Gly		
165	170	175
Asp Tyr Tyr Arg Tyr Leu Ala Glu Val Ala Ala Gly Asp Asp Lys Lys		
180	185	190
Gly Ile Val Asp Gln Ser Gln Gln Ala Tyr Gln Glu Ala Phe Glu Ile		
195	200	205
Ser Lys Lys Glu Met Gln Pro Thr His Pro Ile Arg Leu Gly Leu Ala		
210	215	220
Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Glu Lys		
225	230	235 240
Ala Cys Ser Leu Ala Lys Thr Ala Phe Asp Glu Ala Ile Ala Glu Leu		
245	250	255
Asp Thr Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln		
260	265	270
Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Thr Gln Gly Asp		
275	280	285
Glu Ala Glu Ala Gly Glu Gly Gly Glu Asn		
290	295	

<210> 1254

<211> 173

<212> PRT

<213> Homo sapiens

<400> 1254

Ser Pro Ala Arg Pro Leu Ile Arg Ser Asp Lys Met Lys Glu Thr Ile
1 5 10 15
Met Asn Gln Glu Lys Leu Ala Lys Leu Gln Ala Gln Val Arg Ile Gly
20 25 30
Gly Lys Gly Thr Ala Arg Arg Lys Lys Lys Val Val His Arg Thr Ala
35 40 45
Thr Ala Asp Asp Lys Lys Leu Gln Phe Ser Leu Lys Lys Leu Gly Val
50 55 60

1277

Asn Asn Ile Ser Gly Ile Glu Glu Val Asn Met Phe Thr Asn Gln Gly
 65 70 75 80
 Thr Val Ile His Phe Asn Asn Pro Lys Val Gln Ala Ser Leu Ala Ala
 85 90 95
 Asn Thr Phe Thr Ile Thr Gly His Ala Glu Thr Lys Gln Leu Thr Glu
 100 105 110
 Met Leu Pro Ser Ile Leu Asn Gln Leu Gly Ala Asp Ser Leu Thr Ser
 115 120 125
 Leu Arg Arg Leu Ala Glu Ala Leu Pro Lys Gln Ser Val Asp Gly Lys
 130 135 140
 Ala Pro Leu Ala Thr Gly Glu Asp Asp Asp Glu Val Pro Asp Leu
 145 150 155 160
 Val Glu Asn Phe Asp Glu Ala Ser Lys Asn Glu Ala Asn
 165 170

<210> 1255
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 1255
 Leu Cys Cys Pro Phe His Ile Lys Glu Leu Leu Thr Thr Lys Ala Ala
 1 5 10 15
 Pro Ala Phe Pro Ile Cys Leu Ser Ile Trp Leu Ala Gly Lys Glu Arg
 20 25 30
 Thr Cys Met Leu Val Lys Glu Glu Val Gly Trp Lys Lys Trp Gly Gly
 35 40 45
 Thr Thr Val Lys Ser Arg Val Lys Pro Ser Trp Pro Lys Val Ser Cys
 50 55 60
 Arg Leu
 65

<210> 1256
 <211> 389
 <212> PRT
 <213> Homo sapiens

1278

<400> 1256

Ala Glu Ala Gly Pro Gly Ala Arg Ala Ala Ala Met Ala Ile Lys
 1 5 10 15

Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro Glu Ile Gln
 20 25 30

Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu Trp Thr Ala
 35 40 45

Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro Leu Phe Gly
 50 55 60

Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp Met Arg Val Ile
 65 70 75 80

Leu Ala Ser Asn Arg Gly Thr Leu Met Glu Leu Gly Ile Ser Pro Ile
 85 90 95

Val Thr Ser Gly Leu Ile Met Gln Leu Leu Ala Gly Ala Lys Ile Ile
 100 105 110

Glu Val Gly Asp Thr Pro Lys Asp Arg Ala Leu Phe Asn Gly Ala Gln
 115 120 125

Lys Leu Phe Gly Met Ile Ile Thr Ile Gly Gln Ser Ile Val Tyr Val
 130 135 140

Met Thr Gly Met Tyr Gly Asp Pro Ser Glu Met Gly Ala Gly Ile Cys
 145 150 155 160

Leu Leu Ile Thr Ile Gln Leu Phe Val Ala Gly Leu Ile Val Leu Leu
 165 170 175

Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly Leu Gly Ser Gly Ile Ser
 180 185 190

Leu Phe Ile Ala Thr Asn Ile Cys Glu Thr Ile Val Trp Lys Ala Phe
 195 200 205

Ser Pro Thr Thr Val Asn Thr Gly Arg Gly Met Glu Phe Glu Gly Ala
 210 215 220

Ile Ile Ala Leu Phe His Leu Leu Ala Thr Arg Thr Asp Lys Val Arg
 225 230 235 240

Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn Leu Pro Asn Leu Met Asn
 245 250 255

Leu Ile Ala Thr Ile Phe Val Phe Ala Val Val Ile Tyr Phe Gln Gly

260

265

270

Asn Thr Tyr Pro Ile Lys Leu Phe Tyr Thr Ser Asn Ile Pro Ile Ile
290 295 300

Leu Gln Ser Ala Leu Val Ser Asn Leu Tyr Val Ile Ser Gln Met Leu
305 310 315 320

Ser Ala Arg Phe Ser Gly Asn Leu Leu Val Ser Leu Leu Gly Thr Trp
325 330 335

Ser Asp Thr Ser Ser Gly Gly Pro Ala Arg Ala Tyr Pro Val Gly Gly
340 345 350

Leu Cys Tyr Tyr Leu Ser Pro Pro Trp Ser Met Asn Ser Thr Gly Thr
355 360 365

Ser Pro Gln Pro Arg Pro Leu Val Gly Cys Ala Ser Gly Pro Ser Arg
370 375 380

Ser Trp Leu Thr Ser
385

<210> 1257

<211> 191

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1257

Gly Xaa Pro Ser Ser Ser Arg Ala His Ser Pro Met Ile Ala Val Gly
1 5 10 15

Ser Asp Asp Ser Ser Pro Asn Ala Met Ala Lys Val Gln Ile Phe Glu
20 25 30

Tyr Asn Glu Asn Thr Arg Lys Tyr Ala Lys Ala Glu Thr Leu Met Thr
35 40 45

Val	Thr	Asp	Pro	Val	His	Asp	Ile	Ala	Phe	Ala	Pro	Asn	Leu	Gly	Arg
	50					55					60				

1280

Ser Phe His Ile Leu Ala Ile Ala Thr Lys Asp Val Arg Ile Phe Thr
65 70 75 80

Leu Lys Pro Val Arg Lys Glu Leu Thr Ser Ser Gly Gly Pro Thr Lys
85 90 95

Phe Glu Ile His Ile Val Ala Gln Phe Asp Asn His Asn Ser Gln Val
100 105 110

Trp Arg Val Ser Trp Asn Ile Thr Gly Thr Val Leu Ala Ser Ser Gly
115 120 125

Asp Asp Gly Cys Val Arg Leu Trp Lys Ala Asn Tyr Met Asp Asn Trp
130 135 140

Lys Cys Thr Gly Ile Leu Lys Gly Asn Gly Ser Pro Val Asn Gly Ser
145 150 155 160

Ser Gln Gln Gly Thr Ser Asn Pro Ser Leu Gly Ser Asn Ile Pro Ser
165 170 175

Leu Gln Asn Ser Leu Asn Gly Ser Ser Ala Gly Arg Lys His Ser
180 185 190

<210> 1258

<211> 458

<212> PRT

<213> Homo sapiens

<400> 1258

Pro Gly Ala Arg His Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu
1 5 10 15

Val Ser Cys Glu Asn Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly
20 25 30

Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys
35 40 45

Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val
50 55 60

Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser
65 70 75 80

Lys Asp Val Met Gln Gly Thr Asp Glu His Val Val Cys Lys Val Gln
85 90 95

His Pro Asn Gly Asn Lys Glu Lys Asn Val Pro Leu Pro Val Ile Ala

1281

100	105	110
Glu Leu Pro Pro Lys Val Ser	Val Phe Val Pro Pro Arg Asp Gly Phe	
115	120	125
Phe Gly Asn Pro Arg Lys Ser	Lys Leu Ile Cys Gln Ala Thr Gly Phe	
130	135	140
Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val		
145	150	155
Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser		
165	170	175
Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser		
180	185	190
Asp Trp Leu Ser Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly		
195	200	205
Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp		
210	215	220
Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe		
225	230	235
Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr		
245	250	255
Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val		
260	265	270
Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser		
275	280	285
Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu		
290	295	300
Arg Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys		
305	310	315
Gln Thr Ile Ser Arg Pro Lys Gly Val Ala Leu His Arg Pro Asp Val		
325	330	335
Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala		
340	345	350
Thr Ile Thr Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val		
355	360	365
Gln Trp Met Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr		

1282

370 375 380
 Ser Ala Pro Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His
 385 390 395 400
 Ser Ile Leu Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr
 405 410 415
 Thr Cys Val Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg
 420 425 430
 Thr Val Asp Lys Ser Thr Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu
 435 440 445
 Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
 450 455

<210> 1259

<211> 247

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (25)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1259

Ala Gly Pro Ala Pro Glu Glu Pro Arg Gly Gly Ala Ala Ala Arg Trp
 1 5 10 15
 Asp Cys Gln Pro Cys Gln Ala Ala Xaa Val Val Glu Asn Ser Ala Gln
 20 25 30
 Arg Val Ile His Leu Ala Gly Gln Trp Glu Lys His Arg Val Pro Leu
 35 40 45
 Leu Ala Glu Tyr Arg His Leu Arg Lys Leu Gln Asp Cys Arg Glu Leu
 50 55 60
 Glu Ser Ser Arg Arg Leu Ala Glu Ile Gln Glu Leu His Gln Ser Val
 65 70 75 80
 Arg Ala Ala Ala Glu Glu Ala Arg Arg Lys Glu Glu Val Tyr Lys Gln
 85 90 95
 Leu Met Ser Glu Leu Glu Thr Leu Pro Arg Asp Val Ser Arg Leu Ala
 100 105 110

1283

Tyr Thr Gln Arg Ile Leu Glu Ile Val Gly Asn Ile Arg Lys Gln Lys
 115 120 125
 Glu Glu Ile Thr Lys Ile Leu Ser Asp Thr Lys Glu Leu Gln Lys Glu
 130 135 140
 Ile Asn Ser Leu Ser Gly Lys Leu Asp Arg Thr Phe Ala Val Thr Asp
 145 150 155 160
 Glu Leu Val Phe Lys Asp Ala Lys Lys Asp Asp Ala Val Arg Lys Ala
 165 170 175
 Tyr Lys Tyr Leu Ala Ala Leu His Glu Asn Cys Ser Gln Leu Ile Gln
 180 185 190
 Thr Ile Glu Asp Thr Gly Thr Ile Met Arg Glu Val Arg Asp Leu Glu
 195 200 205
 Glu Gln Ile Glu Thr Glu Leu Gly Lys Lys Thr Leu Ser Asn Leu Glu
 210 215 220
 Lys Ile Arg Glu Asp Tyr Arg Ala Leu Arg Gln Glu Asn Ala Gly Leu
 225 230 235 240
 Leu Gly Arg Val Arg Glu Ala
 245

<210> 1260
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 1260
 Val Gly Ile Lys Trp Ile Glu Glu Ala Val Leu Cys Ala Asn Val Ser
 1 5 10 15
 Phe Ala Ser Asp Arg Tyr Leu Phe Val Ile Arg Arg Val Ala Ser Phe
 20 25 30
 His Leu Gly Ala Glu Asn Ser Arg Gln Leu Leu Thr Asp Lys Phe Asn
 35 40 45
 Leu His Leu Gln Tyr Cys Met Leu Gly Ile Ser Ala Tyr Phe
 50 55 60

<210> 1261
 <211> 243

1284

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (76)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (210)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (226)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1261

Gln	Glu	Arg	Pro	Gly	Asn	Phe	Tyr	Val	Ser	Ser	Glu	Ser	Ile	Arg	Lys
1				5				10						15	

Gly	Pro	Pro	Val	Arg	Pro	Trp	Arg	Asp	Arg	Pro	Gln	Ser	Ser	Ile	Tyr
			20				25						30		

Asp	Pro	Phe	Ala	Gly	Met	Lys	Thr	Pro	Gly	Gln	Arg	Gln	Leu	Ile	Thr
	35						40						45		

Leu	Gln	Glu	Gln	Val	Lys	Leu	Gly	Ile	Val	Asn	Val	Asp	Glu	Ala	Val
	50					55							60		

Leu	His	Phe	Lys	Glu	Trp	Gln	Leu	Asn	Gln	Lys	Xaa	Arg	Ser	Glu	Ser
	65				70					75					80

Phe	Arg	Phe	Gln	Gln	Glu	Asn	Leu	Lys	Arg	Leu	Arg	Asp	Ser	Ile	Thr
			85						90					95	

Arg	Arg	Gln	Arg	Glu	Lys	Gln	Lys	Ser	Gly	Lys	Gln	Thr	Asp	Leu	Glu
			100					105						110	

Ile	Thr	Val	Pro	Ile	Arg	His	Ser	Gln	His	Leu	Pro	Ala	Lys	Val	Glu
		115						120						125	

Phe	Gly	Val	Tyr	Glu	Ser	Gly	Pro	Arg	Lys	Ser	Val	Ile	Pro	Pro	Arg
	130					135						140			

Thr	Glu	Leu	Arg	Arg	Gly	Asp	Trp	Lys	Thr	Asp	Ser	Thr	Ser	Ser	Thr
	145				150					155					160

Ala	Ser	Ser	Thr	Ser	Asn	Arg	Ser	Ser	Thr	Arg	Ser	Leu	Leu	Ser	Val
			165						170					175	

1285

Ser Ser Gly Met Glu Gly Asp Asn Glu Asp Asn Glu Val Pro Glu Val
 180 185 190

Thr Arg Ser Arg Ser Pro Gly Pro Pro Gln Val Asp Gly Thr Pro Thr
 195 200 205

Met Xaa Leu Glu Arg Pro Pro Arg Val Pro Pro Arg Ala Ala Ser Gln
 210 215 220

Arg Xaa Pro Thr Arg Glu Thr Phe His Pro Pro Pro Pro Val Pro Pro
 225 230 235 240

Arg Gly Arg

<210> 1262

<211> 75

<212> PRT

<213> Homo sapiens

<400> 1262

Lys Tyr Val Arg Asn Asp Gln Asn Lys Arg Lys Phe Leu Phe Ser Cys
 1 5 10 15

Lys Tyr Phe Ser Ser Val Ile Thr Leu Lys Tyr Lys Leu Lys Tyr Asn
 20 25 30

Thr Pro Glu Cys Leu Arg His Asp Leu Asp Phe Lys Cys Val Val Phe
 35 40 45

Ile Glu Lys Lys Leu Ser Thr His Leu Val Phe Gln Glu Asn Leu Lys
 50 55 60

Arg Ser Gln Gly Lys Met Ile Cys Met Leu Lys
 65 70 75

<210> 1263

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (249)

<223> Xaa equals any of the naturally occurring L-amino acids

1286

<400> 1263

Arg Thr Gly Leu Gly Arg Asp Val Gly Ala Gly Ala Arg Arg Ala Ala
1 5 10 15

Arg Cys Arg Ala Glu Ala Ala Ala Ala Val Gly Thr Ala Arg Ser Pro
20 25 30

Ala Leu Gly Met Ala Leu Leu Val Leu Gly Leu Val Ser Cys Thr Phe
35 40 45

Phe Leu Ala Val Asn Gly Leu Tyr Ser Ser Ser Asp Asp Val Ile Glu
50 55 60

Leu Thr Pro Ser Asn Phe Asn Arg Glu Val Ile Gln Ser Asp Ser Leu
65 70 75 80

Trp Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Arg Leu
85 90 95

Thr Pro Glu Trp Lys Lys Ala Ala Thr Ala Leu Lys Asp Val Val Lys
100 105 110

Val Gly Ala Val Asp Ala Asp Lys His His Ser Leu Gly Gly Gln Tyr
115 120 125

Gly Val Gln Gly Phe Pro Thr Ile Lys Ile Phe Gly Ser Asn Lys Asn
130 135 140

Arg Pro Glu Asp Tyr Gln Gly Gly Arg Thr Gly Glu Ala Ile Val Asp
145 150 155 160

Ala Ala Leu Ser Ala Leu Arg Gln Leu Val Lys Asp Arg Leu Gly Gly
165 170 175

Arg Ser Gly Gly Tyr Ser Ser Gly Lys Gln Gly Arg Ser Asp Ser Ser
180 185 190

Ser Lys Lys Asp Val Ile Glu Leu Thr Asp Asp Ser Phe Asp Lys Asn
195 200 205

Val Leu Asp Ser Glu Asp Val Trp Met Val Glu Phe Tyr Ala Pro Trp
210 215 220

Cys Gly His Cys Lys Asn Leu Glu Pro Glu Trp Ala Ala Ala Ala Ser
225 230 235 240

Glu Val Lys Glu Gln Thr Lys Gly Xaa Val Lys Leu Ala Ala Val Asp
245 250 255

Ala Thr Val Asn Gln Val Leu Ala Ser Arg Tyr Gly Ile Arg Gly Phe
260 265 270

1287

Pro Thr Ile Lys Ile Phe Gln Lys Gly Glu Ser Pro Val Asp Tyr Asp
 275 280 285
 Gly Gly Arg Thr Arg Ser Asp Ile Val Ser Arg Ala Leu Asp Leu Phe
 290 295 300
 Ser Asp Asn Ala Pro Pro Pro Glu Leu Leu Glu Ile Ile Asn Glu Asp
 305 310 315 320
 Ile Ala Lys Arg Thr Cys Glu Glu His Gln Leu Cys Val Val Ala Val
 325 330 335
 Leu Pro His Ile Leu Asp Thr Gly Ala Ala Gly Arg Asn Ser Tyr Leu
 340 345 350
 Glu Val Leu Leu Lys Leu Ala Asp Lys Tyr Lys Lys Lys Met Trp Gly
 355 360 365
 Trp Leu Trp Thr Glu Ala Gly Ala Gln Ser Glu Leu Glu Thr Ala Leu
 370 375 380
 Gly Ile Gly Gly Phe Gly Tyr Pro Ala Met Ala Ala Ile Asn Ala Arg
 385 390 395 400
 Lys Met Lys Phe Ala Leu Leu Lys Gly Ser Phe Ser Glu Gln Gly Ile
 405 410 415
 Asn Glu Phe Leu Arg Glu Leu Ser Phe Gly Arg Gly Ser Thr Ala Pro
 420 425 430
 Val Gly Gly Gly Ala Phe Pro Thr Ile Val Glu Arg Glu Pro Trp Asp
 435 440 445
 Gly Arg Asp Gly Glu Leu Pro Val Glu Asp Asp Ile Asp Leu Ser Asp
 450 455 460
 Val Glu Leu Asp Asp Leu Gly Lys Asp Glu Leu
 465 470 475

<210> 1264

<211> 398

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (28)

<223> Xaa equals any of the naturally occurring L-amino acids

1288

<400> 1264

His Phe Glu Arg Thr Ser Ser Lys Arg Val Ser Arg Ser Leu Asp Gly
1 5 10 15

Ala Pro Ile Gly Val Met Asp Gln Ser Leu Met Xaa Asp Phe Pro Gly
20 25 30

Ala Ala Gly Glu Ile Ser Ala Tyr Gly Pro Gly Leu Val Ser Ile Ala
35 40 45

Val Val Gln Asp Gly Asp Gly Arg Arg Glu Val Arg Ser Pro Thr Lys
50 55 60

Ala Pro His Leu Gln Leu Ile Glu Gly Lys Ser Ser His Glu Thr Leu
65 70 75 80

Asn Ile Val Glu Glu Lys Lys Arg Ala Glu Val Gly Lys Asp Glu Arg
85 90 95

Val Ile Thr Glu Glu Met Asn Gly Lys Glu Ile Ser Pro Gly Ser Gly
100 105 110

Pro Gly Glu Ile Arg Lys Val Glu Pro Val Thr Gln Lys Asp Ser Thr
115 120 125

Ser Leu Ser Ser Glu Ser Ser Ser Ser Ser Ser Glu Ser Glu Glu Glu
130 135 140

Asp Val Gly Glu Tyr Arg Pro His His Arg Val Thr Glu Gly Thr Ile
145 150 155 160

Arg Glu Glu Gln Glu Tyr Glu Glu Glu Val Glu Glu Glu Pro Arg Pro
165 170 175

Ala Ala Lys Val Val Glu Arg Glu Glu Ala Val Pro Glu Ala Ser Pro
180 185 190

Val Thr Gln Ala Gly Ala Ser Val Ile Thr Val Glu Thr Val Ile Gln
195 200 205

Glu Asn Val Gly Ala Gln Lys Ile Pro Gly Glu Lys Ser Val His Glu
210 215 220

Gly Ala Leu Lys Gln Asp Met Gly Glu Glu Ala Glu Glu Glu Pro Gln
225 230 235 240

Lys Val Asn Gly Glu Val Ser His Val Asp Ile Asp Val Leu Pro Gln
245 250 255

Ile Ile Cys Cys Ser Glu Pro Pro Val Val Lys Thr Glu Met Val Thr

1289

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<210> 1265
<211> 207
<212> PRT
<213> Homo sapiens
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<220>

<221> SITE

<222> (99)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1265

Trp Thr Gly Thr Gly Arg Gly Ala Val Ala Ile Met Ala Asp Pro Asp
1 5 10 15

Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp Phe Asn Tyr Gly Ser
20 25 30

Ser Val Ala Ser Ala Thr Val His Ile Arg Met Ala Phe Leu Arg Lys
35 40 45

Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu Thr Thr Val Thr Ser
50 55 60

1290

Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr Phe Val His Glu Ser
 65 70 75 80
 Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe
 85 90 95
 Ala Leu Xaa Leu Asn Arg His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu
 100 105 110
 Phe Gly Phe Thr Leu Leu Glu Ala Leu Thr Val Ala Val Val Val Thr
 115 120 125
 Phe Tyr Asp Val Tyr Ile Ile Leu Gln Ala Phe Ile Leu Thr Thr Thr
 130 135 140
 Val Phe Phe Gly Leu Thr Val Tyr Thr Leu Gln Ser Lys Lys Asp Phe
 145 150 155 160
 Ser Lys Phe Gly Ala Gly Leu Phe Ala Leu Leu Trp Ile Leu Cys Leu
 165 170 175
 Ser Gly Phe Leu Lys Phe Phe Phe Tyr Ser Glu Ile Met Glu Leu Val
 180 185 190
 Leu Ala Ala Ala Gly Ala Leu Leu Phe Trp Gly Ile His His Leu
 195 200 205

<210> 1266

<211> 289

<212> PRT

<213> Homo sapiens

<400> 1266

Ser Arg Asp Pro Asn Gly Trp Trp Arg Arg Leu Arg Val Ser Ala Glu
 1 5 10 15
 Leu Ala Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu
 20 25 30
 Ala Leu Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg
 35 40 45
 Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg
 50 55 60
 Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser
 65 70 75 80
 Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr

1291

85	90	95
Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn		
100	105	110
Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val		
115	120	125
Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met		
130	135	140
Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys		
145	150	155
Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys		
165	170	175
Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg		
180	185	190
Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro		
195	200	205
Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly Leu Phe Val		
210	215	220
Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg		
225	230	235
Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Ser		
245	250	255
Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val Leu Cys Arg		
260	265	270
Pro Val Ala Lys Arg Thr Gly Glu Gly Arg Gly Asp Met Cys Asp Phe		
275	280	285

Phe

<210> 1267
 <211> 284
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (5)

1292

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1267

Arg Gly Arg Arg Xaa Xaa Ala Ser Leu Arg Gly Trp Pro Val Arg Arg
 1 5 10 15

Gly Met Gly Arg Val Gln Leu Phe Glu Ile Ser Leu Ser His Gly Arg
 20 25 30

Val Val Tyr Ser Pro Gly Glu Pro Leu Ala Gly Thr Val Arg Val Arg
 35 40 45

Leu Gly Ala Pro Leu Pro Phe Arg Ala Ile Arg Val Thr Cys Ile Gly
 50 55 60

Ser Cys Gly Val Ser Asn Lys Ala Asn Asp Thr Ala Trp Val Val Glu
 65 70 75 80

Glu Gly Tyr Phe Asn Ser Ser Leu Ser Leu Ala Asp Lys Gly Ser Leu
 85 90 95

Pro Ala Gly Glu His Ser Phe Pro Phe Gln Phe Leu Leu Pro Ala Thr
 100 105 110

Ala Pro Thr Ser Phe Glu Gly Pro Phe Gly Lys Ile Val His Gln Val
 115 120 125

Arg Ala Ala Ile His Thr Pro Arg Phe Ser Lys Asp His Lys Cys Ser
 130 135 140

Leu Val Phe Tyr Ile Leu Ser Pro Leu Asn Leu Asn Ser Ile Pro Asp
 145 150 155 160

Ile Glu Gln Pro Asn Val Ala Ser Ala Thr Lys Lys Phe Ser Tyr Lys
 165 170 175

Leu Val Lys Thr Gly Ser Val Val Leu Thr Ala Ser Thr Asp Leu Arg
 180 185 190

Gly Tyr Val Val Gly Gln Ala Leu Gln Leu His Ala Asp Val Glu Asn
 195 200 205

Gln Ser Gly Lys Asp Thr Ser Pro Val Val Ala Ser Leu Leu Gln Lys
 210 215 220

Val Ser Tyr Lys Ala Lys Arg Trp Ile His Asp Val Arg Thr Ile Ala

1293

225 230 235 240
 Glu Val Glu Gly Ala Gly Val Lys Ala Trp Arg Arg Ala Gln Trp His
 245 250 255
 Glu Gln Ile Leu Val Pro Ala Leu Pro Gln Ser Ala Leu Pro Ala Ala
 260 265 270
 Ala Ser Ser Thr Ser Thr Thr Thr Tyr Arg Ser Leu
 275 280

<210> 1268
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 1268
 Val Trp Leu Arg Val Glu Asn Val Cys Gln Gly Pro Gly Gln Glu Gly
 1 5 10 15
 Gly Pro Pro Val Thr Met Val Ser Met Ser Phe Lys Arg Asn Arg Ser
 20 25 30
 Asp Arg Phe Tyr Ser Thr Arg Cys Cys Gly Cys Cys His Val Arg Thr
 35 40 45
 Gly Thr Ile Ile Leu Gly Thr Trp Tyr Met Val Val Asn Leu Leu Met
 50 55 60
 Ala Ile Leu Leu Thr Val Glu Val Thr His Pro Asn Ser Met Pro Ala
 65 70 75 80
 Val Asn Ile Gln Tyr Glu Val Ile Gly Asn Tyr Tyr Ser Ser Glu Arg
 85 90 95
 Met Ala Asp Asn Ala Cys Val Leu Phe Ala Val Ser Val Leu Met Phe
 100 105 110
 Ile Ile Ser Ser Met Leu Val Tyr Gly Ala Ile Ser Tyr Gln Val Gly
 115 120 125
 Trp Leu Ile Pro Phe Phe Cys Tyr Arg Leu Phe Asp Phe Val Leu Ser
 130 135 140
 Cys Leu Val Ala Ile Ser Ser Leu Thr Tyr Leu Pro Arg Ile Lys Glu
 145 150 155 160
 Tyr Leu Asp Gln Leu Pro Asp Phe Pro Tyr Lys Asp Asp Leu Leu Ala
 165 170 175

1294

Leu Asp Ser Ser Cys Leu Leu Phe Ile Val Leu Val Phe Phe Ala Leu
 180 185 190

Phe Ile Ile Phe Lys Ala Tyr Leu Ile Asn Cys Val Trp Asn Cys Tyr
 195 200 205

Lys Tyr Ile Asn Asn Arg Asn Val Pro Glu Ile Ala Val Tyr Pro Ala
 210 215 220

Phe Glu Ala Pro Pro Gln Tyr Val Leu Pro Thr Tyr Glu Met Ala Val
 225 230 235 240

Lys Met Pro Glu Lys Glu Pro Pro Pro Pro Tyr Leu Pro Ala
 245 250

<210> 1269

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (49)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (52)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (53)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1269

Lys Ser Ile Leu Val Ile Arg Val Tyr Phe Phe Tyr Arg Thr Arg Trp
 1 5 10 15

Xaa Gly Gly Glu Pro Phe Thr Leu Leu Val Lys Leu Asn His Arg Lys
 20 25 30

Phe Thr Ile Cys Leu Ser Gln Thr Leu Ala Val Arg Gly Met Val Ala

1295

35 40 45
Xaa Ala Cys Xaa Xaa Pro Ala Cys Trp Gly Gly Pro Ser Trp Gly Gly
50 55 60
Leu Pro Glu
65

<210> 1270
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (138)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (152)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (161)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (164)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1270

1296

Gly Ser Pro Gly Thr Xaa Arg Ile Pro Xaa Thr Arg Xaa Glu Thr Cys
 1 5 10 15
 Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr Glu
 20 25 30
 Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala Gly
 35 40 45
 Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly Gly
 50 55 60
 Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr Gly
 65 70 75 80
 Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu Trp
 85 90 95
 Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly Thr
 100 105 110
 Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp Met
 115 120 125
 Met Val Asp Cys Thr Cys Leu Gly Glu Xaa Ser Gly Arg Ile Thr Cys
 130 135 140
 Thr Ser Arg Asn Arg Cys Asn Xaa Gln Asp Thr Arg Thr Ser Ile Glu
 145 150 155 160
 Xaa Glu Thr Xaa

<210> 1271

<211> 363

<212> PRT

<213> Homo sapiens

<400> 1271

Ala Arg Gly Ser Glu Cys Gly Gln Arg Ala Glu Ala Val Ser His Arg
 1 5 10 15
 Arg Arg Arg Arg Ala Gln Ala Ser Ser Phe Gly Trp Gly Ala Ala Glu
 20 25 30
 Leu Thr Ser Asp Ile Ser Ala Pro Phe Thr Arg Arg Asn Pro Gly Ala
 35 40 45
 Gly Ala Arg Ser Ala Gly Val Thr Met Thr Lys Ala Gly Ser Lys Gly

1297

50	55	60
Gly Asn Leu Arg Asp Lys Leu Asp Gly Asn Glu Leu Asp Leu Ser Leu		
65	70	75 80
Ser Asp Leu Asn Glu Val Pro Val Lys Glu Leu Ala Ala Leu Pro Lys		
	85	90 95
Ala Thr Ile Leu Asp Leu Ser Cys Asn Lys Leu Thr Thr Leu Pro Ser		
	100	105 110
Asp Phe Cys Gly Leu Thr His Leu Val Lys Leu Asp Leu Ser Lys Asn		
	115	120 125
Lys Leu Gln Gln Leu Pro Ala Asp Phe Gly Arg Leu Val Asn Leu Gln		
	130	135 140
His Leu Asp Leu Leu Asn Asn Lys Leu Val Thr Leu Pro Val Ser Phe		
	145	150 155 160
Ala Gln Leu Lys Asn Leu Lys Trp Leu Asp Leu Lys Asp Asn Pro Leu		
	165	170 175
Asp Pro Val Leu Ala Lys Val Ala Gly Asp Cys Leu Asp Glu Lys Gln		
	180	185 190
Cys Lys Gln Cys Ala Asn Lys Val Leu Gln His Met Lys Ala Val Gln		
	195	200 205
Ala Asp Gln Glu Arg Glu Arg Gln Arg Arg Leu Glu Val Glu Arg Glu		
	210	215 220
Ala Glu Lys Lys Arg Glu Ala Lys Gln Arg Ala Lys Glu Ala Gln Glu		
	225	230 235 240
Arg Glu Leu Arg Lys Arg Glu Lys Ala Glu Glu Lys Glu Arg Arg Arg		
	245	250 255
Lys Glu Tyr Asp Ala Leu Lys Ala Ala Lys Arg Glu Gln Glu Lys Lys		
	260	265 270
Pro Lys Lys Glu Ala Asn Gln Ala Pro Lys Ser Lys Ser Gly Ser Arg		
	275	280 285
Pro Arg Lys Pro Pro Pro Arg Lys His Thr Arg Ser Trp Ala Val Leu		
	290	295 300
Lys Leu Leu Leu Leu Leu Leu Phe Gly Val Ala Gly Gly Leu Val		
	305	310 315 320
Ala Cys Arg Val Thr Glu Leu Gln Gln Gln Pro Leu Cys Thr Ser Val		

1298

325

330

335

Asn Thr Ile Tyr Asp Asn Ala Val Gln Gly Leu Arg Arg His Glu Ile
 340 345 350

Leu Gln Trp Val Leu Gln Thr Asp Ser Gln Gln
 355 360

<210> 1272

<211> 144

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (112)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (116)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (124)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1272

Gly Leu Val Met Ala Pro Ile Ala Cys Leu Leu Pro Ala Phe Ser Ser
 1 5 10 15

Ala Pro Glu Ala Met His Pro Trp Glu Leu Phe Val Lys Tyr Tyr His
 20 25 30

Ala Lys Asn Gly Arg Ala Tyr Val Glu Ser Pro Ala Arg Lys Leu Ser
 35 40 45

Gln Ser Phe Ala Leu Pro Val Thr Gly Gly Thr Val Val Thr Pro Lys
 50 55 60

Gln Ser Leu Leu Thr Ala Ile His Met Val Leu Thr Glu His Asp Pro
 65 70 75 80

Phe Lys Arg Ser Ala Asp Ser Glu Leu Lys Ala Leu Val Cys Met Ala
 85 90 95

Leu Asn Glu Pro Ala Ser Gly Val Leu Gly Glu Pro His Leu Gln Xaa
 100 105 110

1299

Arg Val Thr Xaa Arg Ala Ser Leu Pro Ala Leu Xaa Leu His Gly Thr
 115 120 125

His Arg Leu Leu Lys Ile Ala Ser Thr Cys Ser Val Ala Ser Thr Thr
 130 135 140

<210> 1273

<211> 252

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (32)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1273

Ala Arg Ala Pro Pro Arg Pro Arg Arg Ala Gly Arg Cys Gln Leu Pro
 1 5 10 15

Gln Arg Pro Ala Glu Ala Arg Cys Met Leu Ser Arg Cys Arg Ser Xaa
 20 25 30

Leu Leu His Val Leu Gly Leu Ser Phe Leu Leu Gln Thr Arg Arg Pro
 35 40 45

Ile Leu Leu Cys Ser Pro Arg Leu Met Lys Pro Leu Val Val Phe Val
 50 55 60

Leu Gly Gly Pro Gly Ala Gly Lys Gly Thr Gln Cys Ala Arg Ile Val
 65 70 75 80

Glu Lys Tyr Gly Tyr Thr His Leu Ser Ala Gly Glu Leu Leu Arg Asp
 85 90 95

Glu Arg Lys Asn Pro Asp Ser Gln Tyr Gly Glu Leu Ile Glu Lys Tyr
 100 105 110

Ile Lys Glu Gly Lys Ile Val Pro Val Glu Ile Thr Ile Ser Leu Leu
 115 120 125

Lys Arg Glu Met Asp Gln Thr Met Ala Ala Asn Ala Gln Lys Asn Lys
 130 135 140

Phe Leu Ile Asp Gly Phe Pro Arg Asn Gln Asp Asn Leu Gln Gly Trp

1300

145 150 155 160
 Asn Lys Thr Met Asp Gly Lys Ala Asp Val Ser Phe Val Leu Phe Phe
 165 170 175
 Asp Cys Asn Asn Glu Ile Cys Ile Glu Arg Cys Leu Glu Arg Gly Lys
 180 185 190
 Ser Ser Gly Arg Ser Asp Asp Asn Arg Glu Ser Leu Glu Lys Arg Ile
 195 200 205
 Gln Thr Tyr Leu Gln Ser Thr Lys Pro Ile Ile Asp Leu Tyr Glu Glu
 210 215 220
 Met Gly Lys Val Lys Lys Ile Asp Ala Ser Lys Ser Val Asp Glu Val
 225 230 235 240
 Phe Asp Glu Val Val Gln Ile Phe Asp Lys Glu Gly
 245 250

<210> 1274

<211> 425

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (35)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1274

Ala Ser Glu Arg Ser Glu Ala Arg Arg Lys Leu Arg Glu Cys Asp Gly
 1 5 10 15
 Leu Val Asp Ala Leu Ile Phe Ile Val Gln Ala Glu Ile Gly Gln Lys
 20 25 30
 Asp Ser Xaa Ser Lys Leu Val Glu Asn Cys Val Cys Leu Leu Arg Asn
 35 40 45
 Leu Ser Tyr Gln Val His Arg Glu Ile Pro Gln Ala Glu Arg Tyr Gln
 50 55 60
 Glu Ala Ala Pro Asn Val Ala Asn Asn Thr Gly Pro His Ala Ala Ser
 65 70 75 80
 Cys Phe Gly Ala Lys Lys Gly Lys Gly Lys Lys Pro Ile Glu Asp Pro
 85 90 95

1301

Ala Asn Asp Thr Val Asp Phe Pro Lys Arg Thr Ser Pro Ala Arg Gly
 100 105 110

Tyr Glu Leu Leu Phe Gln Pro Glu Val Val Arg Ile Tyr Ile Ser Leu
 115 120 125

Leu Lys Glu Ser Lys Thr Pro Ala Ile Leu Glu Ala Ser Ala Gly Ala
 130 135 140

Ile Gln Asn Leu Cys Ala Gly Arg Trp Thr Tyr Gly Arg Tyr Ile Arg
 145 150 155 160

Ser Ala Leu Arg Gln Glu Lys Ala Leu Ser Ala Ile Ala Asp Leu Leu
 165 170 175

Thr Asn Glu His Glu Arg Val Val Lys Ala Ala Ser Gly Ala Leu Arg
 180 185 190

Asn Leu Ala Val Asp Ala Arg Asn Lys Glu Leu Ile Gly Lys His Ala
 195 200 205

Ile Pro Asn Leu Val Lys Asn Leu Pro Gly Gly Gln Gln Asn Ser Ser
 210 215 220

Trp Asn Phe Ser Glu Asp Thr Val Ile Ser Ile Leu Asn Thr Ile Asn
 225 230 235 240

Glu Val Ile Ala Glu Asn Leu Glu Ala Ala Lys Lys Leu Arg Glu Thr
 245 250 255

Gln Gly Ile Glu Lys Leu Val Leu Ile Asn Lys Ser Gly Asn Arg Ser
 260 265 270

Glu Lys Glu Val Arg Ala Ala Ala Leu Val Leu Gln Thr Ile Trp Gly
 275 280 285

Tyr Lys Glu Leu Arg Lys Pro Leu Glu Lys Glu Gly Trp Lys Lys Ser
 290 295 300

Asp Phe Gln Val Asn Leu Asn Asn Ala Ser Arg Ser Gln Ser Ser His
 305 310 315 320

Ser Tyr Asp Asp Ser Thr Leu Pro Leu Ile Asp Arg Asn Gln Lys Ser
 325 330 335

Asp Lys Lys Pro Asp Arg Glu Glu Ile Gln Met Ser Asn Met Gly Ser
 340 345 350

Asn Thr Lys Ser Leu Asp Asn Asn Tyr Ser Thr Pro Asn Glu Arg Gly
 355 360 365

1302

Asp His Asn Arg Thr Leu Asp Arg Ser Gly Asp Leu Gly Asp Met Glu
 370 375 380

Pro Leu Lys Gly Thr Thr Pro Leu Met Gln Asp Glu Gly Gln Glu Ser
 385 390 395 400

Leu Glu Glu Glu Leu Asp Val Leu Val Leu Asp Asp Glu Gly Gly Gln
 405 410 415

Val Ser Tyr Pro Ser Met Gln Lys Ile
 420 425

<210> 1275

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1275

Phe Phe Phe Ser Ser Leu Phe Ser Leu Xaa Phe Leu Lys Lys Gly Lys
 1 5 10 15

Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu
 20 25 30

Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val
 35 40 45

Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro
 50 55 60

Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met
 65 70 75 80

Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp
 85 90 95

Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 100 105 110

<210> 1276

<211> 766

<212> PRT

1303

<213> Homo sapiens

<400> 1276

Gly Asp Phe Ile Met Leu Arg Ala Gly Arg Arg Ala Pro Leu Pro Ser
 1 5 10 15
 Pro Pro Ser Leu Asp Ser Pro Gly Pro Gln Leu Met Pro Ser Pro Arg
 20 25 30
 Pro Val Leu Leu Arg Gly Ala Arg Ala Ala Leu Leu Leu Leu Leu Pro
 35 40 45
 Pro Arg Leu Leu Ala Arg Pro Ser Leu Leu Leu Arg Arg Ser Leu Ser
 50 55 60
 Ala Ala Ser Cys Ala Pro Ile Ser Leu Pro Ala Ala Ala Ser Arg Ser
 65 70 75 80
 Ser Met Asp Gly Ala Gly Ala Glu Glu Val Leu Ala Pro Leu Arg Leu
 85 90 95
 Ala Val Arg Gln Gln Gly Asp Leu Val Arg Lys Leu Lys Glu Asp Lys
 100 105 110
 Ala Pro Gln Val Asp Val Asp Lys Ala Val Ala Glu Leu Lys Ala Arg
 115 120 125
 Lys Arg Val Leu Glu Ala Lys Glu Leu Ala Leu Gln Pro Lys Asp Asp
 130 135 140
 Ile Val Asp Arg Ala Lys Met Glu Asp Thr Leu Lys Arg Arg Phe Phe
 145 150 155 160
 Tyr Asp Gln Ala Phe Ala Ile Tyr Gly Gly Val Ser Gly Leu Tyr Asp
 165 170 175
 Phe Gly Pro Val Gly Cys Ala Leu Lys Asn Asn Ile Ile Gln Thr Trp
 180 185 190
 Arg Gln His Phe Ile Gln Glu Glu Gln Ile Leu Glu Ile Asp Cys Thr
 195 200 205
 Met Leu Thr Pro Glu Pro Val Leu Lys Thr Ser Gly His Val Asp Lys
 210 215 220
 Phe Ala Asp Phe Met Val Lys Asp Val Lys Asn Gly Glu Cys Phe Arg
 225 230 235 240
 Ala Asp His Leu Leu Lys Ala His Leu Gln Lys Leu Met Ser Asp Lys
 245 250 255

1304

Lys Cys Ser Val Glu Lys Lys Ser Glu Met Glu Ser Val Leu Ala Gln
260 265 270

Leu Asp Asn Tyr Gly Gln Gln Glu Leu Ala Asp Leu Phe Val Asn Tyr
275 280 285

Asn Val Lys Ser Pro Ile Thr Gly Asn Asp Leu Ser Pro Pro Val Ser
290 295 300

Phe Asn Leu Met Phe Lys Thr Phe Ile Gly Pro Gly Gly Asn Met Pro
305 310 315 320

Gly Tyr Leu Arg Pro Glu Thr Ala Gln Gly Ile Phe Leu Asn Phe Lys
325 330 335

Arg Leu Leu Glu Phe Asn Gln Gly Lys Leu Pro Phe Ala Ala Ala Gln
340 345 350

Ile Gly Asn Ser Phe Arg Asn Glu Ile Ser Pro Arg Ser Gly Leu Ile
355 360 365

Arg Val Arg Glu Phe Thr Met Ala Glu Ile Glu His Phe Val Asp Pro
370 375 380

Ser Glu Lys Asp His Pro Lys Phe Gln Asn Val Ala Asp Leu His Leu
385 390 395 400

Tyr Leu Tyr Ser Ala Lys Ala Gln Val Ser Gly Gln Ser Ala Arg Lys
405 410 415

Met Arg Leu Gly Asp Ala Val Glu Gln Gly Val Ile Asn Asn Thr Val
420 425 430

Leu Gly Tyr Phe Ile Gly Arg Ile Tyr Leu Tyr Leu Thr Lys Val Gly
435 440 445

Ile Ser Pro Asp Lys Leu Arg Phe Arg Gln His Met Glu Asn Glu Met
450 455 460

Ala His Tyr Ala Cys Asp Cys Trp Asp Ala Glu Ser Lys Thr Ser Tyr
465 470 475 480

Gly Trp Ile Glu Ile Val Gly Cys Ala Asp Arg Ser Cys Tyr Asp Leu
485 490 495

Ser Cys His Ala Arg Ala Thr Lys Val Pro Leu Val Ala Glu Lys Pro
500 505 510

Leu Lys Glu Pro Lys Thr Val Asn Val Val Gln Phe Glu Pro Ser Lys
515 520 525

1305

Gly Ala Ile Gly Lys Ala Tyr Lys Lys Asp Ala Lys Leu Val Met Glu
 530 535 540
 Tyr Leu Ala Ile Cys Asp Glu Cys Tyr Ile Thr Glu Met Glu Met Leu
 545 550 555 560
 Leu Asn Glu Lys Gly Glu Phe Thr Ile Glu Thr Glu Gly Lys Thr Phe
 565 570 575
 Gln Leu Thr Lys Asp Met Ile Asn Val Lys Arg Phe Gln Lys Thr Leu
 580 585 590
 Tyr Val Glu Glu Val Val Pro Asn Val Ile Glu Pro Ser Phe Gly Leu
 595 600 605
 Gly Arg Ile Met Tyr Thr Val Phe Glu His Thr Phe His Val Arg Glu
 610 615 620
 Gly Asp Glu Gln Arg Thr Phe Phe Ser Phe Pro Ala Val Val Ala Pro
 625 630 635 640
 Phe Lys Cys Ser Val Leu Pro Leu Ser Gln Asn Gln Glu Phe Met Pro
 645 650 655
 Phe Val Lys Glu Leu Ser Glu Ala Leu Thr Arg His Gly Val Ser His
 660 665 670
 Lys Val Asp Asp Ser Ser Gly Ser Ile Gly Arg Arg Tyr Ala Arg Thr
 675 680 685
 Asp Glu Ile Gly Val Ala Phe Gly Val Thr Ile Asp Phe Asp Thr Val
 690 695 700
 Asn Lys Thr Pro His Thr Ala Thr Leu Arg Asp Arg Asp Ser Met Arg
 705 710 715 720
 Gln Ile Arg Ala Glu Ile Ser Glu Leu Pro Ser Ile Val Gln Asp Leu
 725 730 735
 Ala Asn Gly Asn Ile Thr Trp Ala Asp Val Glu Ala Arg Tyr Pro Leu
 740 745 750
 Phe Glu Gly Gln Glu Thr Gly Lys Lys Glu Thr Ile Glu Glu
 755 760 765

<210> 1277

<211> 386

<212> PRT

<213> Homo sapiens

1306

<220>

<221> SITE

<222> (75)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1277

Leu Gly Ser Arg Gln Ala Ala Gly Thr Met Arg Gly Gln Arg Ser Leu
 1 5 10 15

Leu Leu Gly Pro Ala Arg Leu Cys Leu Arg Leu Leu Leu Leu Gly
 20 25 30

Tyr Arg Arg Arg Cys Pro Pro Leu Leu Arg Gly Leu Val Gln Arg Trp
 35 40 45

Arg Tyr Gly Lys Val Cys Leu Arg Ser Leu Leu Tyr Asn Ser Phe Gly
 50 55 60

Gly Ser Asp Thr Ala Val Asp Ala Ala Phe Xaa Pro Val Tyr Trp Leu
 65 70 75 80

Val Asp Asn Val Ile Arg Trp Phe Gly Val Val Phe Val Val Leu Val
 85 90 95

Ile Val Leu Thr Gly Ser Ile Val Ala Ile Ala Tyr Leu Cys Val Leu
 100 105 110

Pro Leu Ile Leu Arg Thr Tyr Ser Val Pro Arg Leu Cys Trp His Phe
 115 120 125

Phe Tyr Ser His Trp Asn Leu Ile Leu Ile Val Phe His Tyr Tyr Gln
 130 135 140

Ala Ile Thr Thr Pro Pro Gly Tyr Pro Pro Gln Gly Arg Asn Asp Ile
 145 150 155 160

Ala Thr Val Ser Ile Cys Lys Lys Cys Ile Tyr Pro Lys Pro Ala Arg
 165 170 175

Thr His His Cys Ser Ile Cys Asn Arg Cys Val Leu Lys Met Asp His
 180 185 190

His Cys Pro Trp Leu Asn Asn Cys Val Gly His Tyr Asn His Arg Tyr
 195 200 205

Phe Phe Ser Phe Cys Phe Phe Met Thr Leu Gly Cys Val Tyr Cys Ser
 210 215 220

Tyr Gly Ser Trp Asp Leu Phe Arg Glu Ala Tyr Ala Ala Ile Glu Lys
 225 230 235 240

1307

Met Lys Gln Leu Asp Lys Asn Lys Leu Gln Ala Val Ala Asn Gln Thr
245 250 255

Tyr His Gln Thr Pro Pro Pro Thr Phe Ser Phe Arg Glu Arg Met Thr
260 265 270

His Lys Ser Leu Val Tyr Leu Trp Phe Leu Cys Ser Ser Val Ala Leu
275 280 285

Ala Leu Gly Ala Leu Thr Val Trp His Ala Val Leu Ile Ser Arg Gly
290 295 300

Glu Thr Ser Ile Glu Arg His Ile Asn Lys Lys Glu Arg Arg Arg Leu
305 310 315 320

Gln Ala Lys Gly Arg Val Phe Arg Asn Pro Tyr Asn Tyr Gly Cys Leu
325 330 335

Asp Asn Trp Lys Val Phe Leu Gly Val Asp Thr Gly Arg His Trp Leu
340 345 350

Thr Arg Val Leu Leu Pro Ser Ser His Leu Pro His Gly Asn Gly Met
355 360 365

Ser Trp Glu Pro Pro Pro Trp Val Thr Ala His Ser Ala Ser Val Met
370 375 380

Ala Val
385

<210> 1278

<211> 164

<212> PRT

<213> Homo sapiens

<400> 1278

Val Lys Ala Ser Ala Glu Thr Pro Arg Pro Gln Pro Val Asp Lys Leu
1 5 10 15

Glu Lys Ile Leu Glu Lys Leu Leu Thr Arg Phe Pro Gln Cys Asn Lys
20 25 30

Ala Gln Met Thr Asn Ile Leu Gln Gln Ile Lys Thr Ala Arg Thr Thr
35 40 45

Met Ala Gly Leu Thr Met Glu Glu Leu Ile Gln Leu Val Ala Ala Arg
50 55 60

[illegible]

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<210> 1279
<211> 469
<212> PRT
<213> Homo sapiens
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<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids
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<220>  
<221> SITE  
<222> (81)  
<223> Xaa equals any of the naturally occurring L-amino acids
```

<400> 1279
Pro Val Ala Val Gly Arg Val Arg Val Thr Ala Glu Gly Arg Xaa Met
1 5 10 15

Val Leu Gln Thr Thr Lys Gly Leu Arg Leu Leu Phe Asp Gly Asp Ala
20 25 30

His Leu Leu Met Ser Ile Pro Ser Pro Phe Arg Gly Arg Leu Cys Gly
35 40 45

Leu Cys Gly Asn Phe Asn Gly Asn Trp Ser Asp Asp Phe Val Leu Pro
50 55 60

1309

Asn Gly Ser Ala Ala Ser Ser Val Glu Thr Phe Gly Ala Ala Trp Arg
 65 70 75 80
 Xaa Pro Gly Ser Ser Lys Gly Cys Gly Glu Gly Cys Gly Pro Gln Gly
 85 90 95
 Cys Pro Val Cys Leu Ala Glu Glu Thr Ala Pro Tyr Glu Ser Asn Glu
 100 105 110
 Ala Cys Gly Gln Leu Arg Asn Pro Gln Gly Pro Phe Ala Thr Cys Gln
 115 120 125
 Ala Val Leu Ser Pro Ser Glu Tyr Phe Arg Gln Cys Val Tyr Asp Leu
 130 135 140
 Cys Ala Gln Lys Gly Asp Lys Ala Phe Leu Cys Arg Ser Leu Ala Ala
 145 150 155 160
 Tyr Thr Ala Ala Cys Gln Ala Ala Gly Val Ala Val Lys Pro Trp Arg
 165 170 175
 Thr Asp Ser Phe Cys Pro Leu His Cys Pro Ala His Ser His Tyr Ser
 180 185 190
 Ile Cys Thr Arg Thr Cys Gln Gly Ser Cys Ala Ala Leu Ser Gly Leu
 195 200 205
 Thr Gly Cys Thr Thr Arg Cys Phe Glu Gly Cys Glu Cys Asp Asp Arg
 210 215 220
 Phe Leu Leu Ser Gln Gly Val Cys Ile Pro Val Gln Asp Cys Gly Cys
 225 230 235 240
 Thr His Asn Gly Arg Tyr Leu Pro Val Asn Ser Ser Leu Leu Thr Ser
 245 250 255
 Asp Cys Ser Glu Arg Cys Ser Cys Ser Ser Ser Ser Gly Leu Thr Cys
 260 265 270
 Gln Ala Ala Gly Cys Pro Pro Gly Arg Val Cys Glu Val Lys Ala Glu
 275 280 285
 Ala Arg Asn Cys Trp Ala Thr Arg Gly Leu Cys Val Leu Ser Val Gly
 290 295 300
 Ala Asn Leu Thr Thr Phe Asp Gly Ala Arg Gly Ala Thr Thr Ser Pro
 305 310 315 320
 Gly Val Tyr Glu Leu Ser Ser Arg Cys Pro Gly Leu Gln Asn Thr Ile
 325 330 335

1310

Pro Trp Tyr Arg Val Val Ala Glu Val Gln Ile Cys His Gly Lys Thr
 340 345 350
 Glu Ala Val Gly Gln Val His Ile Phe Phe Gln Asp Gly Met Val Thr
 355 360 365
 Leu Thr Pro Asn Lys Gly Val Trp Val Asn Gly Leu Arg Val Asp Leu
 370 375 380
 Pro Ala Glu Lys Leu Ala Ser Val Ser Val Ser Arg Thr Pro Asp Gly
 385 390 395 400
 Ser Leu Leu Val Arg Gln Lys Ala Gly Val Gln Val Trp Leu Gly Ala
 405 410 415
 Asn Gly Lys Val Ala Val Ile Val Ser Asn Asp His Ala Gly Lys Leu
 420 425 430
 Cys Gly Ala Cys Gly Asn Phe Asp Gly Asp Gln Thr Asn Asp Trp His
 435 440 445
 Asp Ser Gln Glu Lys Pro Ala Met Glu Lys Trp Arg Ala Gln Asp Phe
 450 455 460
 Ser Pro Cys Tyr Gly
 465

<210> 1280

<211> 223

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (216)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (217)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1280

Gly Pro Arg Ala Leu Trp Pro Pro Pro Glu Val Gly Trp Gly Cys Ser
 1 5 10 15

Pro Asn Pro Thr Leu Leu Pro Pro Leu Ser His Phe Pro Leu Leu Arg
 20 25 30

1311

Trp Gly Thr Asn Asn Lys Glu Leu Thr Leu Pro Ala Pro Asn Pro Pro
 35 40 45
 Pro Ala Pro Pro Cys Pro Pro Arg Phe Trp Phe His Phe Ser Ser Val
 50 55 60
 His Lys Leu Pro Leu Asp Ser Cys Val Val Phe Cys Ser Met Phe His
 65 70 75 80
 Ser Ser Thr Ser Val Ile Ala Ala Ala Thr Ser Ala Lys Cys Ser Ser
 85 90 95
 Ser Leu Pro Pro Val Leu Pro Thr Ile Pro Ser Pro Lys Ile Leu Phe
 100 105 110
 Val Gly Lys Arg Gly Trp Gly Met Ala Gly Trp Val Thr Asp Tyr Pro
 115 120 125
 Ser Pro Arg Glu Gly Gly Ala Leu Pro Leu Gly Cys Cys Ser Arg Val
 130 135 140
 Ser Lys Gly Ala Arg Ile Asp His Lys Gly Cys Arg Gly His Leu Leu
 145 150 155 160
 Pro Leu Phe Cys Trp Gly Gly Val Ala Met Ile Cys Pro Ser Leu Gly
 165 170 175
 Leu Pro Leu Trp Phe Pro Ile Cys Ser Tyr Leu Asn Lys Lys Asn Ile
 180 185 190
 Leu Phe Trp Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 195 200 205
 Lys Lys Lys Lys Lys Lys Lys Xaa Xaa Gly Gly Ala Pro Pro Pro
 210 215 220

<210> 1281

<211> 37

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (31)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1281

Thr Gln Ser Lys Trp Arg Leu Glu Val Gln Cys Gly Lys Glu Lys Gln
 1 5 10 15

1312

Val Phe Ile Glu Ser Thr Asn Ser Thr Pro Phe Lys Asn Phe Xaa Gly
 20 25 30

Thr Gln Pro Lys Gly
 35

<210> 1282

<211> 458

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (249)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1282

Gly Pro Gln Arg Leu Ser Pro Gly Ala Met Leu Pro Ala Ala Thr Ala
 1 5 10 15

Ser Leu Leu Gly Pro Leu Leu Thr Ala Cys Ala Leu Leu Pro Phe Ala
 20 25 30

Gln Gly Gln Thr Pro Asn Tyr Thr Arg Pro Val Phe Leu Cys Gly Gly
 35 40 45

Asp Val Lys Gly Glu Ser Gly Tyr Val Ala Ser Glu Gly Phe Pro Asn
 50 55 60

Leu Tyr Pro Pro Asn Lys Glu Cys Ile Trp Thr Ile Thr Val Pro Glu
 65 70 75 80

Gly Gln Thr Val Ser Leu Ser Phe Arg Val Phe Asp Leu Glu Leu His
 85 90 95

Pro Ala Cys Arg Tyr Asp Ala Leu Glu Val Phe Ala Gly Ser Gly Thr
 100 105 110

Ser Gly Gln Arg Leu Gly Arg Phe Cys Gly Thr Phe Arg Pro Ala Pro
 115 120 125

Leu Val Ala Pro Gly Asn Gln Val Thr Leu Arg Met Thr Thr Asp Glu
 130 135 140

Gly Thr Gly Gly Arg Gly Phe Leu Leu Trp Tyr Ser Gly Arg Ala Thr
 145 150 155 160

Ser Gly Thr Glu His Gln Phe Cys Gly Gly Arg Leu Glu Lys Ala Gln

1313

165	170	175
Gly Thr Leu Thr Thr Pro Asn Trp Pro Glu Ser Asp Tyr Pro Pro Gly		
180	185	190
Ile Ser Cys Ser Trp His Ile Ile Ala Pro Pro Asp Gln Val Ile Ala		
195	200	205
Leu Thr Phe Glu Lys Phe Asp Leu Glu Pro Asp Thr Tyr Cys Arg Tyr		
210	215	220
Asp Ser Val Ser Val Phe Asn Gly Ala Val Ser Asp Asp Ser Arg Arg		
225	230	235
Leu Gly Lys Phe Cys Gly Asp Ala Xaa Pro Gly Ser Ile Ser Ser Glu		
245	250	255
Gly Asn Glu Leu Leu Val Gln Phe Val Ser Asp Leu Ser Val Thr Ala		
260	265	270
Asp Gly Phe Ser Ala Ser Tyr Lys Thr Leu Pro Arg Gly Thr Ala Lys		
275	280	285
Glu Gly Gln Gly Pro Gly Pro Lys Arg Gly Thr Glu Pro Lys Val Lys		
290	295	300
Leu Pro Pro Lys Ser Gln Pro Pro Glu Lys Thr Glu Glu Ser Pro Ser		
305	310	315
Ala Pro Asp Ala Pro Thr Cys Pro Lys Gln Cys Arg Arg Thr Gly Thr		
325	330	335
Leu Gln Ser Asn Phe Cys Ala Ser Ser Leu Val Val Thr Ala Thr Val		
340	345	350
Lys Ser Met Val Arg Glu Pro Gly Glu Gly Leu Ala Val Thr Val Ser		
355	360	365
Leu Ile Gly Ala Tyr Lys Thr Gly Gly Leu Asp Leu Pro Ser Pro Pro		
370	375	380
Thr Gly Ala Ser Leu Lys Phe Tyr Val Pro Cys Lys Gln Cys Pro Pro		
385	390	395
Met Lys Lys Gly Val Ser Tyr Leu Leu Met Gly Gln Val Glu Glu Asn		
405	410	415
Arg Gly Pro Val Leu Pro Pro Glu Ser Phe Val Val Leu His Arg Pro		
420	425	430
Asn Gln Asp Gln Ile Leu Thr Asn Leu Ser Lys Arg Lys Cys Pro Ser		

1314

435

440

445

Gln Pro Val Arg Ala Ala Ala Ser Gln Asp
 450 455

<210> 1283

<211> 229

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (45)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (154)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (155)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1283

Cys Arg Ala Pro Leu Gly Ala Gly Leu Ser Pro Ala Val Arg Arg Gln
 1 5 10 15

Glu Pro Pro Phe Pro Leu Gly Val Thr Arg Gly Trp Gly Arg Trp Pro
 20 25 30

Ile Gln Lys Arg Arg Glu Gly Ala Arg Pro Val Pro Xaa Ser Glu Arg
 35 40 45

Ser Gln Glu Asp Gly Arg Gly Pro Ala Ala Arg Ser Ser Gly Thr Leu
 50 55 60

Trp Arg Ile Arg Thr Arg Leu Ser Leu Cys Arg Asp Pro Glu Pro Pro
 65 70 75 80

Pro Pro Leu Cys Leu Leu Arg Val Ser Leu Leu Cys Ala Leu Arg Ala
 85 90 95

Gly Gly Arg Gly Ser Arg Trp Gly Glu Asp Gly Ala Arg Leu Leu Leu
 100 105 110

Leu Pro Pro Ala Arg Ala Ala Gly Asn Gly Glu Ala Glu Pro Ser Gly
 115 120 125

1315

Gly Pro Ser Tyr Ala Gly Arg Met Leu Glu Ser Ser Gly Cys Lys Ala
 130 135 140

Leu Lys Glu Gly Val Leu Glu Lys Arg Xaa Xaa Gly Cys Cys Ser Ser
 145 150 155 160

Gly Arg Lys Ser Val Ala Ser Ser Pro Arg Lys Gly Cys Cys Leu Ser
 165 170 175

Arg Pro Ser Ser Cys Asn Thr Ser Ser Ser Ser Asn Ser Ser Ser Ser
 180 185 190

Ser Ser Asn Asn Ser Pro Gly Arg Gly Arg Pro Ser Arg Pro Asn Pro
 195 200 205

Val Ala Pro Leu Ser Pro Ala Ser Ser Arg Arg Ser Ser Ser Arg Asn
 210 215 220

Cys Thr Ser Pro Thr
 225

<210> 1284

<211> 390

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (52)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1284

Thr Ser Val Ala Ala Ala Ala Arg Gly Arg Ala Gly Cys Pro Leu
 1 5 10 15

Thr Ala Ala Ser Ala Ala Arg Phe Lys Met Ala Ala Cys Ser His Ser
 20 25 30

Phe Ser Ala Glu Arg Leu Leu Thr Phe Ile Val Phe Ser Ala Arg Phe
 35 40 45

Asp Arg Leu Xaa Pro Ala Ala Leu Ser Gly Ile Phe Tyr Gln Ala Glu
 50 55 60

Met His Arg Thr Thr Arg Ile Lys Ile Thr Glu Leu Asn Pro His Leu
 65 70 75 80

Met Cys Val Leu Cys Gly Gly Tyr Phe Ile Asp Ala Thr Thr Ile Ile

1316

85	90	95
Glu Cys Leu His Ser Phe Cys Lys Thr Cys Ile Val Arg Tyr Leu Glu		
100	105	110
Thr Ser Lys Tyr Cys Pro Ile Cys Asp Val Gln Val His Lys Thr Arg		
115	120	125
Pro Leu Leu Asn Ile Arg Ser Asp Lys Thr Leu Gln Asp Ile Val Tyr		
130	135	140
Lys Leu Val Pro Gly Leu Phe Lys Asn Glu Met Lys Arg Arg Arg Asp		
145	150	155
Phe Tyr Ala Ala His Pro Ser Ala Asp Ala Ala Asn Gly Ser Asn Glu		
165	170	175
Asp Arg Gly Glu Val Ala Asp Glu Asp Lys Arg Ile Ile Thr Asp Asp		
180	185	190
Glu Ile Ile Ser Leu Ser Ile Glu Phe Phe Asp Gln Asn Arg Leu Asp		
195	200	205
Arg Lys Val Asn Lys Asp Lys Glu Lys Ser Lys Glu Glu Val Asn Asp		
210	215	220
Lys Arg Tyr Leu Arg Cys Pro Ala Ala Met Thr Val Met His Leu Arg		
225	230	235
Lys Phe Leu Arg Ser Lys Met Asp Ile Pro Asn Thr Phe Gln Ile Asp		
245	250	255
Val Met Tyr Glu Glu Glu Pro Leu Lys Asp Tyr Tyr Thr Leu Met Asp		
260	265	270
Ile Ala Tyr Ile Tyr Thr Trp Arg Arg Asn Gly Pro Leu Pro Leu Lys		
275	280	285
Tyr Arg Val Arg Pro Thr Cys Lys Arg Met Lys Ile Ser His Gln Arg		
290	295	300
Asp Gly Leu Thr Asn Ala Gly Glu Leu Glu Ser Asp Ser Gly Ser Asp		
305	310	315
Lys Ala Asn Ser Pro Ala Gly Gly Ile Pro Ser Thr Ser Ser Cys Leu		
325	330	335
Pro Ser Pro Ser Thr Pro Val Gln Ser Pro His Pro Gln Phe Pro His		
340	345	350
Ile Ser Ser Thr Met Asn Gly Thr Ser Asn Ser Pro Ser Gly Asn His		

1317

355 360 365
Gln Ser Ser Phe Ala Asn Arg Pro Arg Lys Ser Ser Val Asn Gly Ser
370 375 380
Ser Ala Thr Ser Ser Gly
385 390

<210> 1285
<211> 39
<212> PRT
<213> Homo sapiens

<400> 1285
His Ala Ser Ala Gly Ser Gln Leu Phe Glu Met His Glu Lys Leu Ser
1 5 10 15

Cys Met Ala Asn Ser Val Ile Lys Asn Leu Gln Ser Arg Trp Arg Ser
20 25 30

Pro Ser His Glu Asn Ser Ile
35

<210> 1286
<211> 453
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (38)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (101)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (110)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (286)
<223> Xaa equals any of the naturally occurring L-amino acids

1318

<400> 1286

Arg Arg Ser Val Ile Cys Asp Ser Asn Ala Thr Ala Leu Glu Leu Pro
1 5 10 15

Gly Leu Pro Leu Ser Leu Pro Gln Pro Ser Ile Pro Ala Ala Val Pro
20 25 30

Gln Ser Ala Pro Pro Xaa Pro His Arg Glu Glu Thr Val Thr Ala Thr
35 40 45

Ala Thr Ser Gln Val Ala Gln Gln Pro Pro Ala Ala Ala Pro Gly
50 55 60

Glu Gln Ala Val Ala Gly Pro Ala Pro Arg Leu Ser Pro Ala Val Pro
65 70 75 80

Ala Lys Thr Ala Gln Cys Pro Ser Leu Ala Leu Trp Gly Ala Lys Arg
85 90 95

Ser Arg Arg Arg Xaa Lys Val Ala Ala Ala Ala Gln Ala Xaa Lys Glu
100 105 110

Pro Gln Glu Glu Arg Ser Gln Gln Gln Asp Asp Ile Glu Glu Leu Glu
115 120 125

Thr Lys Ala Val Gly Met Ser Asn Asp Gly Arg Phe Leu Lys Phe Asp
130 135 140

Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Lys Gly Leu Asp
145 150 155 160

Thr Glu Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Asp Arg Lys
165 170 175

Leu Thr Lys Ser Glu Arg Gln Arg Phe Lys Glu Glu Ala Glu Met Leu
180 185 190

Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Glu
195 200 205

Ser Thr Val Lys Gly Lys Lys Cys Ile Val Leu Val Thr Glu Leu Met
210 215 220

Thr Ser Gly Thr Leu Lys Thr Tyr Leu Lys Arg Phe Lys Val Met Lys
225 230 235 240

Ile Lys Val Leu Arg Ser Trp Cys Arg Gln Ile Leu Lys Gly Leu Gln
245 250 255

Phe Leu His Thr Arg Thr Pro Pro Ile Ile His Arg Asp Leu Lys Cys

1319

260 265 270

Asp Asn Ile Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Xaa Gly Asp
275 280 285

Leu Gly Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile
290 295 300

Gly Thr Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp
305 310 315 320

Glu Ser Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala
325 330 335

Thr Ser Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Tyr
340 345 350

Arg Arg Val Thr Ser Gly Val Lys Pro Ala Ser Phe Asp Lys Val Ala
355 360 365

Ile Pro Glu Val Lys Glu Ile Ile Glu Gly Cys Ile Arg Gln Asn Lys
370 375 380

Asp Glu Arg Tyr Ser Ile Lys Asp Leu Leu Asn His Ala Phe Phe Gln
385 390 395 400

Glu Glu Thr Gly Val Arg Val Glu Leu Ala Glu Glu Asp Asp Gly Glu
405 410 415

Lys Ile Ala Ile Lys Leu Trp Leu Arg Ile Glu Asp Ile Lys Lys Leu
420 425 430

Lys Gly Lys Tyr Lys Asp Lys Lys Lys Lys Lys Lys Lys Lys Lys
435 440 445

Asn Thr His Arg Ala
450

<210> 1287

<211> 450

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (33)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1320

<221> SITE
 <222> (41)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (43)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (116)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (193)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (314)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (326)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (344)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <400> 1287
 Ala Ala Glu Val Leu Cys Pro Ser Cys Phe Pro Ile Ser Pro Ala Pro
 1 5 10 15
 Trp Met Thr Val Gly Pro Ala Ser Ala Leu Phe Pro Cys Gln Thr Pro
 20 25 30
 Xaa Phe Pro Trp Thr Glu Trp Asn Xaa Trp Xaa Phe Thr Ala His Val
 35 40 45
 Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val Arg Glu Tyr Val
 50 55 60
 Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu Asn Leu Thr Val Arg
 65 70 75 80
 Ile Asp Ile Met Glu Lys Asp Thr Ile Ser Tyr Thr Glu Leu Asp Phe

85

90

95

Leu Lys Glu Xaa Phe Gly Gly Ser Ser Glu Ile Val Asp Gln Leu Glu
115 120 125

Val Glu Ile Arg Asn Met Thr Leu Leu Val Glu Lys Leu Glu Thr Leu
130 135 140

Asp Lys Asn Asn Val Leu Ala Ile Arg Arg Glu Ile Val Ala Leu Lys
145 150 155 160

Thr Lys Leu Lys Glu Cys Glu Ala Ser Lys Asp Gln Asn Thr Pro Val
165 170 175

Val His Pro Pro Pro Thr Pro Gly Ser Cys Gly His Gly Gly Val Val
180 185 190

Xaa Ile Ser Lys Pro Ser Val Val Gln Leu Asn Trp Arg Gly Phe Ser
195 200 205

Tyr Leu Tyr Gly Ala Trp Gly Arg Asp Tyr Ser Pro Gln His Pro Asn
210 215 220

Lys Gly Leu Tyr Trp Val Ala Pro Leu Asn Thr Asp Gly Arg Leu Leu
225 230 235 240

Glu Tyr Tyr Arg Leu Tyr Asn Thr Leu Asp Asp Leu Leu Leu Tyr Ile
245 250 255

Asn Ala Arg Glu Leu Arg Ile Thr Tyr Gly Gln Gly Ser Gly Thr Ala
260 265 270

Val	Tyr	Asn	Asn	Asn	Met	Tyr	Val	Asn	Met	Tyr	Asn	Thr	Gly	Asn	Ile
		275					280					285			

Ala Arg Val Asn Leu Thr Thr Asn Thr Ile Ala Val Thr Gln Thr Leu
290 295 300

Pro Asn Ala Ala Tyr Asn Asn Arg Phe Xaa Tyr Ala Asn Val Ala Trp
305 310 315 320

Gln Asp Ile Asp Phe Xaa Val Asp Glu Asn Gly Leu Trp Val Ile Tyr
325 330 335

Ser Thr Glu Ala Ser Thr Gly Xaa Met Val Ile Ser Lys Leu Asn Asp
340 345 350

Thr Thr Leu Gln Val Leu Asn Thr Trp Tyr Thr Lys Gln Tyr Lys Pro

1322

355 360 365
 Ser Ala Ser Asn Ala Phe Met Val Cys Gly Val Leu Tyr Ala Thr Arg
 370 375 380
 Thr Met Asn Thr Arg Thr Glu Glu Ile Phe Tyr Tyr Tyr Asp Thr Asn
 385 390 395 400
 Thr Gly Lys Glu Gly Lys Leu Asp Ile Val Met His Lys Met Gln Glu
 405 410 415
 Lys Val Gln Ser Ile Asn Tyr Asn Pro Phe Asp Gln Lys Leu Tyr Val
 420 425 430
 Tyr Asn Asp Gly Tyr Leu Leu Asn Tyr Asp Leu Ser Val Leu Gln Lys
 435 440 445
 Pro Gln
 450

<210> 1288
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 1288
 Leu Gln Gln Ala Leu Pro Asn Asn Gly Leu Leu Phe Thr Trp Thr Leu
 1 5 10 15
 Ser Lys Glu Gly Gly Arg Glu Gly Gln Ser Gly Val Ser Phe Gln His
 20 25 30
 Ser Ser Gln Lys Gly Glu Arg Phe Ser Gly Trp Cys His Ala Ile Gly
 35 40 45
 Ile Lys Gln Glu Ala His Gly Trp Leu Leu Asn Glu Glu Gln Asn Leu
 50 55 60
 Gly Ala Leu Trp Leu Thr Thr Ala Ile Cys Gly Ala Gly Thr His Thr
 65 70 75 80
 Ser Arg Gln Leu Gln Phe Cys Thr Phe Ser Leu Leu Asp Ser Lys Ser
 85 90 95
 Arg Cys Cys Leu Ala Ala Leu Arg Gly His Ser Leu Leu Arg Arg Ala
 100 105 110
 Leu Gln Ser Pro Ala Pro Gly Leu Gly Glu Trp Met Arg Leu Leu Pro
 115 120 125

1323

Tyr Asp Thr Cys Gln Asp Ala Leu Pro Pro Pro Leu Lys Val Gly Pro
130 135 140

Gly Gln His Cys Ser Leu Leu Ser Ala Phe Ser Gly Leu Arg Ser Gln
145 150 155 160

Tyr Glu Leu Pro

<210> 1289

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (30)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1289

Trp Met Ser Glu Tyr Xaa Gln Trp Val Phe Leu Ile Ser Leu Arg Ile
1 5 10 15

Cys Leu Arg Val His Tyr Gln Gly Ile Ser Gly Thr Arg Xaa His Ser
20 25 30

Leu His Gln Phe Leu Arg Val Leu
35 40

<210> 1290

<211> 266

<212> PRT

<213> Homo sapiens

<400> 1290

Asp Ile Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His
1 5 10 15

Phe Asn Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg
20 25 30

1324

His Ser Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe
 35 40 45
 Lys Ile Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile
 50 55 60
 Gly Ser Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe
 65 70 75 80
 Lys Glu Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu
 85 90 95
 Glu Lys Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val
 100 105 110
 Val Thr Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu
 115 120 125
 Lys Glu Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp
 130 135 140
 Val Thr Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp
 145 150 155 160
 Cys Val Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro
 165 170 175
 Thr Tyr Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly
 180 185 190
 Gly Phe Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile
 195 200 205
 Gly Glu Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu
 210 215 220
 Ala Ala Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile
 225 230 235 240
 Ser Gln Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser
 245 250 255
 Leu Val Ala Arg Lys Leu Ser Arg Pro Leu
 260 265

<210> 1291

<211> 112

<212> PRT

<213> Homo sapiens

1325

<220>

<221> SITE

<222> (55)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1291

Cys Gly Ser Thr Ile Leu Gln Gly Pro Gln Lys Ala Leu Arg Arg Gly
1 5 10 15
Leu Gly Glu Val Gly Asp Gln Gly Lys Ser Arg Gln Arg Ala Ser Lys
20 25 30
Arg Leu Phe Ala Ser Lys Ala Leu Arg Gly His Leu Arg Pro Val Arg
35 40 45
Gly Gln Gln Pro Gly Arg Xaa Gly Ser Asp Glu Asn Glu Glu Ser Ser
50 55 60
Val Val Asp Tyr Val Glu Val Thr Val Gly Glu Glu Asp Ala Ile Ser
65 70 75 80
Asp Arg Ser Asp Ser Trp Ser Gln Ala Ala Ala Glu Gly Val Ser Glu
85 90 95
Leu Ala Glu Ser Asp Ser Asp Cys Val Pro Ala Glu Ala Gly Gln Ala
100 105 110

<210> 1292

<211> 217

<212> PRT

<213> Homo sapiens

<400> 1292

Gly Ser Thr His Ala Ser Gly Thr Met Arg Ala Ala Ala Ile Ser Thr
1 5 10 15
Pro Lys Leu Asp Lys Met Pro Gly Met Phe Phe Ser Ala Asn Pro Lys
20 25 30
Glu Leu Lys Gly Thr Thr His Ser Leu Leu Asp Asp Lys Met Gln Lys
35 40 45
Arg Arg Pro Lys Thr Phe Gly Met Asp Met Lys Ala Tyr Leu Arg Ser
50 55 60

1326

Met Ile Pro His Leu Glu Ser Gly Met Lys Ser Ser Lys Ser Lys Asp
65 70 75 80

Val Leu Ser Ala Ala Glu Val Met Gln Trp Ser Gln Ser Leu Glu Lys
85 90 95

Leu Leu Ala Asn Gln Thr Gly Gln Asn Val Phe Gly Ser Phe Leu Lys
100 105 110

Ser Glu Phe Ser Glu Glu Asn Ile Glu Phe Trp Leu Ala Cys Glu Asp
115 120 125

Tyr Lys Lys Thr Glu Ser Asp Leu Leu Pro Cys Lys Ala Glu Glu Ile
130 135 140

Tyr Lys Ala Phe Val His Ser Asp Ala Ala Lys Gln Ile Asn Ile Asp
145 150 155 160

Phe Arg Thr Arg Glu Ser Thr Ala Lys Lys Ile Lys Ala Pro Thr Pro
165 170 175

Thr Cys Phe Asp Glu Ala Gln Lys Val Ile Tyr Thr Leu Met Glu Lys
180 185 190

Asp Ser Tyr Pro Arg Phe Leu Lys Ser Asp Ile Tyr Leu Asn Leu Leu
195 200 205

Asn Asp Leu Gln Ala Asn Ser Leu Lys
210 215

<210> 1293

<211> 235

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (229)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1293

Leu His Leu Leu Ala Val Leu Glu Lys Met Ile Ser Gln Gly Asn Asn
1 5 10 15

Asn Lys Asn Gly Lys Asn Glu Thr Gly Asn Asn Asn Asn Lys Asp Gly
20 25 30

Ser Asn His Lys Ala Glu Ser Gly Ala Leu Ile Glu Ala Ala Lys Ser
35 40 45

1327

Lys Ile His Gln Tyr Lys Val Arg Ala Tyr Ile Gln Met Lys Ser Leu
 50 55 60
 Lys Ala Cys Lys Arg Glu Ile Lys Ser Val Met Asn Thr Ala Gly Asn
 65 70 75 80
 Ser Ala Pro Ser Leu Phe Leu Lys Ser Asn Phe Glu Tyr Leu Arg Gly
 85 90 95
 Asn Tyr Arg Lys Ala Val Lys Leu Leu Asn Ser Ser Asn Ile Ala Glu
 100 105 110
 His Pro Gly Phe Met Lys Thr Gly Glu Cys Leu Arg Cys Met Phe Trp
 115 120 125
 Asn Asn Leu Gly Cys Ile His Phe Ala Met Ser Lys His Asn Leu Gly
 130 135 140
 Ile Phe Tyr Phe Lys Lys Ala Leu Gln Glu Asn Asp Asn Val Cys Ala
 145 150 155 160
 Gln Leu Ser Ala Gly Ser Thr Asp Pro Gly Lys Lys Phe Ser Gly Arg
 165 170 175
 Pro Met Cys Thr Leu Leu Thr Asn Lys Arg Tyr Glu Leu Leu Tyr Asn
 180 185 190
 Cys Gly Ile Gln Leu Leu His Ile Gly Arg Pro Leu Ala Ala Phe Glu
 195 200 205
 Cys Leu Ile Glu Ala Val Gln Val Tyr His Ala Asn Pro Arg Leu Trp
 210 215 220
 Leu Arg Leu Ala Xaa Met Leu His Cys Cys Gln
 225 230 235

<210> 1294

<211> 275

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (23)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1328

<222> (49)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (50)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1294

Ala Arg Gly Ala Arg Gly Arg Ala Leu Pro Ala Ser Gly Lys Ala Gly
1 5 10 15

Arg Ala Arg Gly Ser Ala Xaa Gly Ser Ala Ala Arg Gly His Trp Ser
20 25 30

Leu Ala Arg Phe Pro Ala Pro Arg Gly Ser His Leu Pro Ala Arg Arg
35 40 45

Xaa Xaa Gly Arg Val Ser Thr Pro Ile Leu Arg Pro Val Ser Ser Ile
50 55 60

Pro Leu Ala Leu Ser Arg Glu Ser Arg Thr Ala Glu Glu Ser Ser Leu
65 70 75 80

Thr Pro Gln Pro Gln Val Gly Leu Val His Ile Met Thr Ser Phe Glu
85 90 95

Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val Tyr
100 105 110

His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe Asn
115 120 125

Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn Ser
130 135 140

Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val Gln
145 150 155 160

Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser Phe
165 170 175

Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser Arg
180 185 190

Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met Val
195 200 205

Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu Ser
210 215 220

1329

Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu Leu
225 230 235 240

Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly Thr
245 250 255

Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp Glu
260 265 270

Asn Glu Ser
275

<210> 1295

<211> 677

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (144)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (161)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1295

Met Thr Arg Leu Pro Lys Leu Trp Ala Arg Pro Ala Gly Lys Ala Leu
1 5 10 15

Val Ser Pro Val Val Gln Asn Ile Thr Ser Pro Asp Glu Asp Gly Ile
20 25 30

Ser Pro Leu Gly Trp Leu Leu Asp Gln Tyr Leu Glu Cys Gln Glu Ala
35 40 45

Val Phe Asn Pro Gln Ser Arg Gly Pro Ala Phe Phe Ser Arg Val Arg
50 55 60

Arg Leu Thr His Leu Leu Val His Val Glu Pro Cys Glu Ala Pro Pro
65 70 75 80

Pro Val Val Ala Thr Pro Arg Pro Lys Gly Arg Asn Arg Ser His Asp
85 90 95

Trp Ser Ser Leu Ala Thr Arg Gly Leu Pro Ser Ser Ile Met Arg Asn
100 105 110

1330

Leu Thr Arg Cys Trp Arg Ala Val Val Glu Lys Gln Val Asn Asn Phe
115 120 125

Leu Thr Ser Ser Trp Arg Asp Asp Asp Phe Val Pro Arg Tyr Cys Xaa
130 135 140

His Phe Asn Ile Leu Gln Asn Ser Ser Ser Glu Leu Phe Gly Pro Arg
145 150 155 160

Xaa Ala Phe Leu Leu Ala Leu Gln Asn Gly Cys Ala Gly Ala Leu Leu
165 170 175

Lys Leu Pro Phe Leu Lys Ala Ala His Val Ser Glu Gln Phe Ala Arg
180 185 190

His Ile Asp Gln Gln Ile Gln Gly Ser Arg Ile Gly Gly Ala Gln Glu
195 200 205

Met Glu Arg Leu Ala Gln Leu Gln Gln Cys Leu Gln Ala Val Leu Ile
210 215 220

Phe Ser Gly Leu Glu Ile Ala Thr Thr Phe Glu His Tyr Tyr Gln His
225 230 235 240

Tyr Met Ala Asp Arg Leu Leu Gly Val Val Ser Ser Trp Leu Glu Gly
245 250 255

Ala Val Leu Glu Gln Ile Gly Pro Cys Phe Pro Asn Arg Leu Pro Gln
260 265 270

Gln Met Leu Gln Ser Leu Ser Thr Ser Lys Glu Leu Gln Arg Gln Phe
275 280 285

His Val Tyr Gln Leu Gln Gln Leu Asp Gln Glu Leu Leu Lys Leu Glu
290 295 300

Asp Thr Glu Lys Lys Ile Gln Val Gly Leu Gly Ala Ser Gly Lys Glu
305 310 315 320

His Lys Ser Glu Lys Glu Glu Glu Ala Gly Ala Ala Ala Val Val Asp
325 330 335

Val Ala Glu Gly Glu Glu Glu Glu Glu Glu Asn Glu Asp Leu Tyr Tyr
340 345 350

Glu Gly Ala Met Pro Glu Val Ser Val Leu Val Leu Ser Arg His Ser
355 360 365

Trp Pro Val Ala Ser Ile Cys His Thr Leu Asn Pro Arg Thr Cys Leu
370 375 380

1331

Pro Ser Tyr Leu Arg Gly Thr Leu Asn Arg Tyr Ser Asn Phe Tyr Asn
 385 390 395 400
 Lys Ser Gln Ser His Pro Ala Leu Glu Arg Gly Ser Gln Arg Arg Leu
 405 410 415
 Gln Trp Thr Trp Leu Gly Trp Ala Glu Leu Gln Phe Gly Asn Gln Thr
 420 425 430
 Leu His Val Ser Thr Val Gln Met Trp Leu Leu Leu Tyr Leu Asn Asp
 435 440 445
 Leu Lys Ala Val Ser Val Glu Ser Leu Leu Ala Phe Ser Gly Leu Ser
 450 455 460
 Ala Asp Met Leu Asn Gln Ala Ile Gly Pro Leu Thr Ser Ser Arg Gly
 465 470 475 480
 Pro Leu Asp Leu His Glu Gln Lys Asp Ile Pro Gly Gly Val Leu Lys
 485 490 495
 Ile Arg Asp Gly Ser Lys Glu Pro Arg Ser Arg Trp Asp Ile Val Arg
 500 505 510
 Leu Ile Pro Pro Gln Thr Tyr Leu Gln Ala Glu Gly Glu Asp Gly Gln
 515 520 525
 Asn Leu Glu Lys Arg Arg Asn Leu Leu Asn Cys Leu Ile Val Arg Ile
 530 535 540
 Leu Lys Ala His Gly Asp Glu Gly Leu His Ile Asp Gln Leu Val Cys
 545 550 555 560
 Leu Val Leu Glu Ala Trp Gln Lys Gly Pro Cys Pro Pro Arg Gly Leu
 565 570 575
 Val Ser Ser Leu Gly Lys Gly Ser Ala Cys Ser Ser Thr Asp Val Leu
 580 585 590
 Ser Cys Ile Leu His Leu Leu Gly Lys Gly Thr Leu Arg Arg His Asp
 595 600 605
 Asp Arg Pro Gln Val Leu Ser Tyr Ala Val Pro Val Thr Val Met Glu
 610 615 620
 Pro His Thr Glu Ser Leu Asn Pro Gly Ser Ser Gly Pro Asn Pro Pro
 625 630 635 640
 Leu Thr Phe His Thr Leu Gln Ile Arg Ser Arg Gly Val Pro Tyr Ala
 645 650 655

1332

Ser Cys Thr Ala Thr Gln Ser Phe Ser Thr Ser Gly Ser Pro Arg Leu
660 665 670

Gly Val Arg Gly Arg
675

<210> 1296

<211> 578

<212> PRT

<213> Homo sapiens

<400> 1296

Gly Thr Arg Glu Gly Ala Arg Val Gly Gly Ala Arg Gly Gly Arg Asp
1 5 10 15

Gly Arg Lys Met Ala Thr Ala Thr Ile Ala Leu Gln Val Asn Gly Gln
20 25 30

Gln Gly Gly Gly Ser Glu Pro Ala Ala Ala Ala Val Val Ala Ala
35 40 45

Gly Asp Lys Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu
50 55 60

Asn Gly Gln Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro
65 70 75 80

Glu Gln Gln Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln
85 90 95

Ser Ile Lys Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln
100 105 110

Gln Leu Thr Asn Leu Gln Met Ala Ala Val Thr Met Gly Phe Gly Asp
115 120 125

Pro Leu Ser Pro Leu Gln Ser Met Ala Ala Gln Arg Gln Arg Ala Leu
130 135 140

Ala Ile Met Cys Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly
145 150 155 160

Glu Asp Thr Ile Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser
165 170 175

Ile Asp Met Ser Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala
180 185 190

Phe Val Glu Tyr Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln

1333

195	200	205
Met Asn Ser Val Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro		
210	215	220
Ser Asn Ile Gly Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu		
225	230	235 240
Ala Arg Ala Phe Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu		
245	250	255
Ser Asp Asp Asp Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys		
260	265	270
Ser Cys Thr Leu Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr		
275	280	285
Gly Phe Ile Glu Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser		
290	295	300
Ser Met Asn Leu Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys		
305	310	315 320
Ala Val Thr Pro Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly		
325	330	335
Leu Pro Pro Ala Ala Ala Val Ala Ala Ala Ala Ala Thr Ala Lys Ile		
340	345	350
Thr Ala Gln Glu Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly		
355	360	365
Thr Pro Gly Leu Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly		
370	375	380
Thr Leu Pro Gln Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr		
385	390	395 400
Gly Val Thr Pro Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val		
405	410	415
Gly Val Val Asn Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu		
420	425	430
Glu Pro Lys Lys Glu Lys Glu Glu Glu Leu Phe Pro Glu Ser Glu		
435	440	445
Arg Pro Glu Met Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser		
450	455	460
Ser Ala Arg His Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser		

1334

465 470 475 480
 Thr Val Met Val Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp
 485 490 495
 Asp Leu Glu Gly Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val
 500 505 510
 Asn Arg Val Ile Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala
 515 520 525
 Glu Ile Ile Val Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr
 530 535 540
 His Lys Ala Ile Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys
 545 550 555 560
 Val Val Ala Glu Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu
 565 570 575
 Ser Ala

<210> 1297
 <211> 179
 <212> PRT
 <213> Homo sapiens

<400> 1297
 Pro Arg Gly Thr Ser Arg Arg Ser Ala Trp Pro Lys Met Ala Ala Ser
 1 5 10 15
 Val Cys Ser Gly Leu Leu Gly Pro Arg Val Leu Ser Trp Ser Arg Glu
 20 25 30
 Leu Pro Cys Ala Trp Arg Ala Leu His Thr Ser Pro Val Cys Ala Lys
 35 40 45
 Asn Arg Ala Ala Arg Val Arg Val Ser Lys Gly Asp Lys Pro Val Thr
 50 55 60
 Tyr Glu Glu Ala His Ala Pro His Tyr Ile Ala His Arg Lys Gly Trp
 65 70 75 80
 Leu Ser Leu His Thr Gly Asn Leu Asp Gly Glu Asp His Ala Ala Glu
 85 90 95
 Arg Thr Val Glu Asp Val Phe Leu Arg Lys Phe Met Trp Gly Thr Phe
 100 105 110

1335

Pro Gly Cys Leu Ala Asp Gln Leu Val Leu Lys Arg Arg Gly Asn Gln
 115 120 125

Leu Glu Ile Cys Ala Val Val Leu Arg Gln Leu Ser Pro His Lys Tyr
 130 135 140

Tyr Phe Leu Val Gly Tyr Ser Glu Thr Leu Leu Ser Tyr Phe Tyr Lys
 145 150 155 160

Cys Pro Val Arg Leu His Leu Gln Thr Val Pro Ser Lys Val Val Tyr
 165 170 175

Lys Tyr Leu

<210> 1298

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1298

Gly Leu Val Thr Ile Phe Gly Cys Pro Ser Arg Glu Lys Gly Arg Met
 1 5 10 15

Pro Leu Glu Ser Ser Ser Ser Met Pro Leu Ser Phe Pro Ser Leu Leu
 20 25 30

Pro Ser Val Pro His Asn Thr Asn Pro Ser Pro Pro Leu Met Ser Tyr
 35 40 45

Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe Ala Asn Trp
 50 55 60

Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val Ala Lys Ala
 65 70 75 80

Val Pro Glu Lys Leu Gln Pro Leu Leu Asp Ser Leu Glu Gln Leu Ser
 85 90 95

Val Ser Gly Ala Asp Arg Pro Pro Ser Ile Phe Glu Cys Gln Leu His
 100 105 110

Leu Trp Asp Gln Trp Phe Arg Gly Trp Ala Glu Gln Glu Arg Asn Glu
 115 120 125

Phe Val Arg Gln Leu Glu Phe Ser Glu Pro Asp Phe Val Ala Lys Phe
 130 135 140

1336

Tyr Gln Ala Val Ala Ala Thr Ala Gly Lys Asp
145 150 155

<210> 1299

<211> 449

<212> PRT

<213> Homo sapiens

<400> 1299

Ser Asn Arg Lys Phe Ile Pro His Gln Leu Leu Val Ala Ile Asp Leu
1 5 10 15

Leu Ala Arg Gln Ala Val Arg Tyr Ile Asn Glu Asn Leu Ile Val Asn
20 25 30

Thr Asp Glu Leu Gly Arg Asp Cys Leu Ile Asn Ala Ala Lys Thr Ser
35 40 45

Met Ser Ser Lys Ile Ile Gly Ile Asn Gly Asp Phe Phe Ala Asn Met
50 55 60

Val Val Asp Ala Val Leu Ala Ile Lys Tyr Thr Asp Ile Arg Gly Gln
65 70 75 80

Pro Arg Tyr Pro Val Asn Ser Val Asn Ile Leu Lys Ala His Gly Arg
85 90 95

Ser Gln Met Glu Ser Met Leu Ile Ser Gly Tyr Ala Leu Asn Cys Val
100 105 110

Val Gly Ser Gln Gly Met Pro Lys Arg Ile Val Asn Ala Lys Ile Ala
115 120 125

Cys Leu Asp Phe Ser Leu Gln Lys Thr Lys Met Lys Leu Gly Val Gln
130 135 140

Val Val Ile Thr Asp Pro Glu Lys Leu Asp Gln Ile Arg Gln Arg Glu
145 150 155 160

Ser Asp Ile Thr Lys Glu Arg Ile Gln Lys Ile Leu Ala Thr Gly Ala
165 170 175

Asn Val Ile Leu Thr Thr Gly Gly Ile Asp Asp Met Cys Leu Lys Tyr
180 185 190

Phe Val Glu Ala Gly Ala Met Ala Val Arg Arg Val Leu Lys Arg Asp
195 200 205

Leu Lys Arg Ile Ala Lys Ala Ser Gly Ala Thr Ile Leu Ser Thr Leu

1337

210	215	220
Ala Asn Leu Glu Gly Glu Glu Thr Phe Glu Ala Ala Met Leu Gly Gln 225 230 235 240		
Ala Glu Glu Val Val Gln Glu Arg Ile Cys Asp Asp Glu Leu Ile Leu 245 250 255		
Ile Lys Asn Thr Lys Ala Arg Thr Ser Ala Ser Ile Ile Leu Arg Gly 260 265 270		
Ala Asn Asp Phe Met Cys Asp Glu Met Glu Arg Ser Leu His Asp Ala 275 280 285		
Leu Cys Val Val Lys Arg Val Leu Glu Ser Lys Ser Val Val Pro Gly 290 295 300		
Gly Gly Ala Val Glu Ala Ala Leu Ser Ile Tyr Leu Glu Asn Tyr Ala 305 310 315 320		
Thr Ser Met Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu Phe Ala Arg 325 330 335		
Ser Leu Leu Val Ile Pro Asn Thr Leu Ala Val Asn Ala Ala Gln Asp 340 345 350		
Ser Thr Asp Leu Val Ala Lys Leu Arg Ala Phe His Asn Glu Ala Gln 355 360 365		
Val Asn Pro Glu Arg Lys Asn Leu Lys Trp Ile Gly Leu Asp Leu Ser 370 375 380		
Asn Gly Lys Pro Arg Asp Asn Lys Gln Ala Gly Val Phe Glu Pro Thr 385 390 395 400		
Ile Val Lys Val Lys Ser Leu Lys Phe Ala Thr Glu Ala Ala Ile Thr 405 410 415		
Ile Leu Arg Ile Asp Asp Leu Ile Lys Leu His Pro Glu Ser Lys Asp 420 425 430		
Asp Lys His Gly Ser Tyr Glu Asp Ala Val His Ser Gly Ala Leu Asn 435 440 445		

Asp

<210> 1300

<211> 96

1338

<212> PRT

<213> Homo sapiens

<400> 1300

Leu Met Phe Tyr Val Leu Phe Trp Thr Leu Ser Ser Cys Lys Asn Phe
1 5 10 15
Tyr Lys Asn Cys Phe Leu His Pro Cys Gly Ala Tyr Ser Ser Glu Pro
20 25 30
Ser Pro Gln Ser Gln Cys Leu Cys Phe Leu Phe Tyr Phe Cys Ser Ile
35 40 45
Arg Phe Leu Leu Leu Leu Cys Leu Lys Ser Ser Leu Gly Ser Tyr Gln
50 55 60
Gly Phe Ser Phe Cys Val Ala Phe Ala Ala Trp Ile Lys His Trp Leu
65 70 75 80
Thr Val Leu Met Cys Glu Glu Lys Lys Phe Ser Lys Ala Gly Glu Leu
85 90 95

<210> 1301

<211> 332

<212> PRT

<213> Homo sapiens

<400> 1301

Gly Glu Pro Lys Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro
1 5 10 15
Pro Glu Asp Gly Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln
20 25 30
Phe Leu Leu Val Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val
35 40 45
Pro Ala Asn Ser Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu
50 55 60
Asp Cys Ala Phe Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp
65 70 75 80
His Gln Leu Lys Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val
85 90 95

1339

Gly Thr His Asp Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Glu Val
100 105 110

Asn Val Met Val Thr Gly Ser Trp Asp Gln Thr Val Lys Leu Trp Asp
115 120 125

Pro Arg Thr Pro Cys Asn Ala Gly Thr Phe Ser Gln Pro Glu Lys Val
130 135 140

Tyr Thr Leu Ser Val Ser Gly Asp Arg Leu Ile Val Gly Thr Ala Gly
145 150 155 160

Arg Arg Val Leu Val Trp Asp Leu Arg Asn Met Gly Tyr Val Gln Gln
165 170 175

Arg Arg Glu Ser Ser Leu Lys Tyr Gln Thr Arg Cys Ile Arg Ala Phe
180 185 190

Pro Asn Lys Gln Gly Tyr Val Leu Ser Ser Ile Glu Gly Arg Val Ala
195 200 205

Val Glu Tyr Leu Asp Pro Ser Pro Glu Val Gln Lys Lys Lys Tyr Ala
210 215 220

Phe Lys Cys His Arg Leu Lys Glu Asn Asn Ile Glu Gln Ile Tyr Pro
225 230 235 240

Val Asn Ala Ile Ser Phe His Asn Ile His Asn Thr Phe Ala Thr Gly
245 250 255

Gly Ser Asp Gly Phe Val Asn Ile Trp Asp Pro Phe Asn Lys Lys Arg
260 265 270

Leu Cys Gln Phe His Arg Tyr Pro Thr Ser Ile Ala Ser Leu Ala Phe
275 280 285

Ser Asn Asp Gly Thr Thr Leu Ala Ile Ala Ser Ser Tyr Met Tyr Glu
290 295 300

Met Asp Asp Thr Glu His Pro Glu Asp Gly Ile Phe Ile Arg Gln Val
305 310 315 320

Thr Asp Ala Glu Thr Lys Pro Lys Ser Pro Cys Thr
325 330

<210> 1302

<211> 565

<212> PRT

<213> Homo sapiens

1340

<400> 1302

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Leu His Cys Thr Met Cys Gly Ile Trp Ala Leu Phe Gly Ser Asp Asp
 1             5             10             15

Cys Leu Ser Val Gln Cys Leu Ser Ala Met Lys Ile Ala His Arg Gly
      20             25             30

Pro Asp Ala Phe Arg Phe Glu Asn Val Asn Gly Tyr Thr Asn Cys Cys
      35             40             45

Phe Gly Phe His Arg Leu Ala Val Val Asp Pro Leu Phe Gly Met Gln
      50             55             60

Pro Ile Arg Val Lys Lys Tyr Pro Tyr Leu Trp Leu Cys Tyr Asn Gly
      65             70             75             80

Glu Ile Tyr Asn His Lys Lys Met Gln Gln His Phe Glu Phe Glu Tyr
      85             90             95

Gln Thr Lys Val Asp Gly Glu Ile Ile Leu His Leu Tyr Asp Lys Gly
      100             105             110

Gly Ile Glu Gln Thr Ile Cys Met Leu Asp Gly Val Phe Ala Phe Val
      115             120             125

Leu Leu Asp Thr Ala Asn Lys Lys Val Phe Leu Gly Arg Asp Thr Tyr
      130             135             140

Gly Val Arg Pro Leu Phe Lys Ala Met Thr Glu Asp Gly Phe Leu Ala
      145             150             155             160

Val Cys Ser Glu Ala Lys Gly Leu Val Thr Leu Lys His Ser Ala Thr
      165             170             175

Pro Phe Leu Lys Val Glu Pro Phe Leu Pro Gly His Tyr Glu Val Leu
      180             185             190

Asp Leu Lys Pro Asn Gly Lys Val Ala Ser Val Glu Met Val Lys Tyr
      195             200             205

His His Cys Arg Asp Glu Pro Leu His Ala Leu Tyr Asp Asn Val Glu
      210             215             220

Lys Leu Phe Pro Gly Phe Glu Ile Glu Thr Val Lys Asn Asn Leu Arg
      225             230             235             240

Ile Leu Phe Asn Asn Ala Val Lys Lys Arg Leu Met Thr Asp Arg Arg
      245             250             255

Ile Gly Cys Leu Leu Ser Gly Gly Leu Asp Ser Ser Leu Val Ala Ala

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1341

260	265	270
Thr Leu Leu Lys Gln Leu Lys Glu Ala Gln Val Gln Tyr Pro Leu Gln		
275	280	285
Thr Phe Ala Ile Gly Met Glu Asp Ser Pro Asp Leu Leu Ala Ala Arg		
290	295	300
Lys Val Ala Asp His Ile Gly Ser Glu His Tyr Glu Val Leu Phe Asn		
305	310	315
Ser Glu Glu Gly Ile Gln Ala Leu Asp Glu Val Ile Phe Ser Leu Glu		
325	330	335
Thr Tyr Asp Ile Thr Thr Val Arg Ala Ser Val Gly Met Tyr Leu Ile		
340	345	350
Ser Lys Tyr Ile Arg Lys Asn Thr Asp Ser Val Val Ile Phe Ser Gly		
355	360	365
Glu Gly Ser Asp Glu Leu Thr Gln Gly Tyr Ile Tyr Phe His Lys Ala		
370	375	380
Pro Ser Pro Glu Lys Ala Glu Glu Glu Ser Glu Arg Leu Leu Arg Glu		
385	390	395
Leu Tyr Leu Phe Asp Val Leu Arg Ala Asp Arg Thr Thr Ala Ala His		
405	410	415
Gly Leu Glu Leu Arg Val Pro Phe Leu Asp His Arg Phe Ser Ser Tyr		
420	425	430
Tyr Leu Ser Leu Pro Pro Glu Met Arg Ile Pro Lys Asn Gly Ile Glu		
435	440	445
Lys His Leu Leu Arg Glu Thr Phe Glu Asp Ser Asn Leu Ile Pro Lys		
450	455	460
Glu Ile Leu Trp Arg Pro Lys Glu Ala Phe Ser Asp Gly Ile Thr Ser		
465	470	475
Val Lys Asn Ser Trp Phe Lys Ile Leu Gln Glu Tyr Val Glu His Gln		
485	490	495
Val Asp Asp Ala Met Met Ala Asn Ala Ala Gln Lys Phe Pro Phe Asn		
500	505	510
Thr Pro Lys Thr Lys Glu Gly Tyr Tyr Tyr Arg Gln Val Phe Glu Arg		
515	520	525
His Tyr Pro Gly Arg Ala Asp Trp Leu Ser His Tyr Trp Met Pro Lys		

1342

530

535

540

Trp Ile Asn Ala Thr Asp Pro Ser Ala Arg Thr Leu Thr His Tyr Lys
 545 550 555 560

Ser Ala Val Lys Ala
 565

<210> 1303

<211> 441

<212> PRT

<213> Homo sapiens

<400> 1303

Arg Arg Arg Arg Ala Cys Arg Ser Ala Glu Gly Thr Gly Leu Arg Ser
 1 5 10 15

Leu Leu Leu Pro Pro Arg Leu Gln Leu Pro Ala Gly Pro Phe Ser Arg
 20 25 30

Cys Arg Trp Asp Pro Val Ser Ser Pro Arg Pro Ser Thr Met Pro Pro
 35 40 45

Lys Lys Gly Gly Asp Gly Ile Lys Pro Pro Pro Ile Ile Gly Arg Phe
 50 55 60

Gly Thr Ser Leu Lys Ile Gly Ile Val Gly Leu Pro Asn Val Gly Lys
 65 70 75 80

Ser Thr Phe Phe Asn Val Leu Thr Asn Ser Gln Ala Ser Ala Glu Asn
 85 90 95

Phe Pro Phe Cys Thr Ile Asp Pro Asn Glu Ser Arg Val Pro Val Pro
 100 105 110

Asp Glu Arg Phe Asp Phe Leu Cys Gln Tyr His Lys Pro Ala Ser Lys
 115 120 125

Ile Pro Ala Phe Leu Asn Val Val Asp Ile Ala Gly Leu Val Lys Gly
 130 135 140

Ala His Asn Gly Gln Gly Leu Gly Asn Ala Phe Leu Ser His Ile Ser
 145 150 155 160

Ala Cys Asp Gly Ile Phe His Leu Thr Arg Ala Phe Glu Asp Asp Asp
 165 170 175

Ile Thr His Val Glu Gly Ser Val Asp Pro Ile Arg Asp Ile Glu Ile
 180 185 190

1343

Ile His Glu Glu Leu Gln Leu Lys Asp Glu Glu Met Ile Gly Pro Ile
 195 200 205

Ile Asp Lys Leu Glu Lys Val Ala Val Arg Gly Gly Asp Lys Lys Leu
 210 215 220

Lys Pro Glu Tyr Asp Ile Met Cys Lys Val Lys Ser Trp Val Ile Asp
 225 230 235 240

Gln Lys Lys Pro Val Arg Phe Tyr His Asp Trp Asn Asp Lys Glu Ile
 245 250 255

Glu Val Leu Asn Lys His Leu Phe Leu Thr Ser Lys Pro Met Val Tyr
 260 265 270

Leu Val Asn Leu Ser Glu Lys Asp Tyr Ile Arg Lys Lys Asn Lys Trp
 275 280 285

Leu Ile Lys Ile Lys Glu Trp Val Asp Lys Tyr Asp Pro Gly Ala Leu
 290 295 300

Val Ile Pro Phe Ser Gly Ala Leu Glu Leu Lys Leu Gln Glu Leu Ser
 305 310 315 320

Ala Glu Glu Arg Gln Lys Tyr Leu Glu Ala Asn Met Thr Gln Ser Ala
 325 330 335

Leu Pro Lys Ile Ile Lys Ala Gly Phe Ala Ala Leu Gln Leu Glu Tyr
 340 345 350

Phe Phe Thr Ala Gly Pro Asp Glu Val Arg Ala Trp Thr Ile Arg Lys
 355 360 365

Gly Thr Lys Ala Pro Gln Ala Ala Gly Lys Ile His Thr Asp Phe Glu
 370 375 380

Lys Gly Phe Ile Met Ala Glu Val Met Lys Tyr Glu Asp Phe Lys Glu
 385 390 395 400

Glu Gly Ser Glu Asn Ala Val Lys Ala Ala Gly Lys Tyr Arg Gln Gln
 405 410 415

Gly Arg Asn Tyr Ile Val Glu Asp Gly Asp Ile Ile Phe Phe Lys Phe
 420 425 430

Asn Thr Pro Gln Gln Pro Lys Lys Lys
 435 440

1344

<210> 1304

<211> 94

<212> PRT

<213> Homo sapiens

<400> 1304

Glu Lys Lys Arg Gly Arg Glu Asp Lys Pro Gly Thr Met Ala Thr Phe
 1 5 10 15

Pro Pro Ala Thr Ser Ala Pro Gln Gln Pro Pro Gly Pro Glu Asp Glu
 20 25 30

Asp Ser Ser Leu Asp Glu Ser Asp Leu Tyr Ser Leu Ala His Ser Tyr
 35 40 45

Leu Gly Gly Gly Gly Arg Lys Gly Arg Thr Lys Arg Glu Ala Ala Ala
 50 55 60

Asn Thr Asn Arg Pro Ser Pro Gly Gly His Glu Arg Lys Leu Val Thr
 65 70 75 80

Lys Leu Gln Asn Ser Glu Arg Lys Lys Arg Gly Ala Arg Arg
 85 90

<210> 1305

<211> 82

<212> PRT

<213> Homo sapiens

<400> 1305

Val Ile Leu Glu Met Val Ile Val Phe Cys Leu Val Thr Phe Ala Thr
 1 5 10 15

Val Pro Phe Lys Thr Met Trp Lys Pro Gln Val Cys Gly Gln His Arg
 20 25 30

Trp Asn Asp Ile Leu Cys Phe Leu Arg Leu Pro Ser Thr Arg His Ile
 35 40 45

Ser Leu Val Leu Gln Met Ser Ala Gln Val Leu Val Thr Ser Phe Ser
 50 55 60

Cys Cys Pro Gly Lys Ser Val Cys Ala Gly Ala Gly Ala Leu Ala Leu
 65 70 75 80

Phe Arg

1345

<210> 1306

<211> 231

<212> PRT

<213> Homo sapiens

<400> 1306

Ala Arg Glu Met Ala Ala Gln Gln Arg Asp Cys Gly Gly Ala Ala Gln
1 5 10 15

Leu Ala Gly Pro Ala Ala Glu Ala Asp Pro Leu Gly Arg Phe Thr Cys
20 25 30

Pro Val Cys Leu Glu Val Tyr Glu Lys Pro Val Gln Val Pro Cys Gly
35 40 45

His Val Phe Cys Ser Ala Cys Leu Gln Glu Cys Leu Lys Pro Lys Lys
50 55 60

Pro Val Cys Gly Val Cys Arg Ser Ala Leu Ala Pro Gly Val Arg Ala
65 70 75 80

Val Glu Leu Glu Arg Gln Ile Glu Ser Thr Glu Thr Ser Cys His Gly
85 90 95

Cys Arg Lys Asn Phe Phe Leu Ser Lys Ile Arg Ser His Val Ala Thr
100 105 110

Cys Ser Lys Tyr Gln Asn Tyr Ile Met Glu Gly Val Lys Ala Thr Ile
115 120 125

Lys Asp Ala Ser Leu Gln Pro Arg Asn Val Pro Asn Arg Tyr Thr Phe
130 135 140

Pro Cys Pro Tyr Cys Pro Glu Lys Asn Phe Asp Gln Glu Gly Leu Val
145 150 155 160

Glu His Cys Lys Leu Phe His Ser Thr Asp Thr Lys Ser Val Val Cys
165 170 175

Pro Ile Cys Ala Ser Met Pro Trp Gly Asp Pro Asn Tyr Arg Ser Ala
180 185 190

Asn Phe Arg Glu His Ile Gln Arg Arg His Arg Phe Ser Tyr Asp Thr
195 200 205

Phe Val Asp Tyr Asp Val Asp Glu Glu Asp Met Met Asn Gln Val Leu
210 215 220

Gln Arg Ser Ile Ile Asp Gln
225 230

1346

<210> 1307

<211> 170

<212> PRT

<213> Homo sapiens

<400> 1307

Gln Lys Gln Arg Thr Phe Trp Lys Tyr Tyr Tyr Asp Gly Lys Asp Tyr
1 5 10 15

Ile Glu Phe Asn Lys Glu Ile Pro Ala Trp Val Pro Phe Asp Pro Ala
20 25 30

Ala Gln Ile Thr Lys Gln Lys Trp Glu Ala Glu Pro Val Tyr Val Gln
35 40 45

Arg Ala Lys Ala Tyr Leu Glu Glu Glu Cys Pro Ala Thr Leu Arg Lys
50 55 60

Tyr Leu Lys Tyr Ser Lys Asn Ile Leu Asp Arg Gln Asp Pro Pro Ser
65 70 75 80

Val Val Val Thr Ser His Gln Ala Pro Gly Glu Lys Lys Lys Leu Lys
85 90 95

Cys Leu Ala Tyr Asp Phe Tyr Pro Gly Lys Ile Asp Val His Trp Thr
100 105 110

Arg Ala Gly Glu Val Gln Glu Pro Glu Leu Arg Gly Asp Val Leu His
115 120 125

Asn Gly Asn Gly Thr Tyr Gln Ser Trp Val Val Val Ala Val Pro Pro
130 135 140

Gln Asp Thr Ala Pro Tyr Ser Cys His Val Gln His Ser Ser Leu Ala
145 150 155 160

Gln Pro Leu Val Val Pro Trp Glu Ala Ser
165 170

<210> 1308

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

1347

<222> (95)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (104)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1308

Cys Ser Cys Thr Val Arg Ala Arg Arg Arg Leu Asn Arg Gly Leu Arg
 1 5 10 15

Arg Lys Gln His Ser Leu Leu Lys Arg Leu Arg Lys Ala Lys Lys Glu
 20 25 30

Ala Pro Pro Met Glu Lys Pro Glu Val Val Lys Thr His Leu Arg Asp
 35 40 45

Met Ile Ile Leu Pro Glu Met Val Gly Ser Met Val Gly Val Tyr Asn
 50 55 60

Gly Lys Thr Phe Asn Gln Val Glu Ile Lys Pro Glu Met Ile Gly His
 65 70 75 80

Tyr Leu Gly Glu Phe Ser Ile Thr Tyr Lys Pro Val Lys His Xaa Arg
 85 90 95

Pro Gly Ile Gly Ala Thr His Xaa Ser Arg Phe Ile Pro Leu Lys
 100 105 110

<210> 1309

<211> 121

<212> PRT

<213> Homo sapiens

<400> 1309

Pro Val Ser Pro Gln Glu Arg Pro Pro Pro Tyr Leu Ala Val Pro Gly
 1 5 10 15

His Gly Glu Glu Tyr Pro Val Ala Gly Ala His Ser Ser Pro Pro Lys
 20 25 30

Ala Arg Phe Leu Arg Val Pro Ser Glu His Pro Tyr Leu Thr Pro Ser
 35 40 45

Pro Glu Ser Pro Glu His Trp Ala Ser Pro Ser Pro Pro Ser Leu Ser
 50 55 60

Asp Trp Ser Glu Ser Thr Pro Ser Pro Ala Thr Ala Thr Gly Ala Met

1348

65 70 75 80

Ala Thr Thr Thr Gly Ala Leu Pro Ala Gln Pro Leu Pro Leu Ser Val
 85 90 95

Pro Ser Ser Leu Ala Gln Ala Gln Thr Gln Leu Gly Pro Gln Pro Glu
 100 105 110

Val Thr Pro Lys Arg Gln Val Leu Ala
 115 120

<210> 1310
<211> 206
<212> PRT
<213> Homo sapiens

<400> 1310

Gln Cys Pro Gly Arg Ala Gly Ala Pro Gln Thr Arg Ala Pro Arg Ala
1 5 10 15

Arg Glu Arg Gly Gly Ala Met Ala Thr Ala Asn Gly Ala Val Glu Asn
 20 25 30

Gly Gln Pro Asp Arg Lys Pro Pro Ala Leu Pro Arg Pro Ile Arg Asn
 35 40 45

Leu Glu Val Lys Phe Thr Lys Ile Phe Ile Asn Asn Glu Trp His Glu
50 55 60

Ser Lys Ser Gly Lys Lys Phe Ala Thr Cys Asn Pro Ser Thr Arg Glu
65 70 75 80

Gln Ile Cys Glu Val Glu Glu Gly Asp Lys Pro Asp Val Asp Lys Ala
 85 90 95

Val Glu Ala Ala Gln Val Ala Phe Gln Arg Gly Ser Pro Trp Arg Arg
 100 105 110

Leu Asp Ala Leu Ser Arg Gly Arg Leu Leu His Gln Leu Ala Asp Leu
115 120 125

Val Glu Arg Asp Arg Ala Thr Leu Ala Ala Leu Glu Thr Met Asp Thr
130 135 140

Gly Lys Pro Phe Leu His Ala Phe Phe Ile Asp Leu Glu Gly Cys Ile
145 150 155 160

Arg Thr Leu Arg Tyr Phe Ala Gly Trp Ala Asp Lys Ile Gln Gly Lys
 165 170 175

1349

Thr Ile Pro Thr Asp Asp Asn Val Cys Ala Ser Pro Gly Met Ser Pro
180 185 190

Leu Val Ser Val Gly Pro Ser Leu His Gly Thr Ser Pro Cys
195 200 205

<210> 1311

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1311

Ser Trp Glu Thr Glu Lys Met Gln Thr Ala Gly Ala Leu Phe Ile Ser
1 5 10 15

Pro Ala Leu Ile Arg Cys Cys Thr Arg Gly Leu Ile Arg Pro Val Ser
20 25 30

Ala Ser Phe Leu Asn Ser Pro Val Asn Ser Ser Lys Gln Pro Ser Tyr
35 40 45

Ser Asn Phe Pro Leu Gln Val Ala Arg Arg Glu Phe Gln Thr Ser Val
50 55 60

Val Ser Arg Asp Ile Asp Thr Ala Ala Lys Phe Ile Gly Ala Gly Ala
65 70 75 80

Ala Thr Val Gly Val Ala Gly Ser Gly Ala Gly Ile Gly Thr Val Phe
85 90 95

Gly Ser Leu Ile Ile Gly Tyr Ala Arg Asn Pro Ser Leu Lys Gln Gln
100 105 110

Leu Phe Ser Tyr Ala Ile Leu Gly Phe Ala Leu Ser Glu Ala Met Gly
115 120 125

Leu Phe Cys Leu Met Val Ala Phe Leu Ile Leu Phe Ala Met
130 135 140

<210> 1312

<211> 495

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

1350

<222> (121)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (392)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (460)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1312

Arg Arg Met Glu Gly Gln Asp Glu Val Ser Ala Arg Glu Gln His Phe
1 5 10 15

His Ser Gln Val Arg Glu Ser Thr Ile Cys Phe Leu Leu Phe Ala Ile
20 25 30

Leu Tyr Val Val Ser Tyr Phe Ile Ile Thr Arg Tyr Lys Arg Lys Ser
35 40 45

Asp Glu Gln Glu Asp Glu Asp Ala Ile Val Asn Arg Ile Ser Leu Phe
50 55 60

Leu Ser Thr Phe Thr Leu Ala Val Ser Ala Gly Ala Val Leu Leu Leu
65 70 75 80

Pro Phe Ser Ile Ile Ser Asn Glu Ile Leu Leu Ser Phe Pro Gln Asn
85 90 95

Tyr Tyr Ile Gln Trp Leu Asn Gly Ser Leu Ile His Gly Leu Trp Asn
100 105 110

Leu Ala Ser Leu Phe Ser Asn Leu Xaa Leu Phe Val Leu Met Pro Phe
115 120 125

Ala Phe Phe Phe Leu Glu Ser Glu Gly Phe Ala Gly Leu Lys Lys Gly
130 135 140

Ile Arg Ala Arg Ile Leu Glu Thr Leu Val Met Leu Leu Leu Leu Ala
145 150 155 160

Leu Leu Ile Leu Gly Ile Val Trp Val Ala Ser Ala Leu Ile Asp Asn
165 170 175

Asp Ala Ala Ser Met Glu Ser Leu Tyr Asp Leu Trp Glu Phe Tyr Leu
180 185 190

Pro Tyr Leu Tyr Ser Cys Ile Ser Leu Met Gly Cys Leu Leu Leu Leu

1351

195	200	205
Leu Cys Thr Pro Val Gly 210	Leu Ser Arg Met Phe 215	Thr Val Met Gly Gln 220
Leu Leu Val Lys Pro Thr 225	Ile Leu Glu Asp Leu 230	Asp Glu Gln Ile Tyr 235 240
Ile Ile Thr Leu Glu Glu 245	Glu Ala Leu Gln Arg 250	Arg Leu Asn Gly Leu 255
Ser Ser Ser Val Glu Tyr 260	Asn Ile Met Glu Leu 265	Glu Gln Glu Leu Glu 270
Asn Val Lys Thr Leu Lys 275	Thr Lys Leu Asp Pro 280	Trp Ser Ser Phe Ser 285
Val Leu Gln Ser Pro Val 290	Trp His Phe Ala Ala 295	Gln Thr Pro Ala Asp 300
Ile Val Ser Pro Asp Ser 305	His Phe Met Leu Ser 310	Thr Gln Gly Met Ser 315 320
Trp Ala Gln Leu Val Phe 325	Leu Leu Pro Ala Ser 330	Arg Pro Gly Asn Ser 335
Gln Asp Lys Arg Arg Lys 340	Lys Ala Ser Ala Trp 345	Glu Arg Asn Leu Val 350
Tyr Pro Ala Val Met Val 355	Leu Leu Leu Ile Glu 360	Thr Ser Ile Ser Val 365
Leu Leu Val Ala Cys Asn 370	Ile Leu Cys Leu Leu 375	Val Asp Glu Thr Ala 380
Met Pro Lys Gly Thr Arg 385	Gly Xaa Gly Ile Gly 390	Asn Ala Ser Leu Ser 395 400
Thr Phe Gly Phe Val Gly 405	Ala Ala Leu Glu Ile 410	Ile Ile Leu Ile Phe Tyr 415
Leu Met Val Ser Ser Val 420	Val Gly Phe Tyr Ser 425	Leu Arg Phe Phe Gly 430
Asn Phe Thr Pro Lys Lys 435	Asp Asp Thr Thr Met 440	Thr Lys Ile Ile Gly 445
Asn Cys Val Ser Ile Leu 450	Val Leu Ser Ser Ala 455	Xaa Pro Val Met Ser 460
Arg Thr Leu Gly Leu His 465	Lys Leu His Leu Pro 470	Asn Thr Ser Arg Asp 475

1352

465 470 475 480
 Ser Glu Thr Ala Lys Pro Ser Val Asn Gly His Gln Lys Ala Leu
 485 490 495

 <210> 1313
 <211> 790
 <212> PRT
 <213> Homo sapiens

 <400> 1313
 Gly Thr Arg Gly Thr Ala Thr Glu Arg Leu Lys Met Ile Pro Phe Leu
 1 5 10 15
 Pro Met Phe Ser Leu Leu Leu Leu Ile Val Asn Pro Ile Asn Ala
 20 25 30
 Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser Arg Ile Arg Gly Arg
 35 40 45
 Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln Ile Leu Gly Thr Lys
 50 55 60
 Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr Lys Lys Ser Ile Cys
 65 70 75 80
 Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys Pro Gly Tyr Met Arg
 85 90 95
 Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu Pro Ile Asp His Val
 100 105 110
 Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr Thr Gln Arg Tyr Ser
 115 120 125
 Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly Lys Gly Ser Phe Thr
 130 135 140
 Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn Leu Asp Ser Asp Ile
 145 150 155 160
 Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu Leu Leu Asn Ala Leu
 165 170 175
 His Ser His Met Ile Asn Lys Arg Met Leu Thr Lys Asp Leu Lys Asn
 180 185 190
 Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu Gly Leu Phe Ile Asn
 195 200 205

1353

His Tyr Pro Asn Gly Val Val Thr Val Asn Cys Ala Arg Ile Ile His
210 215 220

Gly Asn Gln Ile Ala Thr Asn Gly Val Val His Val Ile Asp Arg Val
225 230 235 240

Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe Ile Glu Ala Glu Asp
245 250 255

Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr Ser Asp Ile Leu Glu
260 265 270

Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe Ala Pro Thr Asn Glu
275 280 285

Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu Arg Ile Met Gly Asp
290 295 300

Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His Ile Leu Asn Thr Leu
305 310 315 320

Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val Phe Glu Thr Leu Glu
325 330 335

Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp Ser Ile Thr Val Asn
340 345 350

Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val Thr Asn Asn Gly Val
355 360 365

Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp Ser Ala Lys Gln Val
370 375 380

Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe Thr Asp Leu Val Ala
385 390 395 400

Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp Gly Glu Tyr Thr Leu
405 410 415

Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp Thr Leu Ser Met Asp
420 425 430

Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His Ile Leu Lys Val Lys
435 440 445

Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile Leu Glu Thr Ile Gly
450 455 460

Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr Ala Val Cys Ile Glu
465 470 475 480

1354

Asn Ser Cys Met Glu Lys Gly Ser Lys Gln Gly Arg Asn Gly Ala Ile		
485	490	495
His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu Lys Ser Leu His Glu		
500	505	510
Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe Leu Ser Leu Leu Glu		
515	520	525
Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro Gly Asp Trp Thr Leu		
530	535	540
Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met Thr Ser Glu Glu Lys		
545	550	555
Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln Asn Ile Ile Leu Tyr		
565	570	575
His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly Phe Glu Pro Gly Val		
580	585	590
Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys Ile Phe Leu Lys Glu		
595	600	605
Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys Ser Lys Glu Ser Asp		
610	615	620
Ile Met Thr Thr Asn Gly Val Ile His Val Val Asp Lys Leu Leu Tyr		
625	630	635
Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu Leu Glu Ile Leu Asn		
645	650	655
Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val Arg Gly Ser Thr Phe		
660	665	670
Lys Glu Ile Pro Val Thr Val Tyr Lys Pro Ile Ile Lys Lys Tyr Thr		
675	680	685
Lys Ile Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg		
690	695	700
Glu Glu Arg Ile Ile Thr Gly Pro Glu Ile Lys Tyr Thr Arg Ile Ser		
705	710	715
Thr Gly Gly Gly Glu Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu		
725	730	735
Glu Val Thr Lys Val Thr Lys Phe Ile Glu Gly Gly Asp Gly His Leu		
740	745	750

1355

Phe Glu Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val
 755 760 765

Arg Lys Leu Gln Ala Asn Lys Lys Val Gln Gly Ser Arg Arg Arg Leu
 770 775 780

Arg Glu Gly Arg Ser Gln
 785 790

<210> 1314

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (20)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (42)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1314

Thr Ser Trp Ala Phe Asp Glu Thr Gly Xaa Asn Thr Ala Val Phe Leu
 1 5 10 15

Leu Glu Ile Xaa Trp Gly Ile Phe Phe Glu Leu Met Gly Thr Ile Arg
 20 25 30

His Asn Cys Leu His Lys Leu Gly Ile Xaa Asp Phe Gly Ile Thr Ile
 35 40 45

Tyr Gln Asn Gly Asp Ile Ser Pro Leu Val Leu Arg Cys Lys Pro Lys
 50 55 60

Asn Ile Met Thr Ser Phe Gln Ala Ser
 65 70

<210> 1315

1356

<211> 268

<212> PRT

<213> Homo sapiens

<400> 1315

Pro Gly Arg Pro Thr Arg Pro Arg Thr Arg Gly Ile Asn Lys Leu Ile
1 5 10 15

Arg Ile Gly Arg Asn Glu Cys Val Val Ile Arg Val Asp Lys Glu
20 25 30

Lys Gly Tyr Ile Asp Leu Ser Lys Arg Arg Val Ser Pro Glu Glu Ala
35 40 45

Ile Lys Cys Glu Asp Lys Phe Thr Lys Ser Lys Thr Val Tyr Ser Ile
50 55 60

Leu Arg His Val Ala Glu Val Leu Glu Tyr Thr Lys Asp Glu Gln Leu
65 70 75 80

Glu Ser Leu Phe Gln Arg Thr Ala Trp Val Phe Asp Asp Lys Tyr Lys
85 90 95

Arg Pro Gly Tyr Gly Ala Tyr Asp Ala Phe Lys His Ala Val Ser Asp
100 105 110

Pro Ser Ile Leu Asp Ser Leu Asp Leu Asn Glu Asp Glu Arg Glu Val
115 120 125

Leu Ile Asn Asn Ile Asn Arg Arg Leu Thr Pro Gln Ala Val Lys Ile
130 135 140

Arg Ala Asp Ile Glu Val Ala Cys Tyr Gly Tyr Glu Gly Ile Asp Ala
145 150 155 160

Val Lys Glu Ala Leu Arg Ala Gly Leu Asn Cys Ser Thr Glu Asn Met
165 170 175

Pro Ile Lys Ile Asn Leu Ile Ala Pro Pro Arg Tyr Val Met Thr Thr
180 185 190

Thr Thr Leu Glu Arg Thr Glu Gly Leu Ser Val Leu Ser Gln Ala Met
195 200 205

Ala Val Ile Lys Glu Lys Ile Glu Glu Lys Arg Gly Val Phe Asn Val
210 215 220

Gln Met Glu Pro Lys Val Val Thr Asp Thr Asp Glu Thr Glu Leu Ala
225 230 235 240

Arg Gln Met Glu Arg Leu Glu Arg Glu Asn Ala Glu Val Asp Gly Asp

1357

245

250

255

Asp Asp Ala Glu Glu Met Glu Ala Lys Ala Glu Asp
 260 265

<210> 1316

<211> 315

<212> PRT

<213> Homo sapiens

<400> 1316

Gly Gln Arg Ala Gly Met Pro His Ala Gln Gly Gly Trp Ser Gly Pro
 1 5 10 15

Ala Ala Asp Ser Ala Glu Pro Ala Leu Pro Ala Gly Glu Pro Gly Gly
 20 25 30

Pro Thr Leu Met Arg Leu Asn Ser Val Gln Ser Ser Glu Arg Pro Leu
 35 40 45

Phe Leu Val His Pro Ile Glu Gly Ser Thr Thr Val Phe His Ser Leu
 50 55 60

Ala Ser Arg Leu Ser Ile Pro Thr Tyr Gly Leu Gln Cys Thr Arg Ala
 65 70 75 80

Ala Pro Leu Asp Ser Ile His Ser Leu Ala Ala Tyr Tyr Ile Asp Cys
 85 90 95

Ile Arg Gln Val Gln Pro Glu Gly Pro Tyr Arg Val Ala Gly Tyr Ser
 100 105 110

Tyr Gly Ala Cys Val Ala Phe Glu Met Cys Ser Gln Leu Gln Ala Gln
 115 120 125

Gln Ser Pro Ala Pro Thr His Asn Ser Leu Phe Leu Phe Asp Gly Ser
 130 135 140

Pro Thr Tyr Val Leu Ala Tyr Thr Gln Ser Tyr Arg Ala Lys Leu Thr
 145 150 155 160

Pro Gly Cys Glu Ala Glu Ala Glu Thr Glu Ala Ile Cys Phe Phe Val
 165 170 175

Gln Gln Phe Thr Asp Met Glu His Asn Arg Val Leu Glu Ala Leu Leu
 180 185 190

Pro Leu Lys Gly Leu Glu Glu Arg Val Ala Ala Ala Val Asp Leu Ile
 195 200 205

1358

Ile Lys Ser His Gln Gly Leu Asp Arg Gln Glu Leu Ser Phe Ala Ala
210 215 220

Arg Ser Phe Tyr Tyr Lys Leu Arg Ala Ala Glu Gln Tyr Thr Pro Lys
225 230 235 240

Ala Lys Tyr His Gly Asn Val Met Leu Leu Arg Ala Lys Thr Gly Gly
245 250 255

Ala Tyr Gly Glu Asp Leu Gly Ala Asp Tyr Asn Leu Ser Gln Val Cys
260 265 270

Asp Gly Lys Val Ser Val His Val Ile Glu Gly Asp His Arg Thr Leu
275 280 285

Leu Glu Gly Ser Gly Leu Glu Ser Ile Ile Ser Ile Ile His Ser Ser
290 295 300

Leu Ala Glu Pro Arg Val Ser Val Arg Glu Gly
305 310 315

<210> 1317

<211> 191

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (20)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1359

<222> (25)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (186)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1317

Thr Thr Xaa Val Xaa Asp Arg Leu Leu Xaa Thr Ser Gly Ser Pro Gly
1 5 10 15

Thr Asp Arg Xaa Phe Gly His Glu Xaa Glu Met Ala Pro Asn Ala Ser
20 25 30

Cys Leu Cys Val His Val Arg Ser Glu Glu Trp Asp Leu Met Thr Phe
35 40 45

Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys Ile Lys Glu His Val Arg
50 55 60

Ser Lys Thr Lys Val Pro Val Gln Asp Gln Val Leu Leu Leu Gly Ser
65 70 75 80

Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser Ser Tyr Gly Ile Asp Lys
85 90 95

Glu Lys Thr Ile His Leu Thr Leu Lys Val Val Lys Pro Ser Asp Glu
100 105 110

Glu Leu Pro Leu Phe Leu Val Glu Ser Gly Asp Glu Ala Lys Arg His
115 120 125

Leu Leu Gln Val Arg Arg Ser Ser Ser Val Ala Gln Val Lys Ala Met
130 135 140

Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu Thr Gln Ile Val Thr Cys
145 150 155 160

Asn Gly Lys Arg Leu Glu Asp Gly Lys Met Met Ala Asp Tyr Gly Ile
165 170 175

Arg Lys Gly Asn Leu Leu Phe Leu Ala Xaa Tyr Cys Ile Gly Gly
180 185 190

<210> 1318

<211> 230

<212> PRT

<213> Homo sapiens

1360

<400> 1318

Arg Asn Leu Gln Glu Thr Ala Ile Met Ala Glu Lys Pro Lys Leu His
 1 5 10 15

Tyr Phe Asn Ala Arg Gly Arg Met Glu Ser Thr Arg Trp Leu Leu Ala
 20 25 30

Ala Ala Gly Val Glu Phe Glu Glu Lys Phe Ile Lys Ser Ala Glu Asp
 35 40 45

Leu Asp Lys Leu Arg Asn Asp Gly Tyr Leu Met Phe Gln Gln Val Pro
 50 55 60

Met Val Glu Ile Asp Gly Met Lys Leu Val Gln Thr Arg Ala Ile Leu
 65 70 75 80

Asn Tyr Ile Ala Ser Lys Tyr Asn Leu Tyr Gly Lys Asp Ile Lys Glu
 85 90 95

Arg Ala Leu Ile Asp Met Tyr Ile Glu Gly Ile Ala Asp Leu Gly Glu
 100 105 110

Met Ile Leu Leu Leu Pro Val Cys Pro Pro Glu Glu Lys Asp Ala Lys
 115 120 125

Leu Ala Leu Ile Lys Glu Lys Ile Lys Asn Arg Tyr Phe Pro Ala Phe
 130 135 140

Glu Lys Val Leu Lys Ser His Gly Gln Asp Tyr Leu Val Gly Asn Lys
 145 150 155 160

Leu Ser Arg Ala Asp Ile His Leu Val Glu Leu Leu Tyr Tyr Val Glu
 165 170 175

Glu Leu Asp Ser Ser Leu Ile Ser Ser Phe Pro Leu Leu Lys Ala Leu
 180 185 190

Lys Thr Arg Ile Ser Asn Leu Pro Thr Val Lys Lys Phe Leu Gln Pro
 195 200 205

Gly Ser Pro Arg Lys Pro Pro Met Asp Glu Lys Ser Leu Glu Glu Ala
 210 215 220

Arg Lys Ile Phe Arg Phe
 225 230

<210> 1319

<211> 279

1361

<212> PRT

<213> Homo sapiens

<400> 1319

Glu Gly Pro Ala Glu Gly Asn Met Ala Ala Lys Val Phe Glu Ser Ile
 1 5 10 15
 Gly Lys Phe Gly Leu Ala Leu Ala Val Ala Gly Gly Val Val Asn Ser
 20 25 30
 Ala Leu Tyr Asn Val Asp Ala Gly His Arg Ala Val Ile Phe Asp Arg
 35 40 45
 Phe Arg Gly Val Gln Asp Ile Val Val Gly Glu Gly Thr His Phe Leu
 50 55 60
 Ile Pro Trp Val Gln Lys Pro Ile Ile Phe Asp Cys Arg Ser Arg Pro
 65 70 75 80
 Arg Asn Val Pro Val Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Asn
 85 90 95
 Ile Thr Leu Arg Ile Leu Phe Arg Pro Val Ala Ser Gln Leu Pro Arg
 100 105 110
 Ile Phe Thr Ser Ile Gly Glu Asp Tyr Asp Glu Arg Val Leu Pro Ser
 115 120 125
 Ile Thr Thr Glu Ile Leu Lys Ser Val Val Ala Arg Phe Asp Ala Gly
 130 135 140
 Glu Leu Ile Thr Gln Arg Glu Leu Val Ser Arg Gln Val Ser Asp Asp
 145 150 155 160
 Leu Thr Glu Arg Ala Ala Thr Phe Gly Leu Ile Leu Asp Asp Val Ser
 165 170 175
 Leu Thr His Leu Thr Phe Gly Lys Glu Phe Thr Glu Ala Val Glu Ala
 180 185 190
 Lys Gln Val Ala Gln Gln Glu Ala Glu Arg Ala Arg Phe Val Val Glu
 195 200 205
 Lys Ala Glu Gln Gln Lys Lys Ala Ala Ile Ile Ser Ala Glu Gly Asp
 210 215 220
 Ser Lys Ala Ala Glu Leu Ile Ala Asn Ser Leu Ala Thr Ala Gly Asp
 225 230 235 240
 Gly Leu Ile Glu Leu Arg Lys Leu Glu Ala Ala Glu Asp Ile Ala Tyr
 245 250 255

1362

Gln Leu Ser Arg Ser Arg Asn Ile Thr Tyr Leu Pro Ala Gly Gln Ser
260 265 270

Val Leu Leu Gln Leu Pro Gln
275

<210> 1320

<211> 406

<212> PRT

<213> Homo sapiens

<400> 1320

Val Thr Ala Cys Ala Ala Pro Ala Ala Trp Leu Pro Ile Leu Val Ala
1 5 10 15

Asp Ile Trp Ser Ser Tyr Asn Met Ala Asp Ile Asp Asn Lys Glu Gln
20 25 30

Ser Glu Leu Asp Gln Asp Leu Asp Asp Val Glu Glu Val Glu Glu Glu
35 40 45

Glu Thr Gly Glu Glu Thr Lys Leu Lys Ala Arg Gln Leu Thr Val Gln
50 55 60

Met Met Gln Asn Pro Gln Ile Leu Ala Ala Leu Gln Glu Arg Leu Asp
65 70 75 80

Gly Leu Val Glu Thr Pro Thr Gly Tyr Ile Glu Ser Leu Pro Arg Val
85 90 95

Val Lys Arg Arg Val Asn Ala Leu Lys Asn Leu Gln Val Lys Cys Ala
100 105 110

Gln Ile Glu Ala Lys Phe Tyr Glu Glu Val His Asp Leu Glu Arg Lys
115 120 125

Tyr Ala Val Leu Tyr Gln Pro Leu Phe Asp Lys Arg Phe Glu Ile Ile
130 135 140

Asn Ala Ile Tyr Glu Pro Thr Glu Glu Glu Cys Glu Trp Lys Pro Asp
145 150 155 160

Glu Glu Asp Glu Ile Ser Glu Glu Leu Lys Glu Lys Ala Lys Ile Glu
165 170 175

Asp Glu Lys Lys Asp Glu Glu Lys Glu Asp Pro Lys Gly Ile Pro Glu
180 185 190

1363

Phe Trp Leu Thr Val Phe Lys Asn Val Asp Leu Leu Ser Asp Met Val
 195 200 205
 Gln Glu His Asp Glu Pro Ile Leu Lys His Leu Lys Asp Ile Lys Val
 210 215 220
 Lys Phe Ser Asp Ala Gly Gln Pro Met Ser Phe Val Leu Glu Phe His
 225 230 235 240
 Phe Glu Pro Asn Glu Tyr Phe Thr Asn Glu Val Leu Thr Lys Thr Tyr
 245 250 255
 Arg Met Arg Ser Glu Pro Asp Asp Ser Asp Pro Phe Ser Phe Asp Gly
 260 265 270
 Pro Glu Ile Met Gly Cys Thr Gly Cys Gln Ile Asp Trp Lys Lys Gly
 275 280 285
 Lys Asn Val Thr Leu Lys Thr Ile Lys Lys Lys Gln Lys His Lys Gly
 290 295 300
 Arg Gly Thr Val Arg Thr Val Thr Lys Thr Val Ser Asn Asp Ser Phe
 305 310 315 320
 Phe Asn Phe Phe Ala Pro Pro Glu Val Pro Glu Ser Gly Asp Leu Asp
 325 330 335
 Asp Asp Ala Glu Ala Ile Leu Ala Ala Asp Phe Glu Ile Gly His Phe
 340 345 350
 Leu Arg Glu Arg Ile Ile Pro Arg Ser Val Leu Tyr Phe Thr Gly Glu
 355 360 365
 Ala Ile Glu Asp Asp Asp Asp Asp Tyr Asp Glu Glu Gly Glu Glu Ala
 370 375 380
 Asp Glu Gly Tyr Gln Leu Phe Glu Glu Val Lys Ser Cys Ser Lys Leu
 385 390 395 400
 Phe Gln Arg Trp Leu Gln
 405

<210> 1321

<211> 173

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

1364

<222> (55)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1321

Gln Ser Ala Cys Ser Leu Leu Pro Glu Met Pro Arg Ile Leu Thr Arg
 1 5 10 15

Thr Pro Ser Ser Arg Met Ile Val Leu Arg Leu Met Pro Val Gly Gly
 20 25 30

Arg Arg Pro Ile Val Thr Ser Phe Gly Gly Cys Ser Thr Ala Pro Arg
 35 40 45

Ala Asn Phe Pro Leu Pro Xaa Pro Ala Leu Arg Gln Ser Arg Ser Lys
 50 55 60

Met Ala Val Val Gly Val Ser Ser Val Ser Arg Leu Leu Gly Arg Ser
 65 70 75 80

Arg Pro Gln Leu Gly Arg Pro Met Ser Ser Gly Ala His Gly Glu Glu
 85 90 95

Gly Ser Ala Arg Met Trp Lys Thr Leu Thr Phe Phe Val Ala Leu Pro
 100 105 110

Gly Val Ala Val Ser Met Leu Asn Val Tyr Leu Lys Ser His His Gly
 115 120 125

Glu His Glu Arg Pro Glu Phe Ile Ala Tyr Pro His Leu Arg Ile Arg
 130 135 140

Thr Lys Pro Phe Pro Trp Gly Asp Gly Asn His Thr Leu Phe His Asn
 145 150 155 160

Pro His Val Asn Pro Leu Pro Thr Gly Tyr Glu Asp Glu
 165 170

<210> 1322

<211> 209

<212> PRT

<213> Homo sapiens

<400> 1322

Lys Thr Gln Ala Ala Ser Val Glu Ala Val Lys Met Leu Asp Glu Ile
 1 5 10 15

Leu Leu Gln Leu Ser Ala Ser Val Pro Val Asp Val Met Pro Gly Glu
 20 25 30

1365

Phe Asp Pro Thr Asn Tyr Thr Leu Pro Gln Gln Pro Leu His Pro Cys
 35 40 45
 Met Phe Pro Leu Ala Thr Ala Tyr Ser Thr Leu Gln Leu Val Thr Asn
 50 55 60
 Pro Tyr Gln Ala Thr Ile Asp Gly Val Arg Phe Leu Gly Thr Ser Gly
 65 70 75 80
 Gln Asn Val Ser Asp Ile Phe Arg Tyr Ser Ser Met Glu Asp His Leu
 85 90 95
 Glu Ile Leu Glu Trp Thr Leu Arg Val Arg His Ile Ser Pro Thr Ala
 100 105 110
 Pro Asp Thr Leu Gly Cys Tyr Pro Phe Tyr Lys Thr Asp Pro Phe Ile
 115 120 125
 Phe Pro Glu Cys Pro His Val Tyr Phe Cys Gly Asn Thr Pro Ser Phe
 130 135 140
 Gly Ser Lys Ile Ile Arg Gly Pro Glu Asp Gln Thr Val Leu Leu Val
 145 150 155 160
 Thr Val Pro Asp Phe Ser Ala Thr Gln Thr Ala Cys Leu Val Asn Leu
 165 170 175
 Arg Ser Leu Ala Cys Gln Pro Ile Ser Phe Ser Gly Phe Gly Ala Glu
 180 185 190
 Asp Asp Asp Leu Gly Gly Leu Gly Trp Ala Pro Asp Ser Lys Lys Trp
 195 200 205
 Phe

<210> 1323

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (30)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (57)

1366

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1323

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Asn Asn Val Ala Thr Thr His Glu Pro Ala Ser Val Pro Ala Pro Gln
 1             5             10             15

Gly Asp Leu Leu Ser Gly Ala Glu Pro Glu Gly Gly Asn Xaa Ala Arg
      20             25             30

Arg Pro Pro Gly Ala Arg Glu Gln Pro Gln Ser Pro Pro Pro Ala Arg
      35             40             45

Gly Gly Ala Gly Ser Leu Ala Thr Xaa Ala Pro Pro Ser Ser Gly Leu
 50             55             60

Ser Cys Pro Gly Cys Phe Arg Leu Arg Leu Trp Met Leu Arg Leu Ser
 65             70             75             80

Glu Arg Asn Met Lys Val Leu Leu Ala Ala Ala Leu Ile Ala Gly Ser
      85             90             95

Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala Ala Asp Glu Lys Lys
      100             105             110

Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe Asp Leu Arg Ile Gly
      115             120             125

Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu Phe Gly Lys Thr Val
      130             135             140

Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala Thr Gly Glu Lys Gly
      145             150             155             160

Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val Ile Lys Asp Phe Met
      165             170             175

Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly Thr Gly Gly Lys Ser
      180             185             190

Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe Lys Leu Lys His Tyr
      195             200             205

Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly Lys Asp Thr Asn Gly
      210             215             220

Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala Trp Leu Asp Gly Lys
      225             230             235             240

His Val Val Phe Gly Lys Val Leu Glu Gly Met Glu Val Val Arg Lys
      245             250             255

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1367

Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys Pro Leu Lys Asp Val
 260 265 270

Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu Lys Pro Phe Ala Ile
 275 280 285

Ala Lys Glu
 290

<210> 1324

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1324

Glu Cys Leu Val Arg Ser Lys Asn Ile Thr Gln Ile Val Gly His Ser
 1 5 10 15

Gly Cys Glu Ala Lys Ser Ile Gln Asn Arg Ala Cys Leu Gly Gln Cys
 20 25 30

Phe Ser Tyr Ser Val Pro Asn Thr Phe Pro Gln Ser Thr Glu Ser Leu
 35 40 45

Val His Cys Asp Ser Cys Met Pro Ala Gln Ser Met Trp Glu Ile Val
 50 55 60

Thr Leu Glu Cys Pro Gly His Glu Glu Val Pro Arg Val Asp Lys Leu
 65 70 75 80

Val Glu Lys Ile Leu His Cys Ser Cys Gln Ala Cys Gly Lys Glu Pro
 85 90 95

Ser His Glu Gly Leu Ser Val Tyr Val Gln Gly Glu Asp Gly Pro Gly
 100 105 110

Ser Gln Pro Gly Thr His Pro His Pro His Pro His Pro His Pro Gly
 115 120 125

Gly Gln Thr Pro Glu Pro Glu Asp Pro Pro Gly Ala Pro His Thr Glu
 130 135 140

Glu Glu Gly Ala Glu Asp
 145 150

<210> 1325

<211> 56

1368

<212> PRT

<213> Homo sapiens

<400> 1325

Glu Ile Asn Ile Ser Arg Lys Gly Glu Ser Arg Phe Tyr Lys Met Ser
1 5 10 15

Gln Leu Ser Asn Ile Trp Gly Ser Asp Ser Phe Phe Val Arg Thr Phe
20 25 30

Glu Thr Ser Lys Gln Pro Leu Phe Leu Lys Asn Ser Gly Phe Thr Leu
35 40 45

Thr His Val Ser Phe Thr Pro Phe
50 55

<210> 1326

<211> 486

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (34)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (438)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (447)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1326

Arg Leu Pro Leu Gly Ser Arg Ser Pro Ser Glu Ala Ala Gly Ala Glu
1 5 10 15

Thr Ala Pro Ser Ser Leu Ser Ala Ala Met Thr Pro Leu Val Ser Arg
20 25 30

Leu Xaa Arg Leu Trp Ala Ile Met Arg Lys Pro Arg Ala Ala Val Gly
35 40 45

Ser Gly His Arg Lys Gln Ala Ala Ser Gln Glu Gly Arg Gln Lys His
50 55 60

1369

Ala Lys Asn Asn Ser Gln Ala Lys Pro Ser Ala Cys Asp Gly Leu Ala
 65 70 75 80
 Arg Gln Pro Glu Glu Val Val Leu Gln Ala Ser Val Ser Ser Tyr His
 85 90 95
 Leu Phe Arg Asp Val Ala Glu Val Thr Ala Phe Arg Gly Ser Leu Leu
 100 105 110
 Ser Trp Tyr Asp Gln Glu Lys Arg Asp Leu Pro Trp Arg Arg Arg Ala
 115 120 125
 Glu Asp Glu Met Asp Leu Asp Arg Arg Ala Tyr Ala Val Trp Val Ser
 130 135 140
 Glu Val Met Leu Gln Gln Thr Gln Val Ala Thr Val Ile Asn Tyr Tyr
 145 150 155 160
 Thr Gly Trp Met Gln Lys Trp Pro Thr Leu Gln Asp Leu Ala Ser Ala
 165 170 175
 Ser Leu Glu Glu Val Asn Gln Leu Trp Ala Gly Leu Gly Tyr Tyr Ser
 180 185 190
 Arg Gly Arg Arg Leu Gln Glu Gly Ala Arg Lys Val Val Glu Glu Leu
 195 200 205
 Gly Gly His Met Pro Arg Thr Ala Glu Thr Leu Gln Gln Leu Leu Pro
 210 215 220
 Gly Val Gly Arg Tyr Thr Ala Gly Ala Ile Ala Ser Ile Ala Phe Gly
 225 230 235 240
 Gln Ala Thr Gly Val Val Asp Gly Asn Val Ala Arg Val Leu Cys Arg
 245 250 255
 Val Arg Ala Ile Gly Ala Asp Pro Ser Ser Thr Leu Val Ser Gln Gln
 260 265 270
 Leu Trp Gly Leu Ala Gln Gln Leu Val Asp Pro Ala Arg Pro Gly Asp
 275 280 285
 Phe Asn Gln Ala Ala Met Glu Leu Gly Ala Thr Val Cys Thr Pro Gln
 290 295 300
 Arg Pro Leu Cys Ser Gln Cys Pro Val Glu Ser Leu Cys Arg Ala Arg
 305 310 315 320
 Gln Arg Val Glu Gln Glu Gln Leu Leu Ala Ser Gly Ser Leu Ser Gly
 325 330 335

1370

Ser Pro Asp Val Glu Glu Cys Ala Pro Asn Thr Gly Gln Cys His Leu
 340 345 350
 Cys Leu Pro Pro Ser Glu Pro Trp Asp Gln Thr Leu Gly Val Val Asn
 355 360 365
 Phe Pro Arg Lys Ala Ser Arg Lys Pro Pro Arg Glu Glu Ser Ser Ala
 370 375 380
 Thr Cys Val Leu Glu Gln Pro Gly Ala Leu Gly Ala Gln Ile Leu Leu
 385 390 395 400
 Val Gln Arg Pro Asn Ser Gly Leu Leu Ala Gly Leu Trp Glu Phe Pro
 405 410 415
 Ser Val Thr Trp Glu Pro Ser Glu Gln Leu Gln Arg Lys Ala Leu Leu
 420 425 430
 Gln Glu Leu Gln Arg Xaa Ala Gly Pro Leu Pro Ala Thr His Xaa Arg
 435 440 445
 His Leu Gly Glu Val Val His Thr Phe Ser His Ile Lys Leu Thr Tyr
 450 455 460
 Gln Val Tyr Gly Leu Ala Leu Glu Gly Gln Thr Pro Val Thr Thr Val
 465 470 475 480
 Pro Pro Gly Ala Arg Cys
 485

<210> 1327

<211> 88

<212> PRT

<213> Homo sapiens

<400> 1327

Lys Thr Leu Phe Thr Tyr Ser Phe His Gly Tyr Asn Thr Leu Ala Asp
 1 5 10 15
 Phe Leu Leu Ala Leu Gly Ala Met Ile Leu Ile Thr Phe Cys Lys Val
 20 25 30
 Thr Asn Val Ile His Ser Thr Leu Cys Gly Ser His Leu Phe Arg Leu
 35 40 45
 Met Cys Phe Gly Glu Arg Lys Lys Phe Leu Ala Glu Tyr Tyr Phe Glu
 50 55 60
 Leu Ser Arg Thr Leu Ser His Gln Arg Gln Phe Phe Ser Val Gln Phe

65 70 75 80

Pro Ile Pro Asp Asn Leu Leu Lys
85

<210> 1328
<211> 424
<212> PRT
<213> Homo sapiens

<400> 1328
Ile Arg Val Ser Phe Met Asn Asn Gln Lys Gln Gln Lys Pro Thr Leu
1 5 10 15
Ser Gly Gln Arg Phe Lys Thr Arg Lys Arg Asp Glu Lys Glu Arg Phe
20 25 30
Asp Pro Thr Gln Phe Gln Asp Cys Ile Ile Gln Gly Leu Thr Glu Thr
35 40 45
Gly Thr Asp Leu Glu Ala Val Ala Lys Phe Leu Asp Ala Ser Gly Ala
50 55 60
Lys Leu Asp Tyr Arg Arg Tyr Ala Glu Thr Leu Phe Asp Ile Leu Val
65 70 75 80
Ala Gly Gly Met Leu Ala Pro Gly Gly Thr Leu Ala Asp Asp Met Met
85 90 95
Arg Thr Asp Val Cys Val Phe Ala Ala Gln Glu Asp Leu Glu Thr Met
100 105 110
Gln Ala Phe Ala Gln Val Phe Asn Lys Leu Ile Arg Arg Tyr Lys Tyr
115 120 125
Leu Glu Lys Gly Phe Glu Asp Glu Val Lys Lys Leu Leu Leu Phe Leu
130 135 140
Lys Gly Phe Ser Glu Ser Glu Arg Asn Lys Leu Ala Met Leu Thr Gly
145 150 155 160
Val Leu Leu Ala Asn Gly Thr Leu Asn Ala Ser Ile Leu Asn Ser Leu
165 170 175
Tyr Asn Glu Asn Leu Val Lys Glu Gly Val Ser Ala Ala Phe Ala Val
180 185 190
Lys Leu Phe Lys Ser Trp Ile Asn Glu Lys Asp Ile Asn Ala Val Ala
195 200 205

1372

Ala Ser Leu Arg Lys Val Ser Met Asp Asn Arg Leu Met Glu Leu Phe
210 215 220

Pro Ala Asn Lys Gln Ser Val Glu His Phe Thr Lys Tyr Phe Thr Glu
225 230 235 240

Ala Gly Leu Lys Glu Leu Ser Glu Tyr Val Arg Asn Gln Gln Thr Ile
245 250 255

Gly Ala Arg Lys Glu Leu Gln Lys Glu Leu Gln Glu Gln Met Ser Arg
260 265 270

Gly Asp Pro Phe Lys Asp Ile Ile Leu Tyr Val Lys Glu Glu Met Lys
275 280 285

Lys Asn Asn Ile Pro Glu Pro Val Val Ile Gly Ile Val Trp Ser Ser
290 295 300

Val Met Ser Thr Val Glu Trp Asn Lys Lys Glu Glu Leu Val Ala Glu
305 310 315 320

Gln Ala Ile Lys His Leu Lys Gln Tyr Ser Pro Leu Leu Ala Ala Phe
325 330 335

Thr Thr Gln Gly Gln Ser Glu Leu Thr Leu Leu Leu Lys Ile Gln Glu
340 345 350

Tyr Cys Tyr Asp Asn Ile His Phe Met Lys Ala Phe Gln Lys Ile Val
355 360 365

Val Leu Phe Tyr Lys Ala Glu Val Leu Ser Glu Glu Pro Ile Leu Lys
370 375 380

Trp Tyr Lys Asp Ala His Val Ala Lys Gly Lys Ser Val Phe Leu Glu
385 390 395 400

Gln Met Lys Lys Phe Val Glu Trp Leu Lys Asn Ala Glu Glu Glu Ser
405 410 415

Glu Ser Glu Ala Glu Glu Gly Asp
420

<210> 1329

<211> 558

<212> PRT

<213> Homo sapiens

<400> 1329

1373

Trp Tyr Cys Ser Val Gly Leu Ala Ser Thr Ala Gly Glu Gln Ala Ala
 1 5 10 15
 Ala Val Ala Ala Ala Phe Ser Leu His Pro Asp Tyr Ala Met Leu Gly
 20 25 30
 Phe Val Gly Arg Val Ala Ala Ala Pro Ala Ser Gly Ala Leu Arg Arg
 35 40 45
 Leu Thr Pro Ser Ala Ser Leu Pro Pro Ala Gln Leu Leu Leu Arg Ala
 50 55 60
 Ala Pro Thr Ala Val His Pro Val Arg Asp Tyr Ala Ala Gln Thr Ser
 65 70 75 80
 Pro Ser Pro Lys Ala Gly Ala Ala Thr Gly Arg Ile Val Ala Val Ile
 85 90 95
 Gly Ala Val Val Asp Val Gln Phe Asp Glu Gly Leu Pro Pro Ile Leu
 100 105 110
 Asn Ala Leu Glu Val Gln Gly Arg Glu Thr Arg Leu Val Leu Glu Val
 115 120 125
 Ala Gln His Leu Gly Glu Ser Thr Val Arg Thr Ile Ala Met Asp Gly
 130 135 140
 Thr Glu Gly Leu Val Arg Gly Gln Lys Val Leu Asp Ser Gly Ala Pro
 145 150 155 160
 Ile Lys Ile Pro Val Gly Pro Glu Thr Leu Gly Arg Ile Met Asn Val
 165 170 175
 Ile Gly Glu Pro Ile Asp Glu Arg Gly Pro Ile Lys Thr Lys Gln Phe
 180 185 190
 Ala Pro Ile His Ala Glu Ala Pro Glu Phe Met Glu Met Ser Val Glu
 195 200 205
 Gln Glu Ile Leu Val Thr Gly Ile Lys Val Val Asp Leu Leu Ala Pro
 210 215 220
 Tyr Ala Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly
 225 230 235 240
 Lys Thr Val Leu Ile Met Glu Leu Ile Asn Asn Val Ala Lys Ala His
 245 250 255
 Gly Gly Tyr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly
 260 265 270

1374

Asn Asp Leu Tyr His Glu Met Ile Glu Ser Gly Val Ile Asn Leu Lys
275 280 285

Asp Ala Thr Ser Lys Val Ala Leu Val Tyr Gly Gln Met Asn Glu Pro
290 295 300

Pro Gly Ala Arg Ala Arg Val Ala Leu Thr Gly Leu Thr Val Ala Glu
305 310 315 320

Tyr Phe Arg Asp Gln Glu Gly Gln Asp Val Leu Leu Phe Ile Asp Asn
325 330 335

Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Ala Leu Leu Gly
340 345 350

Arg Ile Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Thr Asp Met
355 360 365

Gly Thr Met Gln Glu Arg Ile Thr Thr Thr Lys Lys Gly Ser Ile Thr
370 375 380

Ser Val Gln Ala Ile Tyr Val Pro Ala Asp Asp Leu Thr Asp Pro Ala
385 390 395 400

Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Val Leu Ser Arg
405 410 415

Ala Ile Ala Glu Leu Gly Ile Tyr Pro Ala Val Asp Pro Leu Asp Ser
420 425 430

Thr Ser Arg Ile Met Asp Pro Asn Ile Val Gly Ser Glu His Tyr Asp
435 440 445

Val Ala Arg Gly Val Gln Lys Ile Leu Gln Asp Tyr Lys Ser Leu Gln
450 455 460

Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys
465 470 475 480

Leu Thr Val Ser Arg Ala Arg Lys Ile Gln Arg Phe Leu Ser Gln Pro
485 490 495

Phe Gln Val Ala Glu Val Phe Thr Gly His Met Gly Lys Leu Val Pro
500 505 510

Leu Lys Glu Thr Ile Lys Gly Phe Gln Gln Ile Leu Ala Gly Glu Tyr
515 520 525

Asp His Leu Pro Glu Gln Ala Phe Tyr Met Val Gly Pro Ile Glu Glu
530 535 540

1375

Ala Val Ala Lys Ala Asp Lys Leu Ala Glu Glu His Ser Ser
545 550 555

<210> 1330
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1330
Thr Thr Pro Leu Ser Gln Ile Val Ala Arg Gly Leu Ile Ala Arg Gly
1 5 10 15
Val Pro Gly Ala Ile Val Asn Val Ser Ser Gln Cys Ser Gln Arg Ala
20 25 30
Val Thr Asn His Ser Val Tyr Cys Ser Thr Lys Gly Ala Leu Asp Met
35 40 45
Leu Thr Lys Val Met Ala Leu Glu Leu Gly Pro His Lys Ile Arg Val
50 55 60
Asn Ala Val Asn Pro Thr Val Val Met Thr Ser Met Gly Gln Ala Thr
65 70 75 80
Trp Ser Asp Pro His Lys Ala Lys Thr Met Leu Asn Arg Ile Pro Leu
85 90 95
Gly Lys Phe Ala Glu Val Glu His Val Val Asn Ala Ile Leu Phe Leu
100 105 110
Leu Ser Asp Arg Ser Gly Met Thr Thr Gly Ser Thr Leu Pro Val Glu
115 120 125
Gly Gly Phe Trp Ala Cys
130

<210> 1331
<211> 188
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (135)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>

1376

<221> SITE

<222> (137)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1331

Ile Arg His Glu Pro Ser Arg Cys Arg Ser Arg Thr Ala Ala Val Cys
 1 5 10 15

Ser Pro Pro Pro Cys Pro Pro Trp Arg Arg Pro Arg Gly Pro Trp Thr
 20 25 30

Ala Lys Ser Pro Pro Trp Pro Pro Ala Arg Pro Arg Trp Gln Trp Thr
 35 40 45

Arg Ala Leu Asn Ser Thr Ala Ala Pro Pro Arg Ser Pro Pro Ala Pro
 50 55 60

Cys Pro Cys Arg Pro Asn Ser Ala Arg Arg Lys Arg Arg Pro Pro Ala
 65 70 75 80

Asn Cys Arg Ala Ser Ser Gly Trp Leu Ala Ala Trp Lys Pro Ser Arg
 85 90 95

Thr Gly Pro Ala Ala Arg Pro Arg Arg Pro Val Pro Asp Thr Ser Phe
 100 105 110

His Ser Ser Pro Val Gln Ala Ala Val His Phe Val Gly Tyr Lys Ile
 115 120 125

Asn His Gly Pro Ala Met Xaa Leu Xaa Phe Leu Leu Gln Leu Arg Leu
 130 135 140

Gly Arg Gly Pro Gly Leu Pro Arg Glu Asn Val Leu Glu Thr Ala Pro
 145 150 155 160

Val Phe Leu Ala Trp Phe Ile Cys Pro Gly Ser Gly Ser Asp Ser Gly
 165 170 175

Gly Ser Glu Thr Ser Val Ala Leu Ser Tyr Trp Gly
 180 185

<210> 1332

<211> 237

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (5)

1377

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1332

Asp Asp Arg Arg Xaa Asp Ala Glu Ala Asp Lys Met Ala Ala Ala Ala
 1 5 10 15

Val Gln Gly Gly Arg Ser Gly Gly Ser Gly Gly Cys Ser Gly Ala Gly
 20 25 30

Gly Ala Ser Asn Cys Gly Thr Gly Ser Gly Arg Ser Gly Leu Leu Asp
 35 40 45

Lys Trp Lys Ile Asp Asp Lys Pro Val Lys Ile Asp Lys Trp Asp Gly
 50 55 60

Ser Ala Val Lys Asn Ser Leu Asp Asp Ser Ala Lys Lys Val Leu Leu
 65 70 75 80

Glu Lys Tyr Lys Tyr Val Glu Asn Phe Gly Leu Ile Asp Gly Arg Leu
 85 90 95

Thr Ile Cys Thr Ile Ser Cys Phe Phe Ala Ile Val Ala Leu Ile Trp
 100 105 110

Asp Tyr Met His Pro Phe Pro Glu Ser Lys Pro Val Leu Ala Leu Cys
 115 120 125

Val Ile Ser Tyr Phe Val Met Met Gly Ile Leu Thr Ile Tyr Thr Ser
 130 135 140

Tyr Lys Glu Lys Ser Ile Phe Leu Val Ala His Arg Lys Asp Pro Thr
 145 150 155 160

Gly Met Asp Pro Asp Asp Ile Trp Gln Leu Ser Ser Ser Leu Lys Arg
 165 170 175

Phe Asp Asp Lys Tyr Thr Leu Lys Leu Thr Phe Ile Ser Gly Arg Thr
 180 185 190

Lys Gln Gln Arg Glu Ala Glu Phe Thr Lys Ser Ile Ala Lys Phe Phe
 195 200 205

Asp His Ser Gly Thr Leu Val Met Asp Ala Tyr Glu Pro Glu Ile Ser
 210 215 220

Arg Leu His Asp Ser Leu Ala Ile Glu Arg Lys Ile Lys
 225 230 235

<210> 1333

1378

<211> 56

<212> PRT

<213> Homo sapiens

<400> 1333

Thr Thr Ala Asn Pro Leu Lys Thr Arg Gly Leu Ala Leu Val Ala Gln
1 5 10 15

Pro Lys Val Ala Leu Gln Ile Phe Glu Arg Ala Thr Ala Thr Phe Leu
20 25 30

Pro Ser Gln Leu Ser Leu Asp Phe Ser Glu Ser Gly Tyr Cys Tyr Pro
35 40 45

Asn Val Cys Leu Tyr Glu Cys Ile
50 55

<210> 1334

<211> 207

<212> PRT

<213> Homo sapiens

<400> 1334

Ser His Pro Ala Cys Ala Lys Val Glu Tyr Ala Tyr Ser Asp Asn Ser
1 5 10 15

Leu Asp Pro Asp Asp Glu Asp Ser Asp Tyr His Gln Glu Ala Tyr Lys
20 25 30

Glu Ser Tyr Lys Asp Arg Arg Arg Arg Ala His Thr Gln Ala Glu Gln
35 40 45

Lys Arg Arg Asp Ala Ile Lys Arg Gly Tyr Asp Asp Leu Gln Thr Ile
50 55 60

Val Pro Thr Cys Gln Gln Gln Asp Phe Ser Ile Gly Ser Gln Lys Leu
65 70 75 80

Ser Lys Ala Ile Val Leu Gln Lys Thr Ile Asp Tyr Ile Gln Phe Leu
85 90 95

His Lys Glu Lys Lys Lys Gln Glu Glu Glu Val Ser Thr Leu Arg Lys
100 105 110

Asp Val Thr Ala Leu Lys Ile Met Lys Val Asn Tyr Glu Gln Ile Val
115 120 125

Lys Ala His Gln Asp Asn Pro His Glu Gly Glu Asp Gln Val Ser Asp
130 135 140

1379

Gln Val Lys Phe Asn Val Phe Gln Gly Ile Met Asp Ser Leu Phe Gln
 145 150 155 160

Ser Phe Asn Ala Ser Ile Ser Val Ala Ser Phe Gln Glu Leu Ser Ala
 165 170 175

Cys Val Phe Ser Trp Ile Glu Glu His Cys Lys Pro Gln Thr Leu Arg
 180 185 190

Glu Ile Val Ile Gly Val Leu His Gln Leu Lys Asn Gln Leu Tyr
 195 200 205

<210> 1335

<211> 1005

<212> PRT

<213> Homo sapiens

<400> 1335

Arg Val Leu Gln Tyr Val Val Pro Glu Val Lys Asp Leu Tyr Asn Trp
 1 5 10 15

Leu Glu Val Glu Phe Asn Pro Leu Lys Leu Cys Glu Arg Val Thr Lys
 20 25 30

Val Leu Asn Trp Val Arg Glu Gln Pro Glu Lys Glu Pro Glu Leu Gln
 35 40 45

Gln Tyr Val Pro Gln Leu Gln Asn Asn Thr Ile Leu Arg Leu Leu Gln
 50 55 60

Gln Val Ser Gln Ile Tyr Gln Ser Ile Glu Phe Ser Arg Leu Thr Ser
 65 70 75 80

Leu Val Pro Phe Val Asp Ala Phe Gln Leu Glu Arg Ala Ile Val Asp
 85 90 95

Ala Ala Arg His Cys Asp Leu Gln Val Arg Ile Asp His Thr Ser Arg
 100 105 110

Thr Leu Ser Phe Gly Ser Asp Leu Asn Tyr Ala Thr Arg Glu Asp Ala
 115 120 125

Pro Ile Gly Pro His Leu Gln Ser Met Pro Ser Glu Gln Ile Arg Asn
 130 135 140

Gln Leu Thr Ala Met Ser Ser Val Leu Ala Lys Ala Leu Glu Val Ile
 145 150 155 160

1380

Lys Pro Ala His Ile Leu Gln Glu Lys Glu Glu Gln His Gln Leu Ala
165 170 175

Val Thr Ala Tyr Leu Lys Asn Ser Arg Lys Glu His Gln Arg Ile Leu
180 185 190

Ala Arg Arg Gln Thr Ile Glu Glu Arg Lys Glu Arg Leu Glu Ser Leu
195 200 205

Asn Ile Gln Arg Glu Lys Glu Glu Leu Glu Gln Arg Glu Ala Glu Leu
210 215 220

Gln Lys Val Arg Lys Ala Glu Glu Glu Arg Leu Arg Gln Glu Ala Lys
225 230 235 240

Glu Arg Glu Lys Glu Arg Ile Leu Gln Glu His Glu Gln Ile Lys Lys
245 250 255

Lys Thr Val Arg Glu Arg Leu Glu Gln Ile Lys Lys Thr Glu Leu Gly
260 265 270

Ala Lys Ala Phe Lys Asp Ile Asp Ile Glu Asp Leu Glu Glu Leu Asp
275 280 285

Pro Asp Phe Ile Met Ala Lys Gln Val Glu Gln Leu Glu Lys Glu Lys
290 295 300

Lys Glu Leu Gln Glu Arg Leu Lys Asn Gln Glu Lys Lys Ile Asp Tyr
305 310 315 320

Phe Glu Arg Ala Lys Arg Leu Glu Glu Ile Pro Leu Ile Lys Ser Ala
325 330 335

Tyr Glu Glu Gln Arg Ile Lys Asp Met Asp Leu Trp Glu Gln Gln Glu
340 345 350

Glu Glu Arg Ile Thr Thr Met Gln Leu Glu Arg Glu Lys Ala Leu Glu
355 360 365

His Lys Asn Arg Met Ser Arg Met Leu Glu Asp Arg Asp Leu Phe Val
370 375 380

Met Arg Leu Lys Ala Ala Arg Gln Ser Val Tyr Glu Glu Lys Leu Lys
385 390 395 400

Gln Phe Glu Glu Arg Leu Ala Glu Glu Arg His Asn Arg Leu Glu Glu
405 410 415

Arg Lys Arg Gln Arg Lys Glu Glu Arg Arg Ile Thr Tyr Tyr Arg Glu
420 425 430

1381

Lys Glu Glu Glu Glu Gln Arg Arg Ala Glu Glu Gln Met Leu Lys Glu
435 440 445

Arg Glu Glu Arg Glu Arg Ala Glu Arg Ala Lys Arg Glu Glu Glu Leu
450 455 460

Arg Glu Tyr Gln Glu Arg Val Lys Lys Leu Glu Glu Val Glu Arg Lys
465 470 475 480

Lys Arg Gln Arg Glu Leu Glu Ile Glu Glu Arg Glu Arg Arg Arg Glu
485 490 495

Glu Glu Arg Arg Leu Gly Asp Ser Ser Leu Ser Arg Lys Asp Ser Arg
500 505 510

Trp Gly Asp Arg Asp Ser Glu Gly Thr Trp Arg Lys Gly Pro Glu Ala
515 520 525

Asp Ser Glu Trp Arg Arg Gly Pro Pro Glu Lys Glu Trp Arg Arg Gly
530 535 540

Glu Gly Arg Asp Glu Asp Arg Ser His Arg Arg Asp Glu Glu Arg Pro
545 550 555 560

Arg Arg Leu Gly Asp Asp Glu Asp Arg Glu Pro Ser Leu Arg Pro Asp
565 570 575

Asp Asp Arg Val Pro Arg Arg Gly Met Asp Asp Asp Arg Gly Pro Arg
580 585 590

Arg Gly Pro Glu Glu Asp Arg Phe Ser Arg Arg Gly Ala Asp Asp Asp
595 600 605

Arg Pro Ser Trp Arg Asn Thr Asp Asp Asp Arg Pro Pro Arg Arg Ile
610 615 620

Ala Asp Glu Asp Arg Gly Asn Trp Arg His Ala Asp Asp Asp Arg Pro
625 630 635 640

Pro Arg Arg Gly Leu Asp Glu Asp Arg Gly Ser Trp Arg Thr Ala Asp
645 650 655

Glu Asp Arg Gly Pro Arg Arg Gly Met Asp Asp Asp Arg Gly Pro Arg
660 665 670

Arg Gly Gly Ala Asp Asp Glu Arg Ser Ser Trp Arg Asn Ala Asp Asp
675 680 685

Asp Arg Gly Pro Arg Arg Gly Leu Asp Asp Asp Arg Gly Pro Arg Arg
690 695 700

1382

Gly Met Asp Asp Asp Arg Gly Pro Arg Arg Gly Met Asp Asp Asp Arg
705 710 715 720

Gly Pro Arg Arg Gly Met Asp Asp Asp Arg Gly Pro Arg Arg Gly Leu
725 730 735

Asp Asp Asp Arg Gly Pro Trp Arg Asn Ala Asp Asp Asp Arg Ile Pro
740 745 750

Arg Arg Gly Ala Glu Asp Asp Arg Gly Pro Trp Arg Asn Met Asp Asp
755 760 765

Asp Arg Leu Ser Arg Arg Ala Asp Asp Asp Arg Phe Pro Arg Arg Gly
770 775 780

Asp Asp Ser Arg Pro Gly Pro Trp Arg Pro Leu Val Lys Pro Gly Gly
785 790 795 800

Trp Arg Glu Lys Glu Lys Ala Arg Glu Glu Ser Trp Gly Pro Pro Arg
805 810 815

Glu Ser Arg Pro Ser Glu Glu Arg Glu Trp Asp Arg Glu Lys Glu Arg
820 825 830

Asp Arg Asp Asn Gln Asp Arg Glu Glu Asn Asp Lys Asp Pro Glu Arg
835 840 845

Glu Arg Asp Arg Glu Arg Asp Val Asp Arg Glu Asp Arg Phe Arg Arg
850 855 860

Pro Arg Asp Glu Gly Gly Trp Arg Arg Gly Pro Ala Glu Glu Ser Ser
865 870 875 880

Ser Trp Arg Asp Ser Ser Arg Arg Asp Asp Arg Asp Arg Asp Arg
885 890 895

Arg Arg Glu Arg Asp Asp Arg Arg Asp Leu Arg Glu Arg Arg Asp Leu
900 905 910

Arg Asp Asp Arg Asp Arg Arg Gly Pro Pro Leu Arg Ser Glu Arg Glu
915 920 925

Glu Val Ser Ser Trp Arg Arg Ala Asp Asp Arg Lys Asp Asp Arg Val
930 935 940

Glu Glu Arg Asp Pro Pro Arg Arg Val Pro Pro Pro Ala Leu Ser Arg
945 950 955 960

Asp Arg Glu Arg Asp Arg Asp Arg Glu Arg Glu Gly Glu Lys Glu Lys
965 970 975

1383

Ala Ser Trp Arg Ala Glu Lys Asp Arg Glu Ser Leu Arg Arg Thr Lys
980 985 990

Asn Glu Thr Asp Glu Asp Gly Trp Thr Thr Val Arg Arg
995 1000 1005

<210> 1336

<211> 231

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (52)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (64)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (73)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (79)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (82)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (83)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (118)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1336

Ala Gly Ile His Pro Met Asn Ser Ile Ser Ser Leu Asp Arg Thr Arg
1 5 10 15

1384

Met Met Thr Pro Phe Met Gly Ile Ser Pro Leu Pro Gly Gly Glu Arg
 20 25 30
 Phe Pro Tyr Pro Ser Phe His Trp Asp Pro Ile Arg Asp Pro Leu Arg
 35 40 45
 Asp Pro Tyr Xaa Glu Leu Asp Ile His Arg Arg Asp Pro Leu Gly Xaa
 50 55 60
 Asp Phe Leu Leu Arg Asn Asp Pro Xaa His Arg Leu Ser Thr Xaa Arg
 65 70 75 80
 Leu Xaa Xaa Ala Asp Arg Ser Phe Arg Asp Arg Glu Pro His Asp Tyr
 85 90 95
 Ser His His His His His His His His Pro Leu Ser Val Asp Pro Arg
 100 105 110
 Arg Glu His Glu Arg Xaa Gly His Leu Asp Glu Arg Glu Arg Leu His
 115 120 125
 Met Leu Arg Glu Asp Tyr Glu His Thr Arg Leu His Ser Val His Pro
 130 135 140
 Ala Ser Leu Asp Gly His Leu Pro His Pro Ser Leu Ile Thr Pro Gly
 145 150 155 160
 Leu Pro Ser Met His Tyr Pro Arg Ile Ser Pro Thr Ala Gly Asn Gln
 165 170 175
 Asn Gly Leu Leu Asn Lys Thr Pro Pro Thr Ala Ala Leu Ser Ala Pro
 180 185 190
 Pro Pro Leu Ile Ser Thr Leu Gly Gly Arg Pro Val Ser Pro Arg Arg
 195 200 205
 Thr Thr Pro Leu Ser Ala Glu Ile Arg Glu Arg Pro Pro Ser His Thr
 210 215 220
 Leu Lys Asp Ile Glu Ala Arg
 225 230

<210> 1337

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1337

1385

Gly Val Glu Gly Leu Lys Asp Ala Gln Met Arg Asp Leu Leu Ser Pro
 1 5 10 15
 Pro Thr Asp Asn Arg Pro Gly Gln Met Asp Asn Arg Ser Lys Leu Arg
 20 25 30
 Asn Ile Val Glu Leu Arg Leu Ala Gly Leu Asp Ile Thr Asp Ala Ser
 35 40 45
 Leu Arg Leu Ile Ile Arg His Met Pro Leu Leu Ser Lys Leu His Leu
 50 55 60
 Ser Tyr Cys Asn His Val Thr Asp Gln Ser Ile Asn Leu Leu Thr Ala
 65 70 75 80
 Val Gly Thr Thr Thr Arg Asp Ser Leu Thr Glu Ile Asn Leu Ser Asp
 85 90 95
 Cys Asn Lys Val Thr Asp Gln Cys Leu Ser Phe Phe Lys Arg Cys Gly
 100 105 110
 Asn Ile Cys His Ile Asp Leu Arg Tyr Cys Lys Gln Val Thr Lys Glu
 115 120 125
 Gly Cys Glu Gln Phe Ile Ala Glu Met Ser Val Ser Val Gln Phe Gly
 130 135 140
 Gln Val Glu Glu Lys Leu Leu Gln Lys Leu Ser
 145 150 155

<210> 1338

<211> 328

<212> PRT

<213> Homo sapiens

<400> 1338

Asn Asn Ser Gly Val Met Pro Glu Met Pro Glu Asp Met Glu Gln Glu
 1 5 10 15
 Glu Val Asn Ile Pro Asn Arg Arg Val Leu Val Thr Gly Ala Thr Gly
 20 25 30
 Leu Leu Gly Arg Ala Val His Lys Glu Phe Gln Gln Asn Asn Trp His
 35 40 45
 Ala Val Gly Cys Gly Phe Arg Arg Ala Arg Pro Lys Phe Glu Gln Val
 50 55 60
 Asn Leu Leu Asp Ser Asn Ala Val His His Ile Ile His Asp Phe Gln

1386

65		70		75		80
Pro His Val Ile Val His Cys Ala Ala Glu Arg Arg Pro Asp Val Val						
	85			90		95
Glu Asn Gln Pro Asp Ala Ala Ser Gln Leu Asn Val Asp Ala Ser Gly						
	100		105		110	
Asn Leu Ala Lys Glu Ala Ala Ala Val Gly Ala Phe Leu Ile Tyr Ile						
	115		120		125	
Ser Ser Asp Tyr Val Phe Asp Gly Thr Asn Pro Pro Tyr Arg Glu Glu						
	130		135		140	
Asp Ile Pro Ala Pro Leu Asn Leu Tyr Gly Lys Thr Lys Leu Asp Gly						
145		150		155		160
Glu Lys Ala Val Leu Glu Asn Asn Leu Gly Ala Ala Val Leu Arg Ile						
	165		170		175	
Pro Ile Leu Tyr Gly Glu Val Glu Lys Leu Glu Glu Ser Ala Val Thr						
	180		185		190	
Val Met Phe Asp Lys Val Gln Phe Ser Asn Lys Ser Ala Asn Met Asp						
	195		200		205	
His Trp Gln Gln Arg Phe Pro Thr His Val Lys Asp Val Ala Thr Val						
	210		215		220	
Cys Arg Gln Leu Ala Glu Lys Arg Met Leu Asp Pro Ser Ile Lys Gly						
225		230		235		240
Thr Phe His Trp Ser Gly Asn Glu Gln Met Thr Lys Tyr Glu Met Ala						
	245		250		255	
Cys Ala Ile Ala Asp Ala Phe Asn Leu Pro Ser Ser His Leu Arg Pro						
	260		265		270	
Ile Thr Asp Ser Pro Val Leu Gly Ala Gln Arg Pro Arg Asn Ala Gln						
	275		280		285	
Leu Asp Cys Ser Lys Leu Glu Thr Leu Gly Ile Gly Gln Arg Thr Pro						
	290		295		300	
Phe Arg Ile Gly Ile Lys Glu Ser Leu Trp Pro Phe Leu Ile Asp Lys						
305		310		315		320
Arg Trp Arg Gln Thr Val Phe His						
	325					

1387

<210> 1339

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1339

Leu Xaa His Pro Phe Ala Val Thr Ser Tyr Gly Lys Asn Leu Tyr Phe
1 5 10 15

Thr Asp Trp Lys Met Asn Ser Val Val Ala Leu Asp Leu Ala Ile Ser
20 25 30

Lys Glu Thr Asp Ala Phe Gln Pro His Lys Gln Thr Arg Leu Tyr Gly
35 40 45

Ile Thr Thr Ala Leu Ser Gln Cys Pro Gln Ala Ile Thr Thr Ala Gln
50 55 60

<210> 1340

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1340

Arg Lys Met Ala Val Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys
1 5 10 15

Glu Pro Glu Lys Pro Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu
20 25 30

Arg Val Phe Thr Thr Asn Asn Gly Arg His His Arg Met Asp Glu Phe
35 40 45

Ser Arg Gly Asn Val Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met
50 55 60

Asp Ala Thr Leu Lys Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro
65 70 75 80

Glu Ala Arg Lys Lys Gly Thr His Phe Asn Phe Ala Ile Val Phe Thr

1388

85 90 95
Asp Val Lys Arg Pro Gly Tyr Arg Val Lys Glu Ile Gly Ser Thr Met
100 105 110
Ser Gly Arg Lys Gly Thr Asp Asp Ser Met Thr Leu Gln Ser Gln Lys
115 120 125
Phe Gln Ile Gly Asp Tyr Leu Asp Ile Ala Ile Thr Pro Pro Asn Arg
130 135 140
Ala Pro Pro Pro Ser Gly Arg Met Arg Pro Tyr
145 150 155

<210> 1341
<211> 72
<212> PRT
<213> Homo sapiens

<400> 1341
Ala Gln Leu Pro Ser Ser Ser Phe Leu Arg His Arg Gly Val Phe Leu
1 5 10 15
Thr Pro Leu Leu Ala Met Ser Ser His Lys Thr Phe Arg Ile Lys Arg
20 25 30
Phe Leu Ala Lys Lys Gln Lys Gln Asn Arg Pro Ile Pro Gln Trp Ile
35 40 45
Arg Met Lys Thr Gly Asn Lys Ile Arg Tyr Asn Ser Lys Arg Arg His
50 55 60
Trp Arg Arg Thr Lys Leu Gly Leu
65 70

<210> 1342
<211> 270
<212> PRT
<213> Homo sapiens

<400> 1342
Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
1 5 10 15
Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
20 25 30

1389

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
 35 40 45
 Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
 50 55 60
 Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
 65 70 75 80
 Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
 85 90 95
 Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
 100 105 110
 Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
 115 120 125
 Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
 130 135 140
 Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
 145 150 155 160
 Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
 165 170 175
 Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
 180 185 190
 Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
 195 200 205
 Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
 210 215 220
 Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
 225 230 235 240
 Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
 245 250 255
 Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
 260 265 270

<210> 1343

<211> 94

<212> PRT

<213> Homo sapiens

1390

<220>

<221> SITE

<222> (55)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1343

Gln Glu Leu Arg Ser Pro Ser Arg Ser Pro Ser Pro Pro Pro Lys Ser
1 5 10 15

Pro Pro Trp Thr Thr Gly Gly Ser Leu Cys Glu Gln Leu Ala Phe Arg
20 25 30

Lys Pro Leu Ser Val Phe Lys Gln Lys Val Glu Gly Ala Thr Lys Gln
35 40 45

Ala Ala Val Arg Ala Ser Xaa Cys Arg Pro Leu Pro Cys Ser Ser Ser
50 55 60

Ser Phe Ala Ser Ala Ser Ser Val Met Phe Cys Leu Glu Phe Tyr Leu
65 70 75 80

Asp Phe Phe Ser Gly Tyr Phe Ser Val Phe Gln Pro Leu Leu
85 90

<210> 1344

<211> 125

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (118)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (122)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (123)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1344

Tyr Ser Thr Arg Ala Leu Trp Lys Pro Asn His Val His Val Cys Val
1 5 10 15

1391

Cys Val Cys Ala Ser Phe Glu Pro Pro Ser Thr Ala Ala Ser Ser His
 20 25 30
 Asp Thr Lys Leu Leu Ile Ser Thr Phe Leu Trp Val Ala Gln Gly Leu
 35 40 45
 Ile Ala Ser His Ser Ile Thr Arg Ile Glu Ala Arg His Gly Gly Ala
 50 55 60
 Cys Leu Val Val Pro Ala Lys Leu Gly Arg Leu Glu Gly Arg Glu Gly
 65 70 75 80
 Ser Leu Trp Ser Pro Gly Arg Leu Glu Gly Trp Gln Trp Ser His Gly
 85 90 95
 Ser Gly Gly His Trp His Phe Gln Pro Gly Gly Gly Arg Val Glu Thr
 100 105 110
 Phe Val Leu Gln Lys Xaa Lys Lys Lys Xaa Xaa Gly Gly
 115 120 125

<210> 1345

<211> 131

<212> PRT

<213> Homo sapiens

<400> 1345

Pro Arg Val Arg Arg Leu Arg Glu Asp Asp Arg Arg Gly Phe Leu Ser
 1 5 10 15
 Phe Arg Ala Asp Ser Ala His Ala Ser Met Val Asn Val Pro Lys Thr
 20 25 30
 Arg Arg Thr Phe Cys Lys Lys Cys Gly Lys His Gln Pro His Lys Val
 35 40 45
 Thr Gln Tyr Lys Lys Gly Lys Asp Ser Leu Tyr Ala Gln Gly Lys Arg
 50 55 60
 Arg Tyr Asp Arg Lys Gln Ser Gly Tyr Gly Gly Gln Thr Lys Pro Ile
 65 70 75 80
 Phe Arg Lys Lys Ala Lys Thr Thr Lys Lys Ile Val Leu Arg Leu Glu
 85 90 95
 Cys Val Glu Pro Asn Cys Arg Ser Lys Arg Met Leu Ala Ile Lys Arg
 100 105 110
 Cys Lys His Phe Glu Leu Gly Gly Asp Lys Lys Arg Lys Gly Gln Val

1392

115

120

125

Ile Gln Phe

130

<210> 1346

<211> 75

<212> PRT

<213> Homo sapiens

<400> 1346

Asn Lys Arg Asn Cys Lys Phe Pro Leu Leu Lys Ile Thr Lys Ile Thr
 1 5 10 15

Glu Thr Lys Glu Glu Ile Arg Ile Trp Gly Ile Val Leu Asn Asn Leu
 20 25 30

Val Val Lys Lys Asn Asn Cys Ala Cys Leu Asp Leu Asn Lys Pro Pro
 35 40 45

Ser Lys Cys Glu Gly Ser Ser Asn Phe Ser Lys His Met Lys Val Leu
 50 55 60

Ile His Phe Asp Lys Gly Pro Leu Lys Lys Ser
 65 70 75

<210> 1347

<211> 413

<212> PRT

<213> Homo sapiens

<400> 1347

Gly Val Ala Arg Ala Gln Pro Val Pro Ala Val Leu Ser Trp Leu Leu
 1 5 10 15

Ala Leu Leu Arg Cys Ala Ala Thr Met Leu Ser Leu Arg Val Pro Leu
 20 25 30

Ala Pro Ile Thr Asp Pro Gln Gln Leu Gln Leu Ser Pro Leu Lys Gly
 35 40 45

Leu Ser Leu Val Asp Lys Glu Asn Thr Pro Pro Ala Leu Ser Gly Thr
 50 55 60

Arg Val Leu Ala Ser Lys Thr Ala Arg Arg Ile Phe Gln Glu Pro Thr
 65 70 75 80

1393

Glu Pro Lys Thr Lys Ala Ala Ala Pro Gly Val Glu Asp Glu Pro Leu
 85 90 95

Leu Arg Glu Asn Pro Arg Arg Phe Val Ile Phe Pro Ile Glu Tyr His
 100 105 110

Asp Ile Trp Gln Met Tyr Lys Lys Ala Glu Ala Ser Phe Trp Thr Ala
 115 120 125

Glu Glu Val Asp Leu Ser Lys Asp Ile Gln His Trp Glu Ser Leu Lys
 130 135 140

Pro Glu Glu Arg Tyr Phe Ile Ser His Val Leu Ala Phe Phe Ala Ala
 145 150 155 160

Ser Asp Gly Ile Val Asn Glu Asn Leu Val Glu Arg Phe Ser Gln Glu
 165 170 175

Val Gln Ile Thr Glu Ala Arg Cys Phe Tyr Gly Phe Gln Ile Ala Met
 180 185 190

Glu Asn Ile His Ser Glu Met Tyr Ser Leu Leu Ile Asp Thr Tyr Ile
 195 200 205

Lys Asp Pro Lys Glu Arg Glu Phe Leu Phe Asn Ala Ile Glu Thr Met
 210 215 220

Pro Cys Val Lys Lys Lys Ala Asp Trp Ala Leu Arg Trp Ile Gly Asp
 225 230 235 240

Lys Glu Ala Thr Tyr Gly Glu Arg Val Val Ala Phe Ala Ala Val Glu
 245 250 255

Gly Ile Phe Phe Ser Gly Ser Phe Ala Ser Ile Phe Trp Leu Lys Lys
 260 265 270

Arg Gly Leu Met Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg
 275 280 285

Asp Glu Gly Leu His Cys Asp Phe Ala Cys Leu Met Phe Lys His Leu
 290 295 300

Val His Lys Pro Ser Glu Glu Arg Val Arg Glu Ile Ile Ile Asn Ala
 305 310 315 320

Val Arg Ile Glu Gln Glu Phe Leu Thr Glu Ala Leu Pro Val Lys Leu
 325 330 335

Ile Gly Met Asn Cys Thr Leu Met Lys Gln Tyr Ile Glu Phe Val Ala
 340 345 350

1394

Asp Arg Leu Met Leu Glu Leu Gly Phe Ser Lys Val Phe Arg Val Glu
 355 360 365

Asn Pro Phe Asp Phe Met Glu Asn Ile Ser Leu Glu Gly Lys Thr Asn
 370 375 380

Phe Phe Glu Lys Arg Val Gly Glu Tyr Gln Arg Met Gly Val Met Ser
 385 390 395 400

Ser Pro Thr Glu Asn Ser Phe Thr Leu Asp Ala Asp Phe
 405 410

<210> 1348

<211> 243

<212> PRT

<213> Homo sapiens

<400> 1348

Thr Gly Asn Lys Met Gln Asp Pro Asn Ala Asp Thr Glu Trp Asn Asp
 1 5 10 15

Ile Leu Arg Lys Lys Gly Ile Leu Pro Pro Lys Glu Ser Leu Lys Glu
 20 25 30

Leu Glu Glu Glu Ala Glu Glu Glu Gln Arg Ile Leu Gln Gln Ser Val
 35 40 45

Val Lys Thr Tyr Glu Asp Met Thr Leu Glu Glu Leu Glu Asp His Glu
 50 55 60

Asp Glu Phe Asn Glu Glu Asp Glu Arg Ala Ile Glu Met Tyr Arg Arg
 65 70 75 80

Arg Arg Leu Ala Glu Trp Lys Ala Thr Lys Leu Lys Asn Lys Phe Gly
 85 90 95

Glu Val Leu Glu Ile Ser Gly Lys Asp Tyr Val Gln Glu Val Thr Lys
 100 105 110

Ala Gly Glu Gly Leu Trp Val Ile Leu His Leu Tyr Lys Gln Gly Ile
 115 120 125

Pro Leu Cys Ala Leu Ile Asn Gln His Leu Ser Gly Leu Ala Arg Lys
 130 135 140

Phe Pro Asp Val Lys Phe Ile Lys Ala Ile Ser Thr Thr Cys Ile Pro
 145 150 155 160

Asn Tyr Pro Asp Arg Asn Leu Pro Thr Ile Phe Val Tyr Leu Glu Gly

1395

165 170 175
 Asp Ile Lys Ala Gln Phe Ile Gly Pro Leu Val Phe Gly Gly Met Asn
 180 185 190
 Leu Thr Arg Asp Glu Leu Glu Trp Lys Leu Ser Glu Ser Gly Ala Ile
 195 200 205
 Met Thr Asp Leu Glu Glu Asn Pro Lys Lys Pro Ile Glu Asp Val Leu
 210 215 220
 Leu Ser Ser Val Arg Arg Ser Val Leu Met Lys Arg Asp Ser Asp Ser
 225 230 235 240
 Glu Gly Asp

<210> 1349
 <211> 326
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (137)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (142)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1349
 Arg Met Ala Thr Pro Leu Pro Pro Pro Ser Pro Arg His Leu Arg Leu
 1 5 10 15
 Leu Arg Leu Leu Leu Ser Gly Leu Val Leu Gly Ala Ala Leu Arg Gly
 20 25 30
 Ala Ala Ala Gly His Pro Asp Val Ala Ala Cys Pro Gly Ser Leu Asp
 35 40 45
 Cys Ala Leu Lys Arg Arg Ala Arg Cys Pro Pro Gly Ala His Ala Cys
 50 55 60
 Gly Pro Cys Leu Gln Pro Phe Gln Glu Asp Gln Gln Gly Leu Cys Val
 65 70 75 80
 Pro Arg Met Arg Arg Pro Pro Gly Gly Gly Arg Pro Gln Pro Arg Leu

1396

85										90										95																																			
Glu	Asp	Glu	Ile	Asp	Phe	Leu	Ala	Gln	Glu	Leu	Ala	Arg	Lys	Glu	Ser																																								
			100						105					110																																									
Gly	His	Ser	Thr	Pro	Pro	Leu	Pro	Lys	Asp	Arg	Gln	Arg	Leu	Pro	Glu																																								
		115					120					125																																											
Pro	Ala	Thr	Leu	Gly	Phe	Ser	Ala	Xaa	Gly	Gln	Gly	Leu	Xaa	Leu	Gly																																								
		130					135					140																																											
Leu	Pro	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Pro	Thr	Pro	His	Thr	Ser	Leu																																								
		145				150				155				160																																									
Gly	Ser	Pro	Val	Ser	Ser	Asp	Pro	Val	His	Met	Ser	Pro	Leu	Glu	Pro																																								
			165					170					175																																										
Arg	Gly	Gly	Gln	Gly	Asp	Gly	Leu	Ala	Leu	Val	Leu	Ile	Leu	Ala	Phe																																								
			180					185					190																																										
Cys	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ser	Val	Ala	Ser	Leu	Cys	Trp	Cys																																								
		195					200					205																																											
Arg	Leu	Gln	Arg	Glu	Ile	Arg	Leu	Thr	Gln	Lys	Ala	Asp	Tyr	Ala	Thr																																								
		210				215				220																																													
Ala	Lys	Ala	Pro	Gly	Ser	Pro	Ala	Ala	Pro	Arg	Ile	Ser	Pro	Gly	Asp																																								
		225				230				235				240																																									
Gln	Arg	Leu	Ala	Gln	Ser	Ala	Glu	Met	Tyr	His	Tyr	Gln	His	Gln	Arg																																								
			245					250					255																																										
Gln	Gln	Met	Leu	Cys	Leu	Glu	Arg	His	Lys	Glu	Pro	Pro	Lys	Glu	Leu																																								
		260					265					270																																											
Asp	Thr	Ala	Ser	Ser	Asp	Glu	Glu	Asn	Glu	Asp	Gly	Asp	Phe	Thr	Val																																								
		275					280					285																																											
Tyr	Glu	Cys	Pro	Gly	Leu	Ala	Pro	Thr	Gly	Glu	Met	Glu	Val	Arg	Asn																																								
		290				295				300																																													
Pro	Leu	Phe	Asp	His	Ala	Ala	Leu	Ser	Ala	Pro	Leu	Pro	Ala	Pro	Ser																																								
		305				310				315				320																																									
Ser	Pro	Pro	Ala	Leu	Pro																																																		
						325																																																	

<210> 1350

<211> 62

1397

<212> PRT

<213> Homo sapiens

<400> 1350

Val Lys Ser Asp Thr Pro Pro Cys Val Ser Lys Asn Leu Val Pro Pro
1 5 10 15

Leu His Thr Ser Leu Thr Leu Asn Ile Phe His Trp Ile Leu Asp Arg
20 25 30

Ala Lys Gly Arg Thr Gly Ala Ser Gly Gly Pro Trp Leu Phe Lys Ser
35 40 45

Trp Ile Ile Cys Asp Ser Asn His Lys Phe Leu Ala Asn Phe
50 55 60

<210> 1351

<211> 312

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (299)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1351

Glu Pro Arg Pro Gly Cys Gly Asn Lys Met Ala Gly Lys Lys Asn Val
1 5 10 15

Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser Asp
20 25 30

Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys Gly
35 40 45

Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu Gly
50 55 60

Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg Gln
65 70 75 80

Ser Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp Pro
85 90 95

Lys Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val Ala
100 105 110

Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys Ile

1398

115	120	125
Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys Ile		
130	135	140
Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn Tyr		
145	150	155 160
Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu Lys		
	165 170	175
Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro Lys		
	180 185	190
Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu Ala		
	195 200	205
Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala Lys		
	210 215	220
Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr Lys Lys Gly Thr		
	225 230	235 240
Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Thr Ala Ser Thr Ala Val		
	245 250	255
Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro Val		
	260 265	270
Thr Thr Ile Ser Pro Ala His His Pro His His His Ser His Pro Ala		
	275 280	285
Ser Cys Cys His Gly His His Gln Arg Gln Xaa Ser Lys Asp His Arg		
	290 295	300
His Leu Cys Cys Gly Ala Pro Leu		
	305 310	

<210> 1352

<211> 259

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1352

1399

Leu Leu Asp Ser Leu Lys Xaa Asp Tyr Ala Gly Lys Pro Gln Pro Pro
 1 5 10 15
 Ile Lys Ser Glu Arg Arg Asn Pro Pro Ser Tyr Ala Met Ala Gly Lys
 20 25 30
 Lys Val Leu Ile Val Tyr Ala His Gln Glu Pro Lys Ser Phe Asn Gly
 35 40 45
 Ser Leu Lys Asn Val Ala Val Asp Glu Leu Ser Arg Gln Gly Cys Thr
 50 55 60
 Val Thr Val Ser Asp Leu Tyr Ala Met Asn Phe Glu Pro Arg Ala Thr
 65 70 75 80
 Asp Lys Asp Ile Thr Gly Thr Leu Ser Asn Pro Glu Val Phe Asn Tyr
 85 90 95
 Gly Val Glu Thr His Glu Ala Tyr Lys Gln Arg Ser Leu Ala Ser Asp
 100 105 110
 Ile Thr Asp Glu Gln Lys Lys Val Arg Glu Ala Asp Leu Val Ile Phe
 115 120 125
 Gln Phe Pro Leu Tyr Trp Phe Ser Val Pro Ala Ile Leu Lys Gly Trp
 130 135 140
 Met Asp Arg Val Leu Cys Gln Gly Phe Ala Phe Asp Ile Pro Gly Phe
 145 150 155 160
 Tyr Asp Ser Gly Leu Leu Gln Gly Lys Leu Ala Leu Leu Ser Val Thr
 165 170 175
 Thr Gly Gly Thr Ala Glu Met Tyr Thr Lys Thr Gly Val Asn Gly Asp
 180 185 190
 Ser Arg Tyr Phe Leu Trp Pro Leu Gln His Gly Thr Leu His Phe Cys
 195 200 205
 Gly Phe Lys Val Leu Ala Pro Gln Ile Ser Phe Ala Pro Glu Ile Ala
 210 215 220
 Ser Glu Glu Glu Arg Lys Gly Met Val Ala Ala Trp Ser Gln Arg Leu
 225 230 235 240
 Gln Thr Ile Trp Lys Glu Glu Pro Ile Pro Cys Thr Ala His Trp His
 245 250 255
 Phe Gly Gln

1400

<210> 1353

<211> 72

<212> PRT

<213> Homo sapiens

<400> 1353

Asp Leu Ala Ser Glu Glu His Phe Phe Ser Val Lys Phe Leu Tyr Leu
 1 5 10 15

Lys Ile Gln Lys Tyr Phe Arg Ile Leu Leu Ile Leu Ser Pro Val Phe
 20 25 30

Thr Ser Phe Trp Lys Thr Cys Ile Thr Met Ser Leu Glu Lys Gly Gln
 35 40 45

Arg Lys Ala Phe His Val Lys Ile Arg Ser Leu Ala Ile Ser Asn Pro
 50 55 60

Val Leu Phe Ser Leu His Phe Phe
 65 70

<210> 1354

<211> 301

<212> PRT

<213> Homo sapiens

<400> 1354

Lys Arg Arg Arg Arg Leu Glu Gln Arg Gln Gln Pro Asp Glu Gln Arg
 1 5 10 15

Arg Arg Ser Gly Ala Met Val Lys Met Ala Ala Ala Gly Gly Gly Gly
 20 25 30

Gly Gly Gly Arg Tyr Tyr Gly Gly Gly Ser Glu Gly Gly Arg Ala Pro
 35 40 45

Lys Arg Leu Lys Thr Asp Asn Ala Gly Asp Gln His Gly Gly Gly Gly
 50 55 60

Gly Gly Gly Gly Gly Ala Gly Ala Ala Gly Gly Gly Gly Gly Glu
 65 70 75 80

Asn Tyr Asp Asp Pro His Lys Thr Pro Ala Ser Pro Val Val His Ile
 85 90 95

Arg Gly Leu Ile Asp Gly Val Val Glu Ala Asp Leu Val Glu Ala Leu
 100 105 110

1401

Gln Glu Phe Gly Pro Ile Ser Tyr Val Val Val Met Pro Lys Lys Arg
 115 120 125

Gln Ala Leu Val Glu Phe Glu Asp Val Leu Gly Ala Cys Asn Ala Val
 130 135 140

Asn Tyr Ala Ala Asp Asn Gln Ile Tyr Ile Ala Gly His Pro Ala Phe
 145 150 155 160

Val Asn Tyr Ser Thr Ser Gln Lys Ile Ser Arg Pro Gly Asp Ser Asp
 165 170 175

Asp Ser Arg Ser Val Asn Ser Val Leu Leu Phe Thr Ile Leu Asn Pro
 180 185 190

Ile Tyr Ser Ile Thr Thr Asp Val Leu Tyr Thr Ile Cys Asn Pro Cys
 195 200 205

Gly Pro Val Gln Arg Ile Val Ile Phe Arg Lys Asn Gly Val Gln Ala
 210 215 220

Met Val Glu Phe Asp Ser Val Gln Ser Ala Gln Arg Ala Lys Ala Ser
 225 230 235 240

Leu Asn Gly Ala Asp Ile Tyr Ser Gly Cys Cys Thr Leu Lys Ile Glu
 245 250 255

Tyr Ala Lys Pro Thr Arg Leu Asn Val Phe Lys Asn Asp Gln Asp Thr
 260 265 270

Trp Asp Tyr Thr Asn Pro Asn Leu Ser Gly Gln Gly Asn Leu Asp Asp
 275 280 285

His Phe Val Leu Asn Ile Pro Ala Leu Leu Ser Leu Asp
 290 295 300

<210> 1355

<211> 466

<212> PRT

<213> Homo sapiens

<400> 1355

Asn Thr Val Met Gly Arg Lys Lys Lys Lys Gln Leu Lys Pro Trp Cys
 1 5 10 15

Trp Tyr Cys Asn Arg Asp Phe Asp Asp Glu Lys Ile Leu Ile Gln His
 20 25 30

1402

Gln Lys Ala Lys His Phe Lys Cys His Ile Cys His Lys Lys Leu Tyr
35 40 45

Thr Gly Pro Gly Leu Ala Ile His Cys Met Gln Val His Lys Glu Thr
50 55 60

Ile Asp Ala Val Pro Asn Ala Ile Pro Gly Arg Thr Asp Ile Glu Leu
65 70 75 80

Glu Ile Tyr Gly Met Glu Gly Ile Pro Glu Lys Asp Met Asp Glu Arg
85 90 95

Arg Arg Leu Leu Glu Gln Lys Thr Gln Glu Ser Gln Lys Lys Lys Gln
100 105 110

Gln Asp Asp Ser Asp Glu Tyr Asp Asp Asp Asp Ser Ala Ala Ser Thr
115 120 125

Ser Phe Gln Pro Gln Pro Val Gln Pro Gln Gln Gly Tyr Ile Pro Pro
130 135 140

Met Ala Gln Pro Gly Leu Pro Pro Val Pro Gly Ala Pro Gly Met Pro
145 150 155 160

Pro Gly Ile Pro Pro Leu Met Pro Gly Val Pro Pro Leu Met Pro Gly
165 170 175

Met Pro Pro Val Met Pro Gly Met Pro Pro Gly Leu His His Gln Arg
180 185 190

Lys Tyr Thr Gln Ser Phe Cys Gly Glu Asn Ile Met Met Pro Met Gly
195 200 205

Gly Met Met Pro Pro Gly Pro Gly Ile Pro Pro Leu Met Pro Gly Met
210 215 220

Pro Pro Gly Met Pro Pro Pro Val Pro Arg Pro Gly Ile Pro Pro Met
225 230 235 240

Thr Gln Ala Gln Ala Val Ser Ala Pro Gly Ile Leu Asn Arg Pro Pro
245 250 255

Ala Pro Thr Ala Thr Val Pro Ala Pro Gln Pro Pro Val Thr Lys Pro
260 265 270

Leu Phe Pro Ser Ala Gly Gln Ala Gln Ala Ala Val Gln Gly Pro Val
275 280 285

Gly Thr Asp Phe Lys Pro Leu Asn Ser Thr Pro Ala Thr Thr Thr Glu
290 295 300

1403

Pro Pro Lys Pro Thr Phe Pro Ala Tyr Thr Gln Ser Thr Ala Ser Thr
305 310 315 320

Thr Ser Thr Thr Asn Ser Thr Ala Ala Lys Pro Ala Ala Ser Ile Thr
325 330 335

Ser Lys Pro Ala Thr Leu Thr Thr Thr Ser Ala Thr Ser Lys Leu Ile
340 345 350

His Pro Asp Glu Asp Ile Ser Leu Glu Glu Arg Arg Ala Gln Leu Pro
355 360 365

Lys Tyr Gln Arg Asn Leu Pro Arg Pro Gly Gln Ala Pro Ile Gly Asn
370 375 380

Pro Pro Val Gly Pro Ile Gly Gly Met Met Pro Pro Gln Pro Gly Ile
385 390 395 400

Pro Gln Gln Gln Gly Met Arg Pro Pro Met Pro Pro His Gly Gln Tyr
405 410 415

Gly Gly His His Gln Gly Met Pro Gly Tyr Leu Pro Gly Ala Met Pro
420 425 430

Pro Tyr Gly Gln Gly Pro Pro Met Val Pro Pro Tyr Gln Gly Gly Pro
435 440 445

Pro Arg Pro Pro Met Gly Met Arg Pro Pro Val Met Ser Gln Gly Gly
450 455 460

Arg Tyr
465

<210> 1356

<211> 85

<212> PRT

<213> Homo sapiens

<400> 1356

Leu Ser Asp Asp Gln Ser Leu Leu Ile Ile Leu Leu Leu Lys Gly Leu
1 5 10 15

Leu Thr Asn Leu Ser Phe Thr Pro Cys Gly Pro Cys Tyr Trp Tyr Thr
20 25 30

Gln Tyr Val Leu Thr Glu Asp Met Asp Phe Ile Cys Ser Ser Ala Gly
35 40 45

Ile Gly Lys Leu Asp Leu Phe Ser Met Ile Gln Asn Ser Pro Ile Arg

1404

50 55 60
Arg Leu Glu Lys Glu Glu Leu Tyr Ser Ser Leu Cys Tyr Phe Leu Leu
65 70 75 80

Pro Phe Leu Phe Leu
85

<210> 1357

<211> 580

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (526)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1357

Asp Ser Xaa Thr Phe Asp Asp Leu Ala Val Asp Phe Thr Pro Glu Glu
1 5 10 15

Trp Thr Leu Leu Asp Pro Thr Gln Arg Asn Leu Tyr Arg Asp Val Met
20 25 30

Leu Glu Asn Tyr Lys Asn Leu Ala Thr Val Gly Tyr Gln Leu Phe Lys
35 40 45

Pro Ser Leu Ile Ser Trp Leu Glu Gln Glu Glu Ser Arg Thr Val Gln
50 55 60

Arg Gly Asp Phe Gln Ala Ser Glu Trp Lys Val Gln Leu Lys Thr Lys
65 70 75 80

Glu Leu Ala Leu Gln Gln Asp Val Leu Gly Glu Pro Thr Ser Ser Gly
85 90 95

Ile Gln Met Ile Gly Ser His Asn Gly Gly Glu Val Ser Asp Val Lys
100 105 110

Gln Cys Gly Asp Val Ser Ser Glu His Ser Cys Leu Lys Thr His Val
115 120 125

Arg Thr Gln Asn Ser Glu Asn Thr Phe Glu Cys Tyr Leu Tyr Gly Val

1405

130	135	140
Asp Phe Leu Thr Leu His Lys Lys Thr Ser Thr Gly Glu Gln Arg Ser		
145	150	155 160
Val Phe Ser Gln Cys Gly Lys Ala Phe Ser Leu Asn Pro Asp Val Val		
	165	170 175
Cys Gln Arg Thr Cys Thr Gly Glu Lys Ala Phe Asp Cys Ser Asp Ser		
	180	185 190
Gly Lys Ser Phe Ile Asn His Ser His Leu Gln Gly His Leu Arg Thr		
	195	200 205
His Asn Gly Glu Ser Leu His Glu Trp Lys Glu Cys Gly Arg Gly Phe		
	210	215 220
Ile His Ser Thr Asp Leu Ala Val Arg Ile Gln Thr His Arg Ser Glu		
	225	230 235 240
Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Gly Phe Arg Tyr Ser Ala		
	245	250 255
Tyr Leu Asn Ile His Met Gly Thr His Thr Gly Asp Asn Pro Tyr Glu		
	260	265 270
Cys Lys Glu Cys Gly Lys Ala Phe Thr Arg Ser Cys Gln Leu Thr Gln		
	275	280 285
His Arg Lys Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Asp Cys		
	290	295 300
Gly Arg Ala Phe Thr Val Ser Ser Cys Leu Ser Gln His Met Lys Ile		
	305	310 315 320
His Val Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Ile Ala Phe		
	325	330 335
Thr Arg Ser Ser Gln Leu Thr Glu His Leu Lys Thr His Thr Ala Lys		
	340	345 350
Asp Pro Phe Glu Cys Lys Ile Cys Gly Lys Ser Phe Arg Asn Ser Ser		
	355	360 365
Cys Leu Ser Asp His Phe Arg Ile His Thr Gly Ile Lys Pro Tyr Lys		
	370	375 380
Cys Lys Asp Cys Gly Lys Ala Phe Thr Gln Asn Ser Asp Leu Thr Lys		
	385	390 395 400
His Ala Arg Thr His Ser Gly Glu Arg Pro Tyr Glu Cys Lys Glu Cys		

1406

405 410 415
Gly Lys Ala Phe Ala Arg Ser Ser Arg Leu Ser Glu His Thr Arg Thr
420 425 430
His Thr Gly Glu Lys Pro Phe Glu Cys Val Lys Cys Gly Lys Ala Phe
435 440 445
Ala Ile Ser Ser Asn Leu Ser Gly His Leu Arg Ile His Thr Gly Glu
450 455 460
Lys Pro Phe Glu Cys Leu Glu Cys Gly Lys Ala Phe Thr His Ser Ser
465 470 475 480
Ser Leu Asn Asn His Met Arg Thr His Ser Ala Lys Lys Pro Phe Thr
485 490 495
Cys Met Glu Cys Gly Lys Ala Phe Lys Phe Pro Thr Cys Val Asn Leu
500 505 510
His Met Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Xaa Gln Cys
515 520 525
Gly Lys Ser Phe Ser Tyr Ser Asn Ser Phe Gln Leu His Glu Arg Thr
530 535 540
His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe
545 550 555 560
Ser Ser Ser Ser Ser Phe Arg Asn His Glu Arg Arg His Ala Asp Glu
565 570 575
Arg Leu Ser Ala
580

<210> 1358

<211> 612

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (134)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (445)

<223> Xaa equals any of the naturally occurring L-amino acids

1407

<400> 1358

Glu Val Pro Glu Ala His Arg Ala Ser Pro Arg Glu Gly Thr Ser Gly
1 5 10 15

Gly Glu Arg Leu Gln Asp Leu Val Lys Ser Lys Met Ser Glu Thr Ser
20 25 30

Arg Thr Ala Phe Gly Gly Arg Arg Ala Val Pro Pro Asn Asn Ser Asn
35 40 45

Ala Ala Glu Asp Asp Leu Pro Thr Val Glu Leu Gln Gly Val Val Pro
50 55 60

Arg Gly Val Asn Leu Gln Asp Asp Ala Val Tyr Leu Asp Asn Glu Lys
65 70 75 80

Glu Arg Glu Glu Tyr Val Leu Asn Asp Ile Gly Val Ile Phe Tyr Gly
85 90 95

Glu Val Asn Asp Ile Lys Thr Arg Ser Trp Ser Tyr Gly Gln Phe Glu
100 105 110

Asp Gly Ile Leu Asp Thr Cys Leu Tyr Val Met Asp Arg Ala Gln Met
115 120 125

Asp Leu Ser Gly Arg Xaa Asn Pro Ile Lys Val Ser Arg Val Gly Ser
130 135 140

Ala Met Val Asn Ala Lys Asp Asp Glu Gly Val Leu Val Gly Ser Trp
145 150 155 160

Asp Asn Ile Tyr Ala Tyr Gly Val Pro Pro Ser Ala Trp Thr Gly Ser
165 170 175

Val Asp Ile Leu Leu Glu Tyr Arg Ser Ser Glu Asn Pro Val Arg Tyr
180 185 190

Gly Gln Cys Trp Val Phe Ala Gly Val Phe Asn Thr Phe Leu Arg Cys
195 200 205

Leu Gly Ile Pro Ala Arg Ile Val Thr Asn Tyr Phe Ser Ala His Asp
210 215 220

Asn Asp Ala Asn Leu Gln Met Asp Ile Phe Leu Glu Glu Asp Gly Asn
225 230 235 240

Val Asn Ser Lys Leu Thr Lys Asp Ser Val Trp Asn Tyr His Cys Trp
245 250 255

Asn Glu Ala Trp Met Thr Arg Pro Asp Leu Pro Val Gly Phe Gly Gly

1408

260	265	270
Trp Gln Ala Val Asp Ser Thr	Pro Gln Glu Asn Ser Asp Gly Met Tyr	
275	280	285
Arg Cys Gly Pro Ala Ser Val	Gln Ala Ile Lys His Gly His Val Cys	
290	295	300
Phe Gln Phe Asp Ala Pro Phe Val	Phe Ala Glu Val Asn Ser Asp Leu	
305	310	315
Ile Tyr Ile Thr Ala Lys Lys Asp	Gly Thr His Val Val Glu Asn Val	
325	330	335
Asp Ala Thr His Ile Gly Lys Leu	Ile Val Thr Lys Gln Ile Gly Gly	
340	345	350
Asp Gly Met Met Asp Ile Thr Asp	Thr Tyr Lys Phe Gln Glu Gly Gln	
355	360	365
Glu Glu Glu Arg Leu Ala Leu Glu	Thr Ala Leu Met Tyr Gly Ala Lys	
370	375	380
Lys Pro Leu Asn Thr Glu Gly Val	Met Lys Ser Arg Ser Asn Val Asp	
385	390	395
Met Asp Phe Glu Val Glu Asn Ala	Val Leu Gly Lys Asp Phe Lys Leu	
405	410	415
Ser Ile Thr Phe Arg Asn Asn Ser	His Asn Arg Tyr Thr Ile Thr Ala	
420	425	430
Tyr Leu Ser Ala Asn Ile Thr Phe	Tyr Thr Gly Val Xaa Lys Ala Glu	
435	440	445
Phe Lys Lys Glu Thr Phe Asp Val	Thr Leu Glu Pro Leu Ser Phe Lys	
450	455	460
Lys Glu Ala Val Leu Ile Gln Ala	Gly Glu Tyr Met Gly Gln Leu Leu	
465	470	475
Glu Gln Ala Ser Leu His Phe Phe	Val Thr Ala Arg Ile Asn Glu Thr	
485	490	495
Arg Asp Val Leu Ala Lys Gln Lys	Ser Thr Val Leu Thr Ile Pro Glu	
500	505	510
Ile Ile Ile Lys Val Arg Gly Thr	Gln Val Val Gly Ser Asp Met Thr	
515	520	525
Val Thr Val Glu Phe Thr Asn Pro	Leu Lys Glu Thr Leu Arg Asn Val	

1409

530

535

540

Trp Val His Leu Asp Gly Pro Gly Val Thr Arg Pro Met Lys Lys Met
545 550 555 560

Phe Arg Glu Ile Arg Pro Asn Ser Thr Val Gln Trp Glu Glu Val Cys
565 570 575

Arg Pro Trp Val Ser Gly His Arg Lys Leu Ile Ala Ser Met Ser Ser
580 585 590

Asp Ser Leu Arg His Val Tyr Gly Glu Leu Asp Val Gln Ile Gln Arg
595 600 605

Arg Pro Ser Met
610

<210> 1359

<211> 56

<212> PRT

<213> Homo sapiens

<400> 1359

Leu Ser Cys Ile Val Leu Leu Arg Gln Ser Ser Val Lys Leu Tyr Gln
1 5 10 15

Leu Arg Leu Val Ser Ser Asp Phe His Trp Gly Ile Arg Val Leu Ala
20 25 30

Gly Leu Asn Leu Leu Leu Val Gly Ser Val Phe Leu Met Asn Lys Ser
35 40 45

His Ser Thr Glu Leu Gln Val Ile
50 55

<210> 1360

<211> 415

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (368)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (374)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (379)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (381)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (384)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (385)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (386)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (389)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (397)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (404)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (405)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (409)

1411

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1360

Gly	Gly	Gly	Gly	Glu	Lys	Met	Ala	Asp	Asp	Pro	Ser	Ala	Ala	Asp	Arg	1	5	10	15
Asn	Val	Glu	Ile	Trp	Lys	Ile	Lys	Lys	Leu	Ile	Lys	Ser	Leu	Glu	Ala	20	25	30	
Ala	Arg	Gly	Asn	Gly	Thr	Ser	Met	Ile	Ser	Leu	Ile	Ile	Pro	Pro	Lys	35	40	45	
Asp	Gln	Ile	Ser	Arg	Val	Ala	Lys	Met	Leu	Ala	Asp	Glu	Phe	Gly	Thr	50	55	60	
Ala	Ser	Asn	Ile	Lys	Ser	Arg	Val	Asn	Arg	Leu	Ser	Val	Leu	Gly	Ala	65	70	75	80
Ile	Thr	Ser	Val	Gln	Gln	Arg	Leu	Lys	Leu	Tyr	Asn	Lys	Val	Pro	Pro	85	90	95	
Asn	Gly	Leu	Val	Val	Tyr	Cys	Gly	Thr	Ile	Val	Thr	Glu	Glu	Gly	Lys	100	105	110	
Glu	Lys	Lys	Val	Asn	Ile	Asp	Phe	Glu	Pro	Phe	Lys	Pro	Ile	Asn	Thr	115	120	125	
Ser	Leu	Tyr	Leu	Cys	Asp	Asn	Lys	Phe	His	Thr	Glu	Ala	Leu	Thr	Ala	130	135	140	
Leu	Leu	Ser	Asp	Asp	Ser	Lys	Phe	Gly	Phe	Ile	Val	Ile	Asp	Gly	Ser	145	150	155	160
Gly	Ala	Leu	Phe	Gly	Thr	Leu	Gln	Gly	Asn	Thr	Arg	Glu	Val	Leu	His	165	170	175	
Lys	Phe	Thr	Val	Asp	Leu	Pro	Lys	Lys	His	Gly	Arg	Gly	Gly	Gln	Ser	180	185	190	
Ala	Leu	Arg	Phe	Ala	Arg	Leu	Arg	Met	Glu	Lys	Arg	His	Asn	Tyr	Val	195	200	205	
Arg	Lys	Val	Ala	Glu	Thr	Ala	Val	Gln	Leu	Phe	Ile	Ser	Gly	Asp	Lys	210	215	220	
Val	Asn	Val	Ala	Gly	Leu	Val	Leu	Ala	Gly	Ser	Ala	Asp	Phe	Lys	Thr	225	230	235	240
Glu	Leu	Ser	Gln	Ser	Asp	Met	Phe	Asp	Gln	Arg	Leu	Gln	Ser	Lys	Val	245	250	255	

1412

Leu Lys Leu Val Asp Ile Ser Tyr Gly Gly Glu Asn Gly Phe Asn Gln
260 265 270

Ala Ile Glu Leu Ser Thr Glu Val Leu Ser Asn Val Lys Phe Ile Gln
275 280 285

Glu Lys Lys Leu Ile Gly Arg Tyr Phe Asp Glu Ile Ser Gln Asp Thr
290 295 300

Gly Lys Tyr Cys Phe Gly Val Glu Asp Thr Leu Lys Ala Leu Glu Met
305 310 315 320

Gly Ala Val Glu Ile Leu Ile Val Tyr Glu Asn Leu Asp Ile Met Arg
325 330 335

Tyr Val Leu His Cys Gln Gly Thr Glu Glu Glu Lys Ile Leu Tyr Leu
340 345 350

Thr Pro Glu Gln Glu Lys Asp Lys Ser His Phe Thr Asp Lys Glu Xaa
355 360 365

Arg Thr Gly Thr Met Xaa Leu Ser Arg Ala Xaa Pro Xaa Leu Glu Xaa
370 375 380

Xaa Xaa Asn Asn Xaa Lys Lys Leu Gly Leu Pro Trp Xaa Ile Gly Pro
385 390 395 400

Ile Asn Ser Xaa Xaa Arg Gly Gln Xaa Trp Lys Arg Ile Gly Gly
405 410 415

<210> 1361

<211> 119

<212> PRT

<213> Homo sapiens

<400> 1361

His Ala Ser Ala Asp Ala Trp Ala Asp Ala Trp Val Ala Gly Ser Asp
1 5 10 15

Phe Ile Lys Thr Ser Thr Gly Lys Glu Thr Val Asn Ala Thr Phe Pro
20 25 30

Val Ala Ile Val Met Leu Arg Ala Ile Arg Asp Phe Phe Trp Lys Thr
35 40 45

Gly Asn Lys Ile Gly Phe Lys Pro Ala Gly Gly Ile Arg Ser Ala Lys
50 55 60

Asp Ser Leu Ala Trp Leu Ser Leu Val Lys Glu Glu Leu Gly Asp Glu

1413

65 70 75 80

Trp Leu Lys Pro Glu Leu Phe Arg Ile Gly Ala Ser Thr Leu Leu Ser
 85 90 95

Asp Ile Glu Arg Gln Ile Tyr His His Val Thr Gly Arg Tyr Ala Ala
 100 105 110

Tyr His Asp Leu Pro Met Ser
 115

<210> 1362
 <211> 282
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (34)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (35)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1362

Gly Arg Val Gly Gly Arg Val Gly Gly Arg Val Gly Phe Thr Ala Lys
 1 5 10 15

Val Trp Asp Ala Val Ser Gly Asp Glu Leu Met Thr Leu Ala His Lys
 20 25 30

His Xaa Xaa Lys Thr Val Asp Phe Thr Gln Asp Ser Asn Tyr Leu Leu
 35 40 45

Thr Gly Gly Gln Asp Lys Leu Leu Arg Ile Tyr Asp Leu Asn Lys Pro
 50 55 60

Glu Ala Glu Pro Lys Glu Ile Ser Gly His Thr Ser Gly Ile Lys Lys
 65 70 75 80

Ala Leu Trp Cys Ser Glu Asp Lys Gln Ile Leu Ser Ala Asp Asp Lys
 85 90 95

Thr Val Arg Leu Trp Asp His Ala Thr Met Thr Glu Val Lys Ser Leu
 100 105 110

Asn Phe Asn Met Ser Val Ser Ser Met Glu Tyr Ile Pro Glu Gly Glu

1414

115	120	125
Ile Leu Val Ile Thr Tyr Gly Arg Ser Ile Ala Phe His Ser Ala Val		
130	135	140
Ser Leu Asp Pro Ile Lys Ser Phe Glu Ala Pro Ala Thr Ile Asn Ser		
145	150	155 160
Ala Ser Leu His Pro Glu Lys Glu Phe Leu Val Ala Gly Gly Glu Asp		
165	170	175
Phe Lys Leu Tyr Lys Tyr Asp Tyr Asn Ser Gly Glu Glu Leu Glu Ser		
180	185	190
Tyr Lys Gly His Phe Gly Pro Ile His Cys Val Arg Phe Ser Pro Asp		
195	200	205
Gly Glu Leu Tyr Ala Ser Gly Ser Glu Asp Gly Thr Leu Arg Leu Trp		
210	215	220
Gln Thr Val Val Gly Lys Thr Tyr Gly Leu Trp Lys Cys Val Leu Pro		
225	230	235 240
Glu Glu Asp Ser Gly Glu Leu Ala Lys Pro Lys Ile Gly Phe Pro Glu		
245	250	255
Thr Thr Glu Glu Glu Leu Glu Glu Ile Ala Ser Glu Asn Ser Asp Cys		
260	265	270
Ile Phe Pro Ser Ala Pro Asp Val Lys Ala		
275	280	

<210> 1363

<211> 334

<212> PRT

<213> Homo sapiens

<400> 1363

Thr Pro Arg Thr Pro Glu Pro His Lys Pro Gly Leu Ala Met Lys Pro		
1	5	10 15
Gly Phe Ser Pro Arg Gly Gly Gly Phe Gly Gly Arg Gly Gly Phe Gly		
20	25	30
Asp Arg Gly Gly Arg Gly Gly Arg Gly Gly Phe Gly Gly Gly Arg Gly		
35	40	45
Arg Gly Gly Gly Phe Arg Gly Arg Gly Arg Gly Gly Gly Gly Gly		
50	55	60

1415

Gly Gly Gly Gly Gly Gly Gly Arg Gly Gly Gly Gly Phe His Ser Gly
 65 70 75 80
 Gly Asn Arg Gly Arg Gly Arg Gly Gly Lys Arg Gly Asn Gln Ser Gly
 85 90 95
 Lys Asn Val Met Val Glu Pro His Arg His Glu Gly Val Phe Ile Cys
 100 105 110
 Arg Gly Lys Glu Asp Ala Leu Val Thr Lys Asn Leu Val Pro Gly Glu
 115 120 125
 Ser Val Tyr Gly Glu Lys Arg Val Ser Ile Ser Glu Gly Asp Asp Lys
 130 135 140
 Ile Glu Tyr Arg Ala Trp Asn Pro Phe Arg Ser Lys Leu Ala Ala Ala
 145 150 155 160
 Ile Leu Gly Gly Val Asp Gln Ile His Ile Lys Pro Gly Ala Lys Val
 165 170 175
 Leu Tyr Leu Gly Ala Ala Ser Gly Thr Thr Val Ser His Val Ser Asp
 180 185 190
 Ile Val Gly Pro Asp Gly Leu Val Tyr Ala Val Glu Phe Ser His Arg
 195 200 205
 Ser Gly Arg Asp Leu Ile Asn Leu Ala Lys Lys Arg Thr Asn Ile Ile
 210 215 220
 Pro Val Ile Glu Asp Ala Arg His Pro His Lys Tyr Arg Met Leu Ile
 225 230 235 240
 Ala Met Val Asp Val Ile Phe Ala Asp Val Ala Gln Pro Asp Gln Thr
 245 250 255
 Arg Ile Val Ala Leu Asn Ala His Thr Phe Leu Arg Asn Gly Gly His
 260 265 270
 Phe Val Ile Ser Ile Lys Ala Asn Cys Ile Asp Ser Thr Ala Ser Ala
 275 280 285
 Glu Ala Val Phe Ala Ser Glu Val Lys Lys Met Gln Gln Glu Asn Met
 290 295 300
 Lys Pro Gln Glu Gln Leu Thr Leu Glu Pro Tyr Glu Arg Asp His Ala
 305 310 315 320
 Val Val Val Gly Val Tyr Arg Pro Pro Pro Lys Val Lys Asn
 325 330

1416

<210> 1364

<211> 602

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (356)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1364

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Pro Gly Ala Glu Lys Ser Gly Arg Ala Ala Glu Arg Pro Gly Arg Gly
 1             5             10             15

Pro Gly Arg Gly Ala His Ser Arg Pro Thr Ala Pro Arg Glu Arg Ala
      20             25             30

Pro Arg Ser Pro Ala Pro Ser Pro Pro Gly Met Gly Arg Ala Ala Ala
      35             40             45

Ala Glu Ala Pro Ala Trp Pro Gly Arg Thr Arg Pro Glu Ala Glu Gly
      50             55             60

Arg Ala Arg Ala Gln Leu Pro Gly His Gln Ile Gly Ala Arg Arg Ala
      65             70             75             80

Gly Gly Pro Arg Ala Gly Leu Glu Met Ser Trp Pro Arg Arg Leu Leu
      85             90             95

Leu Arg Tyr Leu Phe Pro Ala Leu Leu Leu His Gly Leu Gly Glu Gly
      100            105            110

Ser Ala Leu Leu His Pro Asp Ser Arg Ser His Pro Arg Ser Leu Glu
      115            120            125

Lys Ser Ala Trp Arg Ala Phe Lys Glu Ser Gln Cys His His Met Leu
      130            135            140

Lys His Leu His Asn Gly Ala Arg Ile Thr Val Gln Met Pro Pro Thr
      145            150            155            160

Ile Glu Gly His Trp Val Ser Thr Gly Cys Glu Val Arg Ser Gly Pro
      165            170            175

Glu Phe Ile Thr Arg Ser Tyr Arg Phe Tyr His Asn Asn Thr Phe Lys
      180            185            190

Ala Tyr Gln Phe Tyr Tyr Gly Ser Asn Arg Cys Thr Asn Pro Thr Tyr

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1417

195	200	205
Thr Leu Ile Ile Arg Gly Lys Ile Arg Leu Arg Gln Ala Ser Trp Ile		
210	215	220
Ile Arg Gly Gly Thr Glu Ala Asp Tyr Gln Leu His Asn Val Gln Val		
225	230	235 240
Ile Cys His Thr Glu Ala Val Ala Glu Lys Leu Gly Gln Gln Val Asn		
	245	250 255
Arg Thr Cys Pro Gly Phe Leu Ala Asp Gly Gly Pro Trp Val Gln Asp		
	260	265 270
Val Ala Tyr Asp Leu Trp Arg Glu Glu Asn Gly Cys Glu Cys Thr Lys		
	275	280 285
Ala Val Asn Phe Ala Met His Glu Leu Gln Leu Ile Arg Val Glu Lys		
	290	295 300
Gln Tyr Leu His His Asn Leu Asp His Leu Val Glu Glu Leu Phe Leu		
305	310	315 320
Gly Asp Ile His Thr Asp Ala Thr Gln Arg Met Phe Tyr Arg Pro Ser		
	325	330 335
Ser Tyr Gln Pro Pro Leu Gln Asn Ala Lys Asn His Asp His Ala Cys		
	340	345 350
Ile Ala Cys Xaa Ile Ile Tyr Arg Ser Asp Glu His His Pro Pro Ile		
	355	360 365
Leu Pro Pro Lys Ala Asp Leu Thr Ile Gly Leu His Gly Glu Trp Val		
	370	375 380
Ser Gln Arg Cys Glu Val Arg Pro Glu Val Leu Phe Leu Thr Arg His		
385	390	395 400
Phe Ile Phe His Asp Asn Asn Asn Thr Trp Glu Gly His Tyr Tyr His		
	405	410 415
Tyr Ser Asp Pro Val Cys Lys His Pro Thr Phe Ser Ile Tyr Ala Arg		
	420	425 430
Gly Arg Tyr Ser Arg Gly Val Leu Ser Ser Arg Val Met Gly Gly Thr		
	435	440 445
Glu Phe Val Phe Lys Val Asn His Met Lys Val Thr Pro Met Asp Ala		
	450	455 460
Ala Thr Ala Ser Leu Leu Asn Val Phe Asn Gly Asn Glu Cys Gly Ala		

1418

465 470 475 480
Glu Gly Ser Trp Gln Val Gly Ile Gln Gln Asp Val Thr His Thr Asn
 485 490 495
Gly Cys Val Ala Leu Gly Ile Lys Leu Pro His Thr Glu Tyr Glu Ile
 500 505 510
Phe Lys Met Glu Gln Asp Ala Arg Gly Arg Tyr Leu Leu Phe Asn Gly
 515 520 525
Gln Arg Pro Ser Asp Gly Ser Ser Pro Asp Arg Pro Glu Lys Arg Ala
 530 535 540
Thr Ser Tyr Gln Met Pro Leu Val Gln Cys Ala Ser Ser Ser Pro Arg
545 550 555 560
Ala Glu Asp Leu Ala Glu Asp Ser Gly Ser Ser Leu Tyr Gly Arg Ala
 565 570 575
Pro Gly Arg His Thr Trp Ser Leu Leu Leu Ala Ala Leu Ala Cys Leu
 580 585 590
Val Pro Leu Leu His Trp Asn Ile Arg Arg
 595 600

<210> 1365

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (26)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (40)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (78)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (98)

1419

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (136)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (141)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (142)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1365

Ser	Asn	Ser	Gly	Tyr	Pro	Phe	Trp	Thr	Pro	Ser	Met	Leu	Trp	Lys	Leu
1				5					10					15	

Cys	Thr	Phe	Thr	Leu	Leu	Asn	Lys	Ala	Xaa	Ser	Phe	Phe	Ser	Leu	Ser
			20					25					30		

Val	His	Val	Ser	Phe	Thr	His	Xaa	Gly	Gln	Leu	Pro	His	His	Phe	Phe
	35						40					45			

Gly	Val	Ala	Trp	Gln	Glu	Pro	Gln	Val	Leu	His	Leu	Gly	Glu	Pro	Asp
	50					55					60				

Arg	Arg	Leu	Gln	Lys	Arg	Ile	Lys	Ala	Ile	Lys	Leu	Gln	Xaa	Ile	Leu
65				70						75				80	

Gln	Met	Glu	Pro	Gln	Met	Ser	Ser	Ala	His	Gly	Phe	Tyr	Arg	Gly	Pro
			85						90					95	

Leu	Xaa	Gln	Pro	Ala	Gly	Pro	Ser	Ile	Thr	Leu	Glu	Asn	Ser	Pro	Leu
		100						105					110		

Glu	Asp	Thr	Lys	Leu	Gln	Gly	Pro	Phe	Phe	Thr	Pro	Asn	Gln	Gln	Glu
	115					120						125			

Val	Ala	Arg	Thr	Asp	Cys	His	Xaa	Val	Pro	Asn	Ser	Xaa	Xaa	Gly	Cys
	130					135					140				

Pro	Val	Leu	Glu	Ala	Gly	Phe	Arg	Gly	Gly	Ala	Gln	Leu	Gly
145					150					155			

<210> 1366

1420

<211> 466
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (4)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (12)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (205)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (220)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (347)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1366
 Ser Thr Arg Xaa Arg Glu Gly Asn Ser His Ser Xaa Gly His Lys Thr
 1 5 10 15
 Ile Gln Gly Ser Leu Gly Arg Leu Ser Ser Ala Val Pro Gly Ser Gly
 20 25 30
 Ala Glu Leu Ser Pro Val Pro Asn Thr Asp Gly Thr Met Asn Ser Gly
 35 40 45
 His Ser Phe Ser Gln Thr Pro Ser Ala Ser Phe His Gly Ala Gly Gly
 50 55 60
 Gly Trp Gly Arg Pro Arg Ser Phe Pro Arg Ala Pro Thr Val His Gly
 65 70 75 80
 Gly Ala Gly Gly Ala Arg Ile Ser Leu Ser Phe Thr Thr Arg Ser Cys
 85 90 95
 Pro Pro Pro Gly Ser Trp Gly Ser Gly Arg Ser Ser Pro Leu Leu
 100 105 110

1421

Gly Gly Asn Gly Lys Ala Thr Met Gln Asn Leu Asn Asp Arg Leu Ala
 115 120 125
 Ser Tyr Leu Glu Lys Val Arg Ala Leu Glu Glu Ala Asn Met Lys Leu
 130 135 140
 Glu Ser Arg Ile Leu Lys Trp His Gln Gln Arg Asp Pro Gly Ser Lys
 145 150 155 160
 Lys Asp Tyr Ser Gln Tyr Glu Glu Asn Ile Thr His Leu Gln Glu Gln
 165 170 175
 Ile Val Asp Gly Lys Met Thr Asn Ala Gln Ile Ile Leu Leu Ile Asp
 180 185 190
 Asn Ala Arg Met Ala Val Asp Asp Phe Asn Leu Lys Xaa Glu Asn Glu
 195 200 205
 His Ser Phe Lys Lys Asp Leu Glu Ile Glu Val Xaa Gly Leu Arg Arg
 210 215 220
 Thr Leu Asp Asn Leu Thr Ile Val Thr Thr Asp Leu Glu Gln Glu Val
 225 230 235 240
 Glu Gly Met Arg Lys Glu Leu Ile Leu Met Lys Lys His His Glu Gln
 245 250 255
 Glu Met Glu Lys His His Val Pro Ser Asp Phe Asn Val Asn Val Lys
 260 265 270
 Val Asp Thr Gly Pro Arg Glu Asp Leu Ile Lys Val Leu Glu Asp Met
 275 280 285
 Arg Gln Glu Tyr Glu Leu Ile Ile Lys Lys Lys His Arg Asp Leu Asp
 290 295 300
 Thr Trp Tyr Lys Glu Gln Ser Ala Ala Met Ser Gln Glu Ala Ala Ser
 305 310 315 320
 Pro Ala Thr Val Gln Ser Arg Gln Gly Asp Ile His Glu Leu Lys Arg
 325 330 335
 Thr Phe Gln Ala Leu Glu Ile Asp Leu Gln Xaa Gln Tyr Ser Thr Lys
 340 345 350
 Ser Ala Leu Glu Asn Met Leu Ser Glu Thr Gln Ser Arg Tyr Ser Cys
 355 360 365
 Lys Leu Gln Asp Met Gln Glu Ile Ile Ser His Tyr Glu Glu Glu Leu
 370 375 380

1422

Thr Gln Leu Arg His Glu Leu Glu Arg Gln Asn Asn Glu Tyr Gln Val
385 390 395 400

Leu Leu Gly Ile Lys Thr His Leu Glu Lys Glu Ile Thr Thr Tyr Arg
405 410 415

Arg Leu Leu Glu Gly Glu Ser Glu Gly Thr Arg Glu Glu Ser Lys Ser
420 425 430

Ser Met Lys Val Ser Ala Thr Pro Lys Ile Lys Ala Ile Thr Gln Glu
435 440 445

Thr Ile Asn Gly Arg Leu Val Leu Cys Gln Val Asn Glu Ile Gln Lys
450 455 460

His Ala
465

<210> 1367

<211> 153

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (136)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (138)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (141)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (142)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (143)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1423

<221> SITE

<222> (152)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1367

Leu Arg Phe Ala Ser Pro Gly Pro Gly Ala Gly Arg Ala Arg Asp Ser
1 5 10 15

Gln Arg Lys Trp Arg Arg Leu Arg Ala Arg Pro Leu Leu Gly Pro Gly
20 25 30

Gln Gly Trp Ser Trp Ala Gly Ile Pro Ser Ser Ala Ala Ala Gln Arg
35 40 45

Ala Gly Pro Pro Ala Gly Ala Leu Glu Ala Leu Ser Pro Gly Gly Ala
50 55 60

Arg Ala His Ala Glu Arg Arg Gly Glu Met Arg Ala Thr Pro Leu Ala
65 70 75 80

Ala Pro Ala Gly Ser Leu Ser Arg Lys Lys Arg Leu Glu Leu Asp Asp
85 90 95

Asn Leu Asp Thr Glu Arg Pro Val Gln Lys Arg Ala Arg Ser Gly Pro
100 105 110

Gln Pro Arg Leu Pro Pro Cys Leu Leu Pro Leu Ser Pro Pro Thr Ala
115 120 125

Pro Asp Arg Ala Thr Ala Val Xaa Thr Xaa Ser Arg Xaa Xaa Xaa Tyr
130 135 140

Val Leu Leu Glu Ala Arg Arg Xaa Ala
145 150

<210> 1368

<211> 399

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (13)

<223> Xaa equals any of the naturally occurring L-amino acids

1424

<400> 1368

Ser Asp Asn Xaa Thr Asn Gly Cys Gly Leu Glu Ser Xaa Gly Asn Thr
1 5 10 15

Val Thr Pro Val Asn Val Asn Glu Val Lys Pro Ile Asn Lys Gly Glu
20 25 30

Glu Gln Ile Gly Phe Glu Leu Val Glu Lys Leu Phe Gln Gly Gln Leu
35 40 45

Val Leu Arg Thr Arg Cys Leu Glu Cys Glu Ser Leu Thr Glu Arg Arg
50 55 60

Glu Asp Phe Gln Asp Ile Ser Val Pro Val Gln Glu Asp Glu Leu Ser
65 70 75 80

Lys Val Glu Glu Ser Ser Glu Ile Ser Pro Glu Pro Lys Thr Glu Met
85 90 95

Lys Thr Leu Arg Trp Ala Ile Ser Gln Phe Ala Ser Val Glu Arg Ile
100 105 110

Val Gly Glu Asp Lys Tyr Phe Cys Glu Asn Cys His His Tyr Thr Glu
115 120 125

Ala Glu Arg Ser Leu Leu Phe Asp Lys Met Pro Glu Val Ile Thr Ile
130 135 140

His Leu Lys Cys Phe Ala Ala Ser Gly Leu Glu Phe Asp Cys Tyr Gly
145 150 155 160

Gly Gly Leu Ser Lys Ile Asn Thr Pro Leu Leu Thr Pro Leu Lys Leu
165 170 175

Ser Leu Glu Glu Trp Ser Thr Lys Pro Thr Asn Asp Ser Tyr Gly Leu
180 185 190

Phe Ala Val Val Met His Ser Gly Ile Thr Ile Ser Ser Gly His Tyr
195 200 205

Thr Ala Ser Val Lys Val Thr Asp Leu Asn Ser Leu Glu Leu Asp Lys
210 215 220

Gly Asn Phe Val Val Asp Gln Met Cys Glu Ile Gly Lys Pro Glu Pro
225 230 235 240

Leu Asn Glu Glu Glu Ala Arg Gly Val Val Glu Asn Tyr Asn Asp Glu
245 250 255

Glu Val Ser Ile Arg Val Gly Gly Asn Thr Gln Pro Ser Lys Val Leu

1425

260	265	270
Asn Lys Lys Asn Val Glu Ala Ile Gly Leu Leu Gly Gly Gln Lys Ser		
275	280	285
Lys Ala Asp Tyr Glu Leu Tyr Asn Lys Ala Ser Asn Pro Asp Lys Val		
290	295	300
Ala Ser Thr Ala Phe Ala Glu Asn Arg Asn Ser Glu Thr Ser Asp Thr		
305	310	315
Thr Gly Thr His Glu Ser Asp Arg Asn Lys Glu Ser Ser Asp Gln Thr		
325	330	335
Gly Ile Asn Ile Ser Gly Phe Glu Asn Lys Ile Ser Tyr Val Val Gln		
340	345	350
Ser Leu Lys Glu Tyr Glu Gly Lys Trp Leu Leu Phe Asp Asp Ser Glu		
355	360	365
Val Lys Val Thr Glu Glu Lys Asp Phe Leu Asn Ser Leu Ser Pro Ser		
370	375	380
Thr Ser Pro Thr Ser Thr Pro Tyr Leu Leu Phe Tyr Lys Lys Leu		
385	390	395

<210> 1369

<211> 260

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1369

Val	Phe	Xaa	Ser	Phe	Phe	Ala	Glu	Lys	Glu	Gln	Gln	Glu	Ala	Ile	Glu
1				5					10					15	

His	Ile	Asp	Glu	Val	Gln	Asn	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Gln	Ala
			20						25					30	

Ser	Glu	Glu	Ile	Leu	Lys	Val	Glu	Gln	Lys	Tyr	Asn	Lys	Leu	Arg	Gln
		35						40					45		

Pro	Phe	Phe	Gln	Lys	Arg	Ser	Glu	Leu	Ile	Ala	Lys	Ile	Pro	Asn	Phe
	50						55					60			

1426

Trp Val Thr Thr Phe Val Asn His Pro Gln Val Ser Ala Leu Leu Gly
 65 70 75 80
 Glu Glu Asp Glu Glu Ala Leu His Tyr Leu Thr Arg Val Glu Val Thr
 85 90 95
 Glu Phe Glu Asp Ile Lys Ser Gly Tyr Arg Ile Asp Phe Tyr Phe Asp
 100 105 110
 Glu Asn Pro Tyr Phe Glu Asn Lys Val Leu Ser Lys Glu Phe His Leu
 115 120 125
 Asn Glu Ser Gly Asp Pro Ser Ser Lys Ser Thr Glu Ile Lys Trp Lys
 130 135 140
 Ser Gly Lys Asp Leu Thr Lys Arg Ser Ser Gln Thr Gln Asn Lys Ala
 145 150 155 160
 Ser Arg Lys Arg Gln His Glu Glu Pro Glu Ser Phe Phe Thr Trp Phe
 165 170 175
 Thr Asp His Ser Asp Ala Gly Ala Asp Glu Leu Gly Glu Val Ile Lys
 180 185 190
 Asp Asp Ile Trp Pro Asn Pro Leu Gln Tyr Tyr Leu Val Pro Asp Met
 195 200 205
 Asp Asp Glu Glu Gly Glu Gly Glu Glu Asp Asp Asp Asp Asp Glu Glu
 210 215 220
 Glu Glu Gly Leu Glu Asp Ile Asp Glu Glu Gly Asp Glu Asp Glu Gly
 225 230 235 240
 Glu Glu Asp Glu Asp Asp Asp Glu Gly Glu Glu Gly Glu Glu Asp Glu
 245 250 255
 Gly Glu Asp Asp
 260

<210> 1370

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1370

Lys Gly Glu Ala Ala Ala Phe Ser Ala Thr Phe Pro Ile Ala Arg Gln
 1 5 10 15

Glu Phe Leu Ser Val Thr Thr Ile Ala Val Met Ser Gly Arg Gly Lys

1427

20 25 30
 Gln Gly Gly Lys Ala Arg Ala Lys Ala Lys Ser Arg Ser Ser Arg Ala
 35 40 45
 Gly Leu Gln Phe Pro Val Gly Glu Cys Ile Ala Leu Arg Lys Gly Asn
 50 55 60
 Tyr Ala Glu Arg Val Gly Ala Gly Ala Pro Val Tyr Met Ala Ala Val
 65 70 75 80
 Leu Glu Tyr Leu Thr Ala Glu Ile Leu Glu Leu Ala Gly Asn Ala Ala
 85 90 95
 Arg Asp Asn Lys Lys Thr Arg Ile Ile Pro Arg His Leu Gln Leu Ala
 100 105 110
 Ile Arg Asn Asp Glu Glu Leu Asn Lys Leu Leu Gly Lys Val Thr Ile
 115 120 125
 Ala Gln Gly Gly Val Leu Pro Asn Ile Gln Ala Val Leu Leu Pro Lys
 130 135 140
 Lys Thr Glu Ser His His Lys Ala Lys Gly Lys
 145 150 155

<210> 1371
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 1371
 Phe Pro Gly Arg Thr His Ala Leu Cys Arg Gly Ala Ala Ser Arg Gly
 1 5 10 15
 Leu Leu Cys Lys Trp Ala Pro Trp Pro Ser Ala Pro Val Pro Ala Thr
 20 25 30
 Arg Asp Arg Ala Pro Arg Pro Ala Arg Gly Arg Arg Pro Asp Pro Thr
 35 40 45
 Ser Gln Gln Ala Lys Ala Trp Arg Pro Ser Pro Pro Ala Ala Arg Ser
 50 55 60
 Trp Pro Pro Thr Thr Thr Thr Gly Ala Ala Trp Val Pro Leu Pro Ala
 65 70 75 80
 Thr Ala Pro Ala Ala Val Pro Ser Ala Pro Gly Lys Pro Phe Pro Thr
 85 90 95

1428

Pro Gln Val Ser Pro Arg Leu Thr Arg Val Ile Gly Gly Pro Ala Ser
100 105 110

Phe Ser Gly Ser Pro Pro Ser Arg Ser Trp Pro Arg Cys Trp Ser Pro
115 120 125

Gln Ser Thr Arg Asn Leu Pro Arg Pro Pro Ala Ala
130 135 140

<210> 1372

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (126)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (127)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (128)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (135)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (142)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (147)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1372

Pro Trp Thr Leu Gly Gly Pro Glu Leu Asp Ala Met Gly Gly Cys Ala
1 5 10 15

1429

Gly Ser Arg Arg Arg Phe Ser Asp Ser Glu Gly Glu Glu Thr Val Pro
 20 25 30
 Glu Pro Arg Leu Pro Leu Leu Asp His Gln Gly Ala His Trp Lys Asn
 35 40 45
 Ala Val Gly Phe Trp Leu Leu Gly Leu Cys Asn Asn Phe Ser Tyr Val
 50 55 60
 Val Met Leu Ser Ala Ala His Asp Ile Leu Ser His Lys Arg Thr Ser
 65 70 75 80
 Gly Asn Gln Ser His Val Asp Pro Gly Pro Thr Pro Ile Pro His Asn
 85 90 95
 Ser Ser Ser Arg Phe Asp Cys Asn Ser Val Ser Thr Ala Ala Val Leu
 100 105 110
 Leu Ala Asp Ile Leu Pro Thr Leu Val Ile Lys Leu Leu Xaa Xaa Xaa
 115 120 125
 Gly Leu His Leu Leu Pro Xaa Thr Val Glu Asp Ala Val Xaa Leu Cys
 130 135 140
 Ala Leu Xaa Gly Thr Ala
 145 150

<210> 1373

<211> 128

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (21)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (121)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1373

Arg His Ser Arg Val Asp Pro Arg Val Arg Ala Arg Phe Arg Arg Arg
 1 5 10 15

Arg Ala Phe Ala Xaa Leu Gly Trp Ser Ser Gly Arg Val Ser Arg Pro
 20 25 30

1430

Glu His Val Asp Ala His Pro Pro Leu Ser Leu Met Glu Val Val Thr
 35 40 45
 Phe Gly Asp Val Ala Val His Phe Ser Arg Glu Glu Trp Gln Cys Leu
 50 55 60
 Asp Pro Gly Gln Arg Ala Leu Tyr Arg Glu Val Met Leu Glu Asn His
 65 70 75 80
 Ser Ser Val Ala Gly Leu Ala Gly Phe Leu Val Phe Lys Pro Glu Leu
 85 90 95
 Ile Ser Arg Leu Glu Gln Gly Glu Glu Pro Trp Val Leu Asp Leu Gln
 100 105 110
 Gly Ala Glu Gly Thr Glu Ala Pro Xaa Thr Ser Lys Thr Gly Glu Ala
 115 120 125

<210> 1374

<211> 398

<212> PRT

<213> Homo sapiens

<400> 1374

Ser Ser Trp Leu Arg Ser Arg Ser Gly Met Gln Thr Asp Leu Gln Asn
 1 5 10 15
 Leu Gly Asn Asp Ser Gly Asp His Ser Asp His Met His Tyr Tyr Gln
 20 25 30
 Gly Lys Lys Tyr Phe Arg Asp Arg Arg Gly Gly Gly Arg Asn Ser Asp
 35 40 45
 Trp Ser Ser Asp Thr Asn Arg Gln Gly Gln Gln Ser Ser Ser Asp Cys
 50 55 60
 Tyr Ile Tyr Asp Ser Ala Thr Gly Tyr Tyr Tyr Asp Pro Leu Ala Gly
 65 70 75 80
 Thr Tyr Tyr Asp Pro Asn Thr Gln Gln Glu Val Tyr Val Pro Gln Asp
 85 90 95
 Pro Gly Leu Pro Glu Glu Glu Glu Ile Lys Glu Lys Lys Pro Thr Ser
 100 105 110
 Gln Gly Lys Ser Ser Ser Lys Lys Glu Met Ser Lys Arg Asp Gly Lys

1431

115	120	125
Glu Lys Lys Asp Arg Gly Val Thr Arg Phe Gln Glu Asn Ala Ser Glu		
130	135	140
Gly Lys Ala Pro Ala Glu Asp Val Phe Lys Lys Pro Leu Pro Pro Thr		
145	150	155 160
Val Lys Lys Glu Glu Ser Pro Pro Pro Lys Val Val Asn Pro Leu		
165	170	175
Ile Gly Leu Leu Gly Glu Tyr Gly Gly Asp Ser Asp Tyr Glu Glu Glu		
180	185	190
Glu Glu Glu Glu Gln Thr Pro Pro Pro Gln Pro Arg Thr Ala Gln Pro		
195	200	205
Gln Lys Arg Glu Glu Gln Thr Lys Lys Glu Asn Glu Glu Asp Lys Leu		
210	215	220
Thr Asp Trp Asn Lys Leu Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro		
225	230	235 240
Asn Lys Glu Val Leu Ile Lys His Gln Gln Leu Ser Asp Leu His Lys		
245	250	255
Gln Asn Leu Glu Ile His Arg Lys Ile Lys Gln Ser Glu Gln Glu Leu		
260	265	270
Ala Tyr Leu Glu Arg Arg Glu Arg Glu Gly Lys Phe Lys Gly Arg Gly		
275	280	285
Asn Asp Arg Arg Glu Lys Leu Gln Ser Phe Asp Ser Pro Glu Arg Lys		
290	295	300
Arg Ile Lys Tyr Ser Arg Glu Thr Asp Ser Asp Arg Lys Leu Val Asp		
305	310	315 320
Lys Glu Asp Ile Asp Thr Ser Ser Lys Gly Gly Cys Val Gln Gln Ala		
325	330	335
Thr Gly Trp Arg Lys Gly Thr Gly Leu Gly Tyr Gly His Pro Gly Leu		
340	345	350
Ala Ser Ser Glu Glu Ala Glu Gly Arg Met Arg Gly Pro Ser Val Gly		
355	360	365
Ala Ser Gly Arg Thr Ser Lys Arg Gln Ser Asn Glu Thr Tyr Arg Asp		
370	375	380
Ala Val Arg Arg Val Met Phe Ala Arg Tyr Lys Glu Leu Asp		

1432

385

390

395

<210> 1375

<211> 167

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (157)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (161)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (163)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1375

His Arg Gly Lys Arg Tyr Thr Asp Ser Thr Val Arg Asn Ser Arg Val
1 5 10 15

Asp Pro Arg Val Arg Ser Ala Lys Pro Glu Ser Cys Pro Phe Ser Leu
20 25 30

Pro Gly Gln His Glu Leu His His Ser Leu His Leu Leu His Gln Leu
35 40 45

Pro Val Pro Gly Leu Cys Pro Gly Ala Gln Leu Arg Arg Pro Ala Gly
50 55 60

Gln Gln Arg Gly Gln Arg Leu Cys Arg Arg Trp Gly Leu Trp Phe Pro
65 70 75 80

Asp Leu Arg Val Pro Leu His Gln Leu Gln Gly Arg His Gly Val Arg
85 90 95

Gly Pro Gly His Arg Asp Ser Arg Gly Ser Gly Arg Asn Gly Ser Ile
100 105 110

Gln Asn Glu Lys Glu Thr Met Gln Lys Leu Asn Asp Arg Leu Ala Ser
115 120 125

Tyr Leu Asp Lys Met Lys Glu Pro Gly Asp Arg Glu Thr Gly Gly Trp
130 135 140

1433

Lys Ala Lys Thr Arg Glu His Phe Gly Glu Glu Gly Xaa Gln Val Arg
 145 150 155 160

Xaa Trp Xaa Pro Leu Ile Gln
 165

<210> 1376

<211> 448

<212> PRT

<213> Homo sapiens

<400> 1376

Leu Pro Asp Val Glu Lys Leu Gly Arg Arg Arg Gly Arg Lys Met Asp
 1 5 10 15

Ser Val Glu Lys Gly Ala Ala Thr Ser Val Ser Asn Pro Arg Gly Arg
 20 25 30

Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg Gly Gly
 35 40 45

Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu Ile Leu
 50 55 60

Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys His Leu
 65 70 75 80

Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu Asp Ser
 85 90 95

Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu Ile Glu
 100 105 110

Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser Ser Glu
 115 120 125

Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu Phe Leu
 130 135 140

Asn Tyr His Asn Glu Val Asp Ile Val Gly Asn Ile Gln Ala Thr Ser
 145 150 155 160

Pro Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met Ile Arg
 165 170 175

Glu Glu Gly Tyr Asp Ser Val Phe Ser Val Val Arg Arg His Gln Phe
 180 185 190

1434

Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu Pro Leu
195 200 205

Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp Gly Glu
210 215 220

Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu Ile Glu
225 230 235 240

Met Gly Tyr Leu Gln Gly Gly Lys Met Ala Tyr Tyr Glu Met Arg Ala
245 250 255

Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile Ala Glu
260 265 270

Gln Arg Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu Lys Glu
275 280 285

Ile Lys Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn Gly His
290 295 300

Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp Val Lys
305 310 315 320

Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu Val Arg
325 330 335

Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser Leu Lys
340 345 350

Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala Val Val
355 360 365

Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val Ala Tyr
370 375 380

Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val Gly Leu
385 390 395 400

Ser Gly Ala Pro Ala Asp Ala Cys Ser Thr Ala Gln Lys Ala Val Gly
405 410 415

Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu Phe Ala
420 425 430

Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys Gln Lys
435 440 445

1435

<210> 1377

<211> 469

<212> PRT

<213> Homo sapiens

<400> 1377

Gly Gly Pro Ala Lys Met Ala Ala Ser Cys Leu Val Leu Leu Ala Leu
1 5 10 15

Cys Leu Leu Leu Pro Leu Leu Leu Leu Gly Gly Trp Lys Arg Trp Arg
20 25 30

Arg Gly Arg Ala Ala Arg His Val Val Ala Val Val Leu Gly Asp Val
35 40 45

Gly Arg Ser Pro Arg Met Gln Tyr His Ala Leu Ser Leu Ala Met His
50 55 60

Gly Phe Ser Val Thr Leu Leu Gly Phe Cys Asn Ser Lys Pro His Asp
65 70 75 80

Glu Leu Leu Gln Asn Asn Arg Ile Gln Ile Val Gly Leu Thr Glu Leu
85 90 95

Gln Ser Leu Ala Val Gly Pro Arg Val Phe Gln Tyr Gly Val Lys Val
100 105 110

Val Leu Gln Ala Met Tyr Leu Leu Trp Lys Leu Met Trp Arg Glu Pro
115 120 125

Gly Ala Tyr Ile Phe Leu Gln Asn Pro Pro Gly Leu Pro Ser Ile Ala
130 135 140

Val Cys Trp Phe Val Gly Cys Leu Cys Gly Ser Lys Leu Val Ile Asp
145 150 155 160

Trp His Asn Tyr Gly Tyr Ser Ile Met Gly Leu Val His Gly Pro Asn
165 170 175

His Pro Leu Val Leu Leu Ala Lys Trp Tyr Glu Lys Phe Phe Gly Arg
180 185 190

Leu Ser His Leu Asn Leu Cys Val Thr Asn Ala Met Arg Glu Asp Leu
195 200 205

Ala Asp Asn Trp His Ile Arg Ala Val Thr Val Tyr Asp Lys Pro Ala
210 215 220

Ser Phe Phe Lys Glu Thr Pro Leu Asp Leu Gln His Arg Leu Phe Met

1436

225		230		235		240									
Lys	Leu	Gly	Ser	Met	His	Ser	Pro	Phe	Arg	Ala	Arg	Ser	Glu	Pro	Glu
				245					250					255	
Asp	Pro	Val	Thr	Glu	Arg	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Ala	Gly	Ser
			260					265					270		
Gly	Leu	Val	Thr	Arg	Leu	Arg	Glu	Arg	Pro	Ala	Leu	Leu	Val	Ser	Ser
		275					280						285		
Thr	Ser	Trp	Thr	Glu	Asp	Glu	Asp	Phe	Ser	Ile	Leu	Leu	Ala	Ala	Leu
	290						295					300			
Glu	Lys	Phe	Glu	Gln	Leu	Thr	Leu	Asp	Gly	His	Asn	Leu	Pro	Ser	Leu
305					310					315					320
Val	Cys	Val	Ile	Thr	Gly	Lys	Gly	Pro	Leu	Arg	Glu	Tyr	Tyr	Ser	Arg
				325					330					335	
Leu	Ile	His	Gln	Lys	His	Phe	Gln	His	Ile	Gln	Val	Cys	Thr	Pro	Trp
			340					345					350		
Leu	Glu	Ala	Glu	Asp	Tyr	Pro	Leu	Leu	Leu	Gly	Ser	Ala	Asp	Leu	Gly
		355					360					365			
Val	Cys	Leu	His	Thr	Ser	Ser	Ser	Gly	Leu	Asp	Leu	Pro	Met	Lys	Val
	370						375				380				
Val	Asp	Met	Phe	Gly	Cys	Cys	Leu	Pro	Val	Cys	Ala	Val	Asn	Phe	Lys
385					390					395					400
Cys	Leu	His	Glu	Leu	Val	Lys	His	Glu	Glu	Asn	Gly	Leu	Val	Phe	Glu
				405					410					415	
Asp	Ser	Glu	Glu	Leu	Ala	Ala	Gln	Leu	Gln	Met	Leu	Phe	Ser	Asn	Phe
			420					425					430		
Pro	Asp	Pro	Ala	Gly	Lys	Leu	Asn	Gln	Phe	Arg	Lys	Asn	Leu	Arg	Glu
		435					440					445			
Ser	Gln	Gln	Leu	Arg	Trp	Asp	Glu	Ser	Trp	Val	Gln	Thr	Val	Leu	Pro
	450					455					460				
Leu	Val	Met	Asp	Thr											
465															

<210> 1378

<211> 314

1437

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (93)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1378

Glu Lys Ala Ala Gly Ala Gly Lys Ser His Leu Ala Ile Val Gln Lys
 1 5 10 15

Val Asn Asn Glu Gly Glu Gly Asp Pro Phe Tyr Glu Val Leu Gly Leu
 20 25 30

Val Thr Leu Glu Asp Val Ile Glu Glu Ile Ile Lys Ser Glu Ile Leu
 35 40 45

Asp Glu Ser Asp Met Tyr Thr Asp Asn Arg Ser Arg Lys Arg Val Ser
 50 55 60

Glu Lys Asn Lys Arg Asp Phe Ser Ala Phe Lys Asp Ala Asp Asn Glu
 65 70 75 80

Leu Lys Val Lys Ile Ser Pro Gln Leu Leu Leu Ala Xaa His Arg Phe
 85 90 95

Leu Ala Thr Glu Val Ser Gln Phe Ser Pro Ser Leu Ile Ser Glu Lys
 100 105 110

Ile Leu Leu Arg Leu Leu Lys Tyr Pro Asp Val Ile Gln Glu Leu Lys
 115 120 125

Phe Asp Glu His Asn Lys Tyr Tyr Ala Arg His Tyr Leu Tyr Thr Arg
 130 135 140

Asn Lys Pro Ala Asp Tyr Phe Ile Leu Ile Leu Gln Gly Lys Val Glu
 145 150 155 160

Val Glu Ala Gly Lys Glu Asn Met Lys Phe Glu Thr Gly Ala Phe Ser
 165 170 175

Tyr Tyr Gly Thr Met Ala Leu Thr Ser Val Pro Ser Asp Arg Ser Pro
 180 185 190

Ala His Pro Thr Pro Leu Ser Arg Ser Ala Ser Leu Ser Tyr Pro Asp
 195 200 205

Arg Thr Asp Val Ser Thr Ala Ala Thr Leu Ala Gly Ser Ser Asn Gln
 210 215 220

1438

Phe Gly Ser Ser Val Leu Gly Gln Tyr Ile Ser Asp Phe Ser Val Arg
 225 230 235 240

Ala Leu Val Asp Leu Gln Tyr Ile Lys Ile Thr Arg Gln Gln Tyr Gln
 245 250 255

Asn Gly Leu Leu Ala Ser Arg Met Glu Asn Ser Pro Gln Phe Pro Ile
 260 265 270

Asp Gly Cys Thr Thr His Met Glu Asn Leu Ala Glu Lys Ser Glu Leu
 275 280 285

Pro Val Val Asp Glu Thr Thr Thr Leu Leu Asn Glu Arg Asn Ser Leu
 290 295 300

Leu His Lys Ala Ser His Glu Asn Ala Ile
 305 310

<210> 1379

<211> 131

<212> PRT

<213> Homo sapiens

<400> 1379

Ser Cys Pro Val Leu Lys Met Phe Pro Glu Gln Gln Lys Glu Glu Phe
 1 5 10 15

Val Ser Val Trp Val Arg Asp Pro Arg Ile Gln Lys Glu Asp Phe Trp
 20 25 30

His Ser Tyr Ile Asp Tyr Glu Ile Cys Ile His Thr Asn Ser Met Cys
 35 40 45

Phe Thr Met Lys Thr Ser Cys Val Arg Arg Arg Tyr Arg Glu Phe Val
 50 55 60

Trp Leu Arg Gln Arg Leu Gln Ser Asn Ala Leu Leu Val Gln Leu Pro
 65 70 75 80

Glu Leu Pro Ser Lys Asn Leu Phe Phe Asn Met Asn Asn Arg Gln His
 85 90 95

Val Asp Gln Arg Arg Gln Gly Leu Gly Asn Phe Leu Arg Lys Val Leu
 100 105 110

Gln Met His Phe Cys Phe Gln Ile Ala Ala Phe Thr Ser Ser Leu Gln
 115 120 125

Ser His Leu

1439

130

<210> 1380

<211> 219

<212> PRT

<213> Homo sapiens

<400> 1380

Pro Gly Ala Ala Trp Ser Arg Pro Asp Leu Arg Gly Cys Cys Thr Gly
1 5 10 15

Pro Gln Pro Ala Leu Arg Met Leu Val Leu Pro Ser Pro Cys Pro Gln
20 25 30

Pro Leu Ala Phe Ser Ser Val Glu Thr Met Glu Gly Pro Pro Arg Arg
35 40 45

Thr Cys Arg Ser Pro Glu Pro Gly Pro Ser Ser Ser Ile Gly Ser Pro
50 55 60

Gln Ala Ser Ser Pro Pro Arg Pro Asn His Tyr Leu Leu Ile Asp Thr
65 70 75 80

Gln Gly Val Pro Tyr Thr Val Leu Val Asp Glu Glu Ser Gln Arg Glu
85 90 95

Pro Gly Ala Ser Gly Ala Pro Gly Gln Lys Lys Cys Tyr Ser Cys Pro
100 105 110

Val Cys Ser Arg Val Phe Glu Tyr Met Ser Tyr Leu Gln Arg His Ser
115 120 125

Ile Thr His Ser Glu Val Lys Pro Phe Glu Cys Asp Ile Cys Gly Lys
130 135 140

Ala Phe Lys Arg Ala Ser His Leu Ala Arg His His Ser Ile His Leu
145 150 155 160

Ala Gly Gly Gly Arg Pro His Gly Cys Pro Leu Cys Pro Arg Arg Phe
165 170 175

Arg Asp Ala Gly Glu Leu Ala Gln His Ser Arg Val His Ser Gly Glu
180 185 190

Arg Pro Phe Gln Cys Pro His Cys Pro Arg Arg Phe Met Glu Gln Asn
195 200 205

Thr Leu Gln Lys His Thr Arg Trp Lys His Pro
210 215

1440

<210> 1381

<211> 275

<212> PRT

<213> Homo sapiens

<400> 1381

Gly Val Ala Leu Phe Lys Ser Ala Ala Gly Asp Gln Pro Thr Ala Ala
1 5 10 15

Cys Ile Cys Ile Gln Arg Gln Val Pro Pro Val Pro Ala Ala Arg Ala
20 25 30

Pro Gln Ser Arg Thr Arg Ser Ala Gln Ala Lys Leu Ala Leu Thr Met
35 40 45

Pro Val Lys Gly Gly Thr Lys Cys Ile Lys Tyr Leu Leu Phe Gly Phe
50 55 60

Asn Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu
65 70 75 80

Trp Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu Thr
85 90 95

Asn Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile Gly
100 105 110

Ala Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly Ala
115 120 125

Val Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu Leu
130 135 140

Val Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser His
145 150 155 160

Lys Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr Tyr
165 170 175

Asn Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys Ala
180 185 190

Ile His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu Gln
195 200 205

Phe Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe Thr
210 215 220

[44]

Val Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys Phe
 225 230 235 240

His Ile Ile Gly Ala Val Gly Ile Gly Ile Ala Val Val Met Ile Phe
 245 250 255

Gly Met Ile Phe Ser Met Ile Leu Cys Cys Ala Ile Arg Arg Asn Arg
 260 265 270

Glu Met Val
 275

<210> 1382

<211> 766

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (13)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (123)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1382

Pro Cys Trp Glu Leu Val Gly Pro Pro Gly Trp Gln Xaa Ile Arg Ala
 1 5 10 15

Xaa Pro Ala Thr Val His Arg Ala Glu Ile Leu Ser Phe Pro Arg Ser
 20 25 30

Lys Thr Ser Glu Pro Ala Lys Arg Gly Arg Thr Ala Ser Ala Ala Met
 35 40 45

Ala Leu Lys Asp Tyr Ala Leu Glu Lys Glu Lys Val Lys Lys Phe Leu
 50 55 60

Gln Glu Phe Tyr Gln Asp Asp Glu Leu Gly Lys Lys Gln Phe Lys Tyr
 65 70 75 80

Gly Asn Gln Leu Val Arg Leu Ala His Arg Glu Gln Val Ala Leu Tyr

85

90

95

Ile Cys Glu Asn Ala Arg Arg Tyr Ala Lys Xaa Phe Ala Asp Ala Val
115 120 125

Gln Glu Leu Leu Pro Gln Tyr Lys Glu Arg Glu Val Val Asn Lys Asp
130 135 140

Val Leu Asp Val Tyr Ile Glu His Arg Leu Met Met Glu Gln Arg Ser
145 150 155 160

Arg Asp Pro Gly Met Val Arg Ser Pro Gln Asn Gln Tyr Pro Ala Glu
165 170 175

Leu Met Arg Arg Phe Glu Leu Tyr Phe Gln Gly Pro Ser Ser Asn Lys
180 185 190

Pro Arg Val Ile Arg Glu Val Arg Ala Asp Ser Val Gly Lys Leu Val
195 200 205

Thr	Val	Arg	Gly	Ile	Val	Thr	Arg	Val	Ser	Glu	Val	Lys	Pro	Lys	Met
210						215					220				

Val	Val	Ala	Thr	Tyr	Thr	Cys	Asp	Gln	Cys	Gly	Ala	Glu	Thr	Tyr	Gln
225					230					235					240

Pro Ile Gln Ser Pro Thr Phe Met Pro Leu Ile Met Cys Pro Ser Gln
245 250 255

Glu Cys Gln Thr Asn Arg Ser Gly Gly Arg Leu Tyr Leu Gln Thr Arg
260 265 270

Gly Ser Arg Phe Ile Lys Phe Gln Glu Met Lys Met Gln Glu His Ser
275 280 285

Asp Gln Val Pro Val Gly Asn Ile Pro Arg Ser Ile Thr Val Leu Val
290 295 300

Glu Gly Glu Asn Thr Arg Ile Ala Gln Pro Gly Asp His Val Ser Val
305 310 315 320

Thr Gly Ile Phe Leu Pro Ile Leu Arg Thr Gly Phe Arg Gln Val Val
325 330 335

Gln Gly Leu Leu Ser Glu Thr Tyr Leu Glu Ala His Arg Ile Val Lys
340 345 350

Met Asn Lys Ser Glu Asp Asp Glu Ser Gly Ala Gly Glu Leu Thr Arg

1443

355	360	365
Glu Glu Leu Arg Gln Ile Ala Glu Glu Asp Phe Tyr Glu Lys Leu Ala		
370	375	380
Ala Ser Ile Ala Pro Glu Ile Tyr Gly His Glu Asp Val Lys Lys Ala		
385	390	395 400
Leu Leu Leu Leu Leu Val Gly Gly Val Asp Gln Ser Pro Arg Gly Met		
405	410	415
Lys Ile Arg Gly Asn Ile Asn Ile Cys Leu Met Gly Asp Pro Gly Val		
420	425	430
Ala Lys Ser Gln Leu Leu Ser Tyr Ile Asp Arg Leu Ala Pro Arg Ser		
435	440	445
Gln Tyr Thr Thr Gly Arg Gly Ser Ser Gly Val Gly Leu Thr Ala Ala		
450	455	460
Val Leu Arg Asp Ser Val Ser Gly Glu Leu Thr Leu Glu Gly Gly Ala		
465	470	475 480
Leu Val Leu Ala Asp Gln Gly Val Cys Cys Ile Asp Glu Phe Asp Lys		
485	490	495
Met Ala Glu Ala Asp Arg Thr Ala Ile His Glu Val Met Glu Gln Gln		
500	505	510
Thr Ile Ser Ile Ala Lys Ala Gly Ile Leu Thr Thr Leu Asn Ala Arg		
515	520	525
Cys Ser Ile Leu Ala Ala Ala Asn Pro Ala Tyr Gly Arg Tyr Asn Pro		
530	535	540
Arg Arg Ser Leu Glu Gln Asn Ile Gln Leu Pro Ala Ala Leu Leu Ser		
545	550	555 560
Arg Phe Asp Leu Leu Trp Leu Ile Gln Asp Arg Pro Asp Arg Asp Asn		
565	570	575
Asp Leu Arg Leu Ala Gln His Ile Thr Tyr Val His Gln His Ser Arg		
580	585	590
Gln Pro Pro Ser Gln Phe Glu Pro Leu Asp Met Lys Leu Met Arg Arg		
595	600	605
Tyr Ile Ala Met Cys Arg Glu Lys Gln Pro Met Val Pro Glu Ser Leu		
610	615	620
Ala Asp Tyr Ile Thr Ala Ala Tyr Val Glu Met Arg Arg Glu Ala Trp		

1444

625	630	635	640
Ala Ser Lys Asp	Ala Thr Tyr Thr Ser	Ala Arg Thr Leu Leu	Ala Ile
645	650	655	
Leu Arg Leu Ser	Thr Ala Leu Ala Arg	Leu Arg Met Val	Asp Val Val
660	665	670	
Glu Lys Glu Asp	Val Asn Glu Ala Ile	Arg Leu Met Glu	Met Ser Lys
675	680	685	
Asp Ser Leu Leu	Gly Asp Lys Gly Gln	Thr Ala Arg Thr	Gln Arg Pro
690	695	700	
Ala Asp Val Ile	Phe Ala Thr Val Arg	Glu Leu Val Ser	Gly Gly Arg
705	710	715	720
Ser Val Arg Phe	Ser Glu Ala Glu	Gln Arg Cys Val	Ser Arg Gly Phe
725	730	735	
Thr Pro Ala Gln	Phe Gln Ala Ala	Leu Asp Glu Tyr	Glu Glu Leu Asn
740	745	750	
Val Trp Gln Val	Asn Ala Ser Arg	Thr Arg Ile Thr	Phe Val
755	760	765	

<210> 1383
 <211> 296
 <212> PRT
 <213> Homo sapiens

<400> 1383
 Phe Arg Pro Gly Ser Pro Arg Gln Pro Arg Ala Gln Pro Ile Ser Ala
 1 5 10 15
 Pro Asp Cys Thr Arg Ala Met Val Gly Arg Arg Ala Leu Ile Val Leu
 20 25 30
 Ala His Ser Glu Arg Thr Ser Phe Asn Tyr Ala Met Lys Glu Ala Ala
 35 40 45
 Ala Ala Ala Leu Lys Lys Lys Gly Trp Glu Val Val Glu Ser Asp Leu
 50 55 60
 Tyr Ala Met Asn Phe Asn Pro Ile Ile Ser Arg Lys Asp Ile Thr Gly
 65 70 75 80
 Lys Leu Lys Asp Pro Ala Asn Phe Gln Tyr Pro Ala Glu Ser Val Leu
 85 90 95

1445

Ala Tyr Lys Glu Gly His Leu Ser Pro Asp Ile Val Ala Glu Gln Lys
 100 105 110
 Lys Leu Glu Ala Ala Asp Leu Val Ile Phe Gln Phe Pro Leu Gln Trp
 115 120 125
 Phe Gly Val Pro Ala Ile Leu Lys Gly Trp Phe Glu Arg Val Phe Ile
 130 135 140
 Gly Glu Phe Ala Tyr Thr Tyr Ala Ala Met Tyr Asp Lys Gly Pro Phe
 145 150 155 160
 Arg Ser Lys Lys Ala Val Leu Ser Ile Thr Thr Gly Gly Ser Gly Ser
 165 170 175
 Met Tyr Ser Leu Gln Gly Ile His Gly Asp Met Asn Val Ile Leu Trp
 180 185 190
 Pro Ile Gln Ser Gly Ile Leu His Phe Cys Gly Phe Gln Val Leu Glu
 195 200 205
 Pro Gln Leu Thr Tyr Ser Ile Gly His Thr Pro Ala Asp Ala Arg Ile
 210 215 220
 Gln Ile Leu Glu Gly Trp Lys Lys Arg Leu Glu Asn Ile Trp Asp Glu
 225 230 235 240
 Thr Pro Leu Tyr Phe Ala Pro Ser Ser Leu Phe Asp Leu Asn Phe Gln
 245 250 255
 Ala Gly Phe Leu Met Lys Lys Glu Val Gln Asp Glu Glu Lys Asn Lys
 260 265 270
 Lys Phe Gly Leu Ser Val Gly His His Leu Gly Lys Ser Ile Pro Thr
 275 280 285
 Asp Asn Gln Ile Lys Ala Arg Lys
 290 295

<210> 1384

<211> 165

<212> PRT

<213> Homo sapiens

<400> 1384

Asp Pro Arg Thr Met Asn Leu Ala Ile Ser Ile Ala Leu Leu Thr
 1 5 10 15

1446

Val Leu Gln Val Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys
 20 25 30
 Leu Val Asp Gln Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser
 35 40 45
 Ser Ser Pro Ile Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys
 50 55 60
 His Val Leu Phe Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser
 65 70 75 80
 Arg Thr Asn Phe Thr Ser Lys Tyr Asn Met Lys Val Leu Tyr Leu Ser
 85 90 95
 Ala Phe Thr Ser Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His
 100 105 110
 Ser Gly His Ser Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg
 115 120 125
 Asp Lys Leu Val Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr
 130 135 140
 Ser Trp Leu Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr
 145 150 155 160
 Asp Phe Met Ser Leu
 165

<210> 1385

<211> 399

<212> PRT

<213> Homo sapiens

<400> 1385

His Glu Arg Thr Pro Ser Arg Pro Gln Pro Asp Thr Pro Arg Gly Pro
 1 5 10 15
 Pro Val Ser Arg Gly Cys Ser Pro Arg His Gly Thr Gly Pro Arg Leu
 20 25 30
 Thr Met Ala Ala Ala Arg His Ser Thr Leu Asp Phe Met Leu Gly Ala
 35 40 45
 Lys Ala Asp Gly Glu Thr Ile Leu Lys Gly Leu Gln Ser Ile Phe Gln
 50 55 60
 Glu Gln Gly Met Ala Glu Ser Val His Thr Trp Gln Asp His Gly Tyr

1447

65	70	75	80
Leu Ala Thr Tyr Thr Asn Lys Asn Gly Ser Phe Ala Asn Leu Arg Ile	85	90	95
Tyr Pro His Gly Leu Val Leu Leu Asp Leu Gln Ser Tyr Asp Gly Asp	100	105	110
Ala Gln Gly Lys Glu Glu Ile Asp Ser Ile Leu Asn Lys Val Glu Glu	115	120	125
Arg Met Lys Glu Leu Ser Gln Asp Ser Thr Gly Arg Val Lys Arg Leu	130	135	140
Pro Pro Ile Val Arg Gly Gly Ala Ile Asp Arg Tyr Trp Pro Thr Ala	145	150	155
Asp Gly Arg Leu Val Glu Tyr Asp Ile Asp Glu Val Val Tyr Asp Glu	165	170	175
Asp Ser Pro Tyr Gln Asn Ile Lys Ile Leu His Ser Lys Gln Phe Gly	180	185	190
Asn Ile Leu Ile Leu Ser Gly Asp Val Asn Leu Ala Glu Ser Asp Leu	195	200	205
Ala Tyr Thr Arg Ala Ile Met Gly Ser Gly Lys Glu Asp Tyr Thr Gly	210	215	220
Lys Asp Val Leu Ile Leu Gly Gly Gly Asp Gly Gly Ile Leu Cys Glu	225	230	235
Ile Val Lys Leu Lys Pro Lys Met Val Thr Met Val Glu Ile Asp Gln	245	250	255
Met Val Ile Asp Gly Cys Lys Lys Tyr Met Arg Lys Thr Cys Gly Asp	260	265	270
Val Leu Asp Asn Leu Lys Gly Asp Cys Tyr Gln Val Leu Ile Glu Asp	275	280	285
Cys Ile Pro Val Leu Lys Arg Tyr Ala Lys Glu Gly Arg Glu Phe Asp	290	295	300
Tyr Val Ile Asn Asp Leu Thr Ala Val Pro Ile Ser Thr Ser Pro Glu	305	310	315
Glu Asp Ser Thr Trp Glu Phe Leu Arg Leu Ile Leu Asp Leu Ser Met	325	330	335
Lys Val Leu Lys Gln Asp Gly Lys Tyr Phe Thr Gln Gly Asn Cys Val			

1448

340 345 350
 Asn Leu Thr Glu Ala Leu Ser Leu Tyr Glu Glu Gln Leu Gly Arg Leu
 355 360 365
 Tyr Cys Pro Val Glu Phe Ser Lys Glu Ile Val Cys Val Pro Ser Tyr
 370 375 380
 Leu Glu Leu Trp Val Phe Tyr Thr Val Trp Lys Lys Ala Lys Pro
 385 390 395

<210> 1386
 <211> 287
 <212> PRT
 <213> Homo sapiens

<400> 1386
 Phe Asp Cys Arg Asp Val Ala Phe Thr Val Gly Glu Gly Glu Asp His
 1 5 10 15
 Asp Ile Pro Ile Gly Ile Asp Lys Ala Leu Glu Lys Met Gln Arg Glu
 20 25 30
 Glu Gln Cys Ile Leu Tyr Leu Gly Pro Arg Tyr Gly Phe Gly Glu Ala
 35 40 45
 Gly Lys Pro Lys Phe Gly Ile Glu Pro Asn Ala Glu Leu Ile Tyr Glu
 50 55 60
 Val Thr Leu Lys Ser Phe Glu Lys Ala Lys Glu Ser Trp Glu Met Asp
 65 70 75 80
 Thr Lys Glu Lys Leu Glu Gln Ala Ala Ile Val Lys Glu Lys Gly Thr
 85 90 95
 Val Tyr Phe Lys Gly Gly Lys Tyr Met Gln Ala Val Ile Gln Tyr Gly
 100 105 110
 Lys Ile Val Ser Trp Leu Glu Met Glu Tyr Gly Leu Ser Glu Lys Glu
 115 120 125
 Ser Lys Ala Ser Glu Ser Phe Leu Leu Ala Ala Phe Leu Asn Leu Ala
 130 135 140
 Met Cys Tyr Leu Lys Leu Arg Glu Tyr Thr Lys Ala Val Glu Cys Cys
 145 150 155 160
 Asp Lys Ala Leu Gly Leu Asp Ser Ala Asn Glu Lys Gly Leu Tyr Arg
 165 170 175

1449

Arg Gly Glu Ala Gln Leu Leu Met Asn Glu Phe Glu Ser Ala Lys Gly
 180 185 190
 Asp Phe Glu Lys Val Leu Glu Val Asn Pro Gln Asn Lys Ala Ala Arg
 195 200 205
 Leu Gln Ile Ser Met Cys Gln Lys Lys Ala Lys Glu His Asn Glu Arg
 210 215 220
 Asp Arg Arg Tyr Thr Pro Thr Cys Ser Arg Ser Leu Gln Ser Arg Met
 225 230 235 240
 Pro Arg Lys Arg Pro Ile Lys Gln Trp Ala Arg Arg Leu Gln Lys Gly
 245 250 255
 Ser Leu Met Lys Lys Glu Gln Thr Val Lys Gln Trp Lys Lys Arg Asn
 260 265 270
 Leu Arg Ala Thr Tyr Asp Ala Thr Pro Arg Arg Glu Glu Ser Gln
 275 280 285

<210> 1387
 <211> 206
 <212> PRT
 <213> Homo sapiens

<400> 1387
 Arg Leu Pro Ile Arg Gln Ser Ala Ala Asp Gly Leu Arg Ala Arg Pro
 1 5 10 15
 Leu Gly Ser Asn Thr Ala Pro Ala Leu Arg Val Met Val Gln Ala Trp
 20 25 30
 Tyr Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp
 35 40 45
 Pro Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu
 50 55 60
 Tyr Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu
 65 70 75 80
 Lys Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile
 85 90 95
 Cys Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr
 100 105 110

1450

Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly
 115 120 125
 Ser Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile
 130 135 140
 Phe Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His
 145 150 155 160
 Arg Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe
 165 170 175
 Val Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe
 180 185 190
 Glu Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
 195 200 205

<210> 1388

<211> 394

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1388

Phe His Xaa Ala Ala His Tyr Ser Leu Pro Asp Gly Arg His Gly Arg
 1 5 10 15
 Leu Asp Ser Pro Thr Phe His Leu Thr Leu His Tyr Pro Thr Glu His
 20 25 30
 Val Gln Phe Trp Val Gly Ser Pro Ser Thr Pro Ala Gly Trp Val Arg
 35 40 45
 Glu Gly Asp Thr Val Gln Leu Leu Cys Arg Gly Asp Gly Ser Pro Ser
 50 55 60
 Pro Glu Tyr Thr Leu Phe Arg Leu Gln Asp Glu Gln Glu Glu Val Leu
 65 70 75 80
 Asn Val Asn Leu Glu Gly Asn Leu Thr Leu Glu Gly Val Thr Arg Gly
 85 90 95
 Gln Ser Gly Thr Tyr Gly Cys Arg Val Glu Asp Tyr Asp Ala Ala Asp
 100 105 110

1451

Asp Val Gln Leu Ser Lys Thr Leu Glu Leu Arg Val Ala Tyr Leu Asp
 115 120 125

Pro Leu Glu Leu Ser Glu Gly Lys Val Leu Ser Leu Pro Leu Asn Ser
 130 135 140

Ser Ala Val Val Asn Cys Ser Val His Gly Leu Pro Thr Pro Ala Leu
 145 150 155 160

Arg Trp Thr Lys Asp Ser Thr Pro Leu Gly Asp Gly Pro Met Leu Ser
 165 170 175

Leu Ser Ser Ile Thr Phe Asp Ser Asn Gly Thr Tyr Val Cys Glu Ala
 180 185 190

Ser Leu Pro Thr Val Pro Val Leu Ser Arg Thr Gln Asn Phe Thr Leu
 195 200 205

Leu Val Gln Gly Ser Pro Glu Leu Lys Thr Ala Glu Ile Glu Pro Lys
 210 215 220

Ala Asp Gly Ser Trp Arg Glu Gly Asp Glu Val Thr Leu Ile Cys Ser
 225 230 235 240

Ala Arg Gly His Pro Asp Pro Lys Leu Ser Trp Ser Gln Leu Gly Gly
 245 250 255

Ser Pro Ala Glu Pro Ile Pro Gly Arg Gln Gly Trp Val Ser Ser Ser
 260 265 270

Leu Thr Leu Lys Val Thr Ser Ala Leu Ser Arg Asp Gly Ile Ser Cys
 275 280 285

Glu Ala Ser Asn Pro His Gly Asn Lys Arg His Val Phe His Phe Gly
 290 295 300

Thr Val Ser Pro Gln Thr Ser Gln Ala Gly Val Ala Val Met Ala Val
 305 310 315 320

Ala Val Ser Val Gly Leu Leu Leu Leu Val Val Ala Val Phe Tyr Cys
 325 330 335

Val Arg Arg Lys Gly Gly Pro Cys Cys Arg Gln Arg Arg Glu Lys Gly
 340 345 350

Ala Pro Pro Pro Gly Glu Pro Gly Leu Ser His Ser Gly Ser Glu Gln
 355 360 365

Pro Glu Gln Thr Gly Leu Leu Met Gly Gly Ala Ser Gly Gly Ala Arg
 370 375 380

1452

Gly Gly Ser Gly Gly Phe Gly Asp Glu Cys
385 390

<210> 1389

<211> 264

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (16)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1389

Val Gly Cys Arg Trp Ser Arg Val Gly Pro Gln Asn Pro Arg Val Xaa
1 5 10 15

Leu Pro Pro Pro Thr Leu Ala Met Phe Leu Thr Arg Ser Glu Tyr Asp
20 25 30

Arg Gly Val Asn Thr Phe Ser Pro Glu Gly Arg Leu Phe Gln Val Glu
35 40 45

Tyr Ala Ile Glu Ala Ile Lys Leu Gly Ser Thr Ala Ile Gly Ile Gln
50 55 60

Thr Ser Glu Gly Val Cys Leu Ala Val Glu Lys Arg Ile Thr Ser Pro
65 70 75 80

Leu Met Glu Pro Ser Ser Ile Glu Lys Ile Val Glu Ile Asp Ala His
85 90 95

Ile Gly Cys Ala Met Ser Gly Leu Ile Ala Asp Ala Lys Thr Leu Ile
100 105 110

Asp Lys Ala Arg Val Glu Thr Gln Asn His Trp Phe Thr Tyr Asn Glu
115 120 125

Thr Met Thr Val Glu Ser Val Thr Gln Ala Val Ser Asn Leu Ala Leu
130 135 140

Gln Phe Gly Glu Glu Asp Ala Asp Pro Gly Ala Met Ser Arg Pro Phe
145 150 155 160

Gly Val Ala Leu Leu Phe Gly Gly Val Asp Glu Lys Gly Pro Gln Leu
165 170 175

Phe His Met Asp Pro Ser Gly Thr Phe Val Gln Cys Asp Ala Arg Ala

1453

180 185 190
 Ile Gly Ser Ala Ser Glu Gly Ala Gln Ser Ser Leu Gln Glu Val Tyr
 195 200 205
 His Lys Ser Met Thr Leu Lys Glu Ala Ile Lys Ser Ser Leu Ile Ile
 210 215 220
 Leu Lys Gln Val Met Glu Glu Lys Leu Asn Ala Thr Asn Ile Glu Leu
 225 230 235 240
 Ala Thr Val Gln Pro Gly Gln Asn Phe His Met Phe Thr Lys Glu Glu
 245 250 255
 Leu Glu Glu Val Ile Lys Asp Ile
 260

<210> 1390

<211> 178

<212> PRT

<213> Homo sapiens

<400> 1390

Gln Lys Leu Glu Leu His Arg Gly Gly Gly Arg Ser Arg Thr Ser Gly
 1 5 10 15
 Ser Pro Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala Ala
 20 25 30
 Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser Phe
 35 40 45
 Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro Pro
 50 55 60
 Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu Asn
 65 70 75 80
 Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro Val
 85 90 95
 Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser Ile
 100 105 110
 Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr Arg
 115 120 125
 Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu Trp Ser Arg
 130 135 140

1454

Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro
 145 150 155 160

Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro Glu
 165 170 175

Asp Glu

<210> 1391

<211> 133

<212> PRT

<213> Homo sapiens

<400> 1391

Val Ile Ile Thr Ser Ile Asn Gln Lys Ile Phe His Pro Leu Arg Ala
 1 5 10 15

Leu Lys Leu Ser Thr Ser Ala Thr Phe Leu Ile Leu Val Leu Gly Gly
 20 25 30

His Val Tyr Gly Leu Phe Asn Phe His Val Pro Tyr Cys Pro Leu Pro
 35 40 45

Ala Val Ala Lys Ala Ser Cys Phe Ser Pro Thr Glu Glu Thr Val Leu
 50 55 60

Cys His Asp Asp Arg Ala Leu Leu Gly Leu Val Phe Leu Val Phe Pro
 65 70 75 80

Phe Trp Gln Cys Gly Leu Gln Glu Leu Asp Val Tyr Ala Gln Gly Ile
 85 90 95

Glu Phe Thr Leu Lys Leu Gly Asn Gly Val Phe Asn Leu Cys Ser Cys
 100 105 110

Leu Phe Ile Leu Leu Phe Ile Phe Cys His Pro Ala Leu Tyr Trp Ala
 115 120 125

Asn Asn Glu Ile Lys
 130

<210> 1392

<211> 401

<212> PRT

<213> Homo sapiens

1455

<400> 1392

Asn Thr Val Leu Lys Lys Met Asp Glu Glu Pro Glu Arg Thr Lys Arg
1 5 10 15

Trp Glu Gly Gly Tyr Glu Arg Thr Trp Glu Ile Leu Lys Glu Asp Glu
20 25 30

Ser Gly Ser Leu Lys Ala Thr Ile Glu Asp Ile Leu Phe Lys Ala Lys
35 40 45

Arg Lys Arg Val Phe Glu His His Gly Gln Val Arg Leu Gly Met Met
50 55 60

Arg His Leu Tyr Val Val Val Asp Gly Ser Arg Thr Met Glu Asp Gln
65 70 75 80

Asp Leu Lys Pro Asn Arg Leu Thr Cys Thr Leu Lys Leu Leu Glu Tyr
85 90 95

Phe Val Glu Glu Tyr Phe Asp Gln Asn Pro Ile Ser Gln Ile Gly Ile
100 105 110

Ile Val Thr Lys Ser Lys Arg Ala Glu Lys Leu Thr Glu Leu Ser Gly
115 120 125

Asn Pro Arg Lys His Ile Thr Ser Leu Lys Lys Ala Val Asp Met Thr
130 135 140

Cys His Gly Glu Pro Ser Leu Tyr Asn Ser Leu Ser Ile Ala Met Gln
145 150 155 160

Thr Leu Lys His Met Pro Gly His Thr Ser Arg Glu Val Leu Ile Ile
165 170 175

Phe Ser Ser Leu Thr Thr Cys Asp Pro Ser Asn Ile Tyr Asp Leu Ile
180 185 190

Lys Thr Leu Lys Ala Ala Lys Ile Arg Val Ser Val Ile Gly Leu Ser
195 200 205

Ala Glu Val Arg Val Cys Thr Val Leu Ala Arg Glu Thr Gly Gly Thr
210 215 220

Tyr His Val Ile Leu Asp Glu Ser His Tyr Lys Glu Leu Leu Thr His
225 230 235 240

His Val Ser Pro Pro Pro Ala Ser Ser Ser Ser Glu Cys Ser Leu Ile
245 250 255

Arg Met Gly Phe Pro Gln His Thr Ile Ala Ser Leu Ser Asp Gln Asp

1456

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<210> 1393
<211> 318
<212> PRT
<213> Homo sapiens
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<400> 1393
Pro Glu Gly Leu Pro Arg Phe Asn Asn Asn Phe Met Ala Pro Gly Ser
 1             5             10             15
Ala Ser Ser Pro Ser Pro Ser Phe Pro Ala Ser Arg Pro Trp Ala Ala
 20             25             30
Val Gly Thr Met Ala Ala Ala Ala Ala Ala Gly Pro Ser Pro Gly Ser
 35             40             45
Gly Pro Gly Asp Ser Pro Glu Gly Pro Glu Gly Glu Ala Pro Glu Arg
 50             55             60
Arg Arg Lys Ala His Gly Met Leu Lys Leu Tyr Tyr Gly Leu Ser Glu
 65             70             75             80

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1457

Gly Glu Ala Ala Gly Arg Pro Ala Gly Pro Asp Pro Leu Asp Pro Thr
85 90 95

Asp Leu Asn Gly Ala His Phe Asp Pro Glu Val Tyr Leu Asp Lys Leu
100 105 110

Arg Arg Glu Cys Pro Leu Ala Gln Leu Met Asp Ser Glu Thr Asp Met
115 120 125

Val Arg Gln Ile Arg Ala Leu Asp Ser Asp Met Gln Thr Leu Val Tyr
130 135 140

Glu Asn Tyr Asn Lys Phe Ile Ser Ala Thr Asp Thr Ile Arg Lys Met
145 150 155 160

Lys Asn Asp Phe Arg Lys Met Glu Asp Glu Met Asp Arg Leu Ala Thr
165 170 175

Asn Met Ala Val Ile Thr Asp Phe Ser Ala Arg Ile Ser Ala Thr Leu
180 185 190

Gln Asp Arg His Glu Arg Ile Thr Lys Leu Ala Gly Val His Ala Leu
195 200 205

Leu Arg Lys Leu Gln Phe Leu Phe Glu Leu Pro Ser Arg Leu Thr Lys
210 215 220

Cys Val Glu Leu Gly Ala Tyr Gly Gln Ala Val Arg Tyr Gln Gly Arg
225 230 235 240

Ala Gln Ala Val Leu Gln Gln Tyr Gln His Leu Pro Ser Phe Arg Ala
245 250 255

Ile Gln Asp Asp Cys Gln Val Ile Thr Ala Arg Leu Ala Gln Gln Leu
260 265 270

Arg Gln Arg Phe Arg Glu Gly Gly Ser Gly Ala Pro Glu Gln Ala Glu
275 280 285

Cys Val Glu Leu Leu Leu Ala Leu Gly Glu Pro Ala Glu Glu Leu Cys
290 295 300

Glu Glu Phe Trp Arg Thr Pro Ala Ala Gly Trp Arg Arg Ser
305 310 315

<210> 1394

<211> 1285

<212> PRT

1458

<213> Homo sapiens

<400> 1394

Phe Ser Phe Pro Leu Ser Ser Glu Pro Phe Gln Gly Ser Tyr Lys Val
1 5 10 15

Val Val Gln Lys Lys Ser Gly Gly Arg Thr Glu His Pro Phe Thr Val
20 25 30

Glu Glu Phe Val Leu Pro Lys Phe Glu Val Gln Val Thr Val Pro Lys
35 40 45

Ile Ile Thr Ile Leu Glu Glu Glu Met Asn Val Ser Val Cys Gly Leu
50 55 60

Tyr Thr Tyr Gly Lys Pro Val Pro Gly His Val Thr Val Ser Ile Cys
65 70 75 80

Arg Lys Tyr Ser Asp Ala Ser Asp Cys His Gly Glu Asp Ser Gln Ala
85 90 95

Phe Cys Glu Lys Phe Ser Gly Gln Leu Asn Ser His Gly Cys Phe Tyr
100 105 110

Gln Gln Val Lys Thr Lys Val Phe Gln Leu Lys Arg Lys Glu Tyr Glu
115 120 125

Met Lys Leu His Thr Glu Ala Gln Ile Gln Glu Glu Gly Thr Val Val
130 135 140

Glu Leu Thr Gly Arg Gln Ser Ser Glu Ile Thr Arg Thr Ile Thr Lys
145 150 155 160

Leu Ser Phe Val Lys Val Asp Ser His Phe Arg Gln Gly Ile Pro Phe
165 170 175

Phe Gly Gln Val Arg Leu Val Asp Gly Lys Gly Val Pro Ile Pro Asn
180 185 190

Lys Val Ile Phe Ile Arg Gly Asn Glu Ala Asn Tyr Tyr Ser Asn Ala
195 200 205

Thr Thr Asp Glu His Gly Leu Val Gln Phe Ser Ile Asn Thr Thr Asn
210 215 220

Val Met Gly Thr Ser Leu Thr Val Arg Val Asn Tyr Lys Asp Arg Ser
225 230 235 240

Pro Cys Tyr Gly Tyr Gln Trp Val Ser Glu Glu His Glu Glu Ala His
245 250 255

1459

His Thr Ala Tyr Leu Val Phe Ser Pro Ser Lys Ser Phe Val His Leu
260 265 270

Glu Pro Met Ser His Glu Leu Pro Cys Gly His Thr Gln Thr Val Gln
275 280 285

Ala His Tyr Ile Leu Asn Gly Gly Thr Leu Leu Gly Leu Lys Lys Leu
290 295 300

Ser Phe Tyr Tyr Leu Ile Met Ala Lys Gly Gly Ile Val Arg Thr Gly
305 310 315 320

Thr His Gly Leu Leu Val Lys Gln Glu Asp Met Lys Gly His Phe Ser
325 330 335

Ile Ser Ile Pro Val Lys Ser Asp Ile Ala Pro Val Ala Arg Leu Leu
340 345 350

Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp Ser Ala Lys
355 360 365

Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu Ser Phe Ser
370 375 380

Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg Val Thr Ala
385 390 395 400

Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln Ser Val Leu
405 410 415

Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val Tyr Asn Leu
420 425 430

Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu Asn Asp Gln
435 440 445

Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile Asn Gly Ile
450 455 460

Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met Tyr Ser Phe
465 470 475 480

Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys Ile Arg Lys
485 490 495

Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His Gly Pro Glu
500 505 510

Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly Arg Gly His
515 520 525

1460

Ala Arg Leu Val His Val Glu Glu Pro His Thr Glu Thr Val Arg Lys
530 535 540

Tyr Phe Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala
545 550 555 560

Gly Val Ala Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp
565 570 575

Lys Ala Gly Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser
580 585 590

Ser Thr Ala Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr
595 600 605

Met Pro Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr
610 615 620

Val Leu Asn Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu
625 630 635 640

Ala Ser Pro Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro
645 650 655

His Cys Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr
660 665 670

Pro Lys Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu
675 680 685

Glu Ser Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His
690 695 700

Gly Arg Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly
705 710 715 720

Leu Glu Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly
725 730 735

Glu Val Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu
740 745 750

Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser
755 760 765

Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly
770 775 780

Glu Gln Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr
785 790 795 800

1461

Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser Lys Ala Ile
805 810 815

Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr
820 825 830

Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly
835 840 845

Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg
850 855 860

Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp
865 870 875 880

Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser
885 890 895

Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu
900 905 910

Ser Ala Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr
915 920 925

His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys
930 935 940

Thr Ala Gln Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu
945 950 955 960

Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu
965 970 975

Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val
980 985 990

His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr
995 1000 1005

Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu
1010 1015 1020

Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr
1025 1030 1035 1040

Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln
1045 1050 1055

Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu
1060 1065 1070

1462

Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln
1075 1080 1085

Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp
1090 1095 1100

Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro
1105 1110 1115 1120

Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln
1125 1130 1135

Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe
1140 1145 1150

Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala
1155 1160 1165

His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg
1170 1175 1180

Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe
1185 1190 1195 1200

Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val
1205 1210 1215

Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys
1220 1225 1230

Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val
1235 1240 1245

Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr
1250 1255 1260

Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys
1265 1270 1275 1280

Asp Leu Gly Asn Ala
1285

<210> 1395

<211> 75

<212> PRT

<213> Homo sapiens

<400> 1395

Ile Thr Lys Asn Ile Tyr Ser Asp Leu Lys Asp Leu Ser Ala Lys Asn

1463

1 5 10 15
 Gln Ser Ile Ser Cys Pro Ser Ile Ile Val His Ala Cys Leu Leu Leu
 20 25 30
 Phe Thr Cys Ser Ser Ala Gln Thr Val Ser Asn Leu Gly Thr Pro Phe
 35 40 45
 Gly Ala Asp Lys Tyr Ser Ser Ala Phe Ser Pro Gln Ile Tyr Asn Asp
 50 55 60
 Phe Asn Ile Pro Lys Asn Ile Gly Ile Ser Glu
 65 70 75

<210> 1396
 <211> 920
 <212> PRT
 <213> Homo sapiens

<400> 1396
 Arg Thr Arg Gly Ile His Gly Glu Met Arg Leu Phe Val Ser Asp Gly
 1 5 10 15
 Val Pro Gly Cys Leu Pro Val Leu Ala Ala Ala Gly Arg Ala Arg Gly
 20 25 30
 Arg Ala Glu Val Leu Ile Ser Thr Val Gly Pro Glu Asp Cys Val Val
 35 40 45
 Pro Phe Leu Thr Arg Pro Lys Val Pro Val Leu Gln Leu Asp Ser Gly
 50 55 60
 Asn Tyr Leu Phe Ser Thr Ser Ala Ile Cys Arg Tyr Phe Phe Leu Leu
 65 70 75 80
 Ser Gly Trp Glu Gln Asp Asp Leu Thr Asn Gln Trp Leu Glu Trp Glu
 85 90 95
 Ala Thr Glu Leu Gln Pro Ala Leu Ser Ala Ala Leu Tyr Tyr Leu Val
 100 105 110
 Val Gln Gly Lys Lys Gly Glu Asp Val Leu Gly Ser Val Arg Arg Ala
 115 120 125
 Leu Thr His Ile Asp His Ser Leu Ser Arg Gln Asn Cys Pro Phe Leu
 130 135 140
 Ala Gly Glu Thr Glu Ser Leu Ala Asp Ile Val Leu Trp Gly Ala Leu
 145 150 155 160

1464

Tyr Pro Leu Leu Gln Asp Pro Ala Tyr Leu Pro Glu Glu Leu Ser Ala
165 170 175

Leu His Ser Trp Phe Gln Thr Leu Ser Thr Gln Glu Pro Cys Gln Arg
180 185 190

Ala Ala Glu Thr Val Leu Lys Gln Gln Gly Val Leu Ala Leu Arg Pro
195 200 205

Tyr Leu Gln Lys Gln Pro Gln Pro Ser Pro Ala Glu Gly Arg Ala Val
210 215 220

Thr Asn Glu Pro Glu Glu Glu Glu Leu Ala Thr Leu Ser Glu Glu Glu
225 230 235 240

Ile Ala Met Ala Val Thr Ala Trp Glu Lys Gly Leu Glu Ser Leu Pro
245 250 255

Pro Leu Arg Pro Gln Gln Asn Pro Val Leu Pro Val Ala Gly Glu Arg
260 265 270

Asn Val Leu Ile Thr Ser Ala Leu Pro Tyr Val Asn Asn Val Pro His
275 280 285

Leu Gly Asn Ile Ile Gly Cys Val Leu Ser Ala Asp Val Phe Ala Arg
290 295 300

Tyr Ser Arg Leu Arg Gln Trp Asn Thr Leu Tyr Leu Cys Gly Thr Asp
305 310 315 320

Glu Tyr Gly Thr Ala Thr Glu Thr Lys Ala Leu Glu Glu Gly Leu Thr
325 330 335

Pro Gln Glu Ile Cys Asp Lys Tyr His Ile Ile His Ala Asp Ile Tyr
340 345 350

Arg Trp Phe Asn Ile Ser Phe Asp Ile Phe Gly Arg Thr Thr Thr Pro
355 360 365

Gln Gln Thr Lys Ile Thr Gln Asp Ile Phe Gln Gln Leu Leu Lys Arg
370 375 380

Gly Phe Val Leu Gln Asp Thr Val Glu Gln Leu Arg Cys Glu His Cys
385 390 395 400

Ala Arg Phe Leu Ala Asp Arg Phe Val Glu Gly Val Cys Pro Phe Cys
405 410 415

Gly Tyr Glu Glu Ala Arg Gly Asp Gln Cys Asp Lys Cys Gly Lys Leu
420 425 430

1465

Ile Asn Ala Val Glu Leu Lys Lys Pro Gln Cys Lys Val Cys Arg Ser
 435 440 445

Cys Pro Val Val Gln Ser Ser Gln His Leu Phe Leu Asp Leu Pro Lys
 450 455 460

Leu Glu Lys Arg Leu Glu Glu Trp Leu Gly Arg Thr Leu Pro Gly Ser
 465 470 475 480

Asp Trp Thr Pro Asn Ala Gln Phe Ile Thr Arg Ser Trp Leu Arg Asp
 485 490 495

Gly Leu Lys Pro Arg Cys Ile Thr Arg Asp Leu Lys Trp Gly Thr Pro
 500 505 510

Val Pro Leu Glu Gly Phe Glu Asp Lys Val Phe Tyr Val Trp Phe Asp
 515 520 525

Ala Thr Ile Gly Tyr Leu Ser Ile Thr Ala Asn Tyr Thr Asp Gln Trp
 530 535 540

Glu Arg Trp Trp Lys Asn Pro Glu Gln Val Asp Leu Tyr Gln Phe Met
 545 550 555 560

Ala Lys Asp Asn Val Pro Phe His Ser Leu Val Phe Pro Cys Ser Ala
 565 570 575

Leu Gly Ala Glu Asp Asn Tyr Thr Leu Val Ser His Leu Ile Ala Thr
 580 585 590

Glu Tyr Leu Asn Tyr Glu Asp Gly Lys Phe Ser Lys Ser Arg Gly Val
 595 600 605

Gly Val Phe Gly Asp Met Ala Gln Asp Thr Gly Ile Pro Ala Asp Ile
 610 615 620

Trp Arg Phe Tyr Leu Leu Tyr Ile Arg Pro Glu Gly Gln Asp Ser Ala
 625 630 635 640

Phe Ser Trp Thr Asp Leu Leu Leu Lys Asn Asn Ser Glu Leu Leu Asn
 645 650 655

Asn Leu Gly Asn Phe Ile Asn Arg Ala Gly Met Phe Val Ser Lys Phe
 660 665 670

Phe Gly Gly Tyr Val Pro Glu Met Val Leu Thr Pro Asp Asp Gln Arg
 675 680 685

Leu Leu Ala His Val Thr Leu Glu Leu Gln His Tyr His Gln Leu Leu
 690 695 700

1466

Glu Lys Val Arg Ile Arg Asp Ala Leu Arg Ser Ile Leu Thr Ile Ser
705 710 715 720

Arg His Gly Asn Gln Tyr Ile Gln Val Asn Glu Pro Trp Lys Arg Ile
725 730 735

Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala Gly Thr Val Thr Gly Leu
740 745 750

Ala Val Asn Ile Ala Ala Leu Leu Ser Val Met Leu Gln Pro Tyr Met
755 760 765

Pro Thr Val Ser Ala Thr Ile Gln Ala Gln Leu Gln Leu Pro Pro Pro
770 775 780

Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu Cys Thr Leu Pro Ala Gly
785 790 795 800

His Gln Ile Gly Thr Val Ser Pro Leu Phe Gln Lys Leu Glu Asn Asp
805 810 815

Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly Gly Gly Gln Ala Lys Thr
820 825 830

Ser Pro Lys Pro Ala Val Val Glu Thr Val Thr Thr Ala Lys Pro Gln
835 840 845

Gln Ile Gln Ala Leu Met Asp Glu Val Thr Lys Gln Gly Asn Ile Val
850 855 860

Arg Glu Leu Lys Ala Gln Lys Ala Asp Lys Asn Glu Val Ala Ala Glu
865 870 875 880

Val Ala Lys Leu Leu Asp Leu Lys Lys Gln Leu Ala Val Ala Glu Gly
885 890 895

Asn Pro Leu Lys Pro Leu Lys Ala Arg Arg Lys Ser Lys Arg Pro Trp
900 905 910

Leu Ile Glu Ser His Phe Asn Arg
915 920

<210> 1397

<211> 476

<212> PRT

<213> Homo sapiens

<220>

1467

<221> SITE

<222> (127)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1397

Lys Met Ala Ala Leu Thr Thr Leu Phe Lys Tyr Ile Asp Glu Asn Gln
 1 5 10 15

Asp Arg Tyr Ile Lys Lys Leu Ala Lys Trp Val Ala Ile Gln Ser Val
 20 25 30

Ser Ala Trp Pro Glu Lys Arg Gly Glu Ile Arg Arg Met Met Glu Val
 35 40 45

Ala Ala Ala Asp Val Lys Gln Leu Gly Gly Ser Val Glu Leu Val Asp
 50 55 60

Ile Gly Lys Gln Lys Leu Pro Asp Gly Ser Glu Ile Pro Leu Pro Pro
 65 70 75 80

Ile Leu Leu Gly Arg Leu Gly Ser Asp Pro Gln Lys Lys Thr Val Cys
 85 90 95

Ile Tyr Gly His Leu Asp Val Gln Pro Ala Ala Leu Glu Asp Gly Trp
 100 105 110

Asp Ser Glu Pro Phe Thr Leu Val Glu Arg Asp Gly Lys Leu Xaa Gly
 115 120 125

Arg Gly Ser Thr Asp Asp Lys Gly Pro Val Ala Gly Trp Ile Asn Ala
 130 135 140

Leu Glu Ala Tyr Gln Lys Thr Gly Gln Glu Ile Pro Val Asn Val Arg
 145 150 155 160

Phe Cys Leu Glu Gly Met Glu Glu Ser Gly Ser Glu Gly Leu Asp Glu
 165 170 175

Leu Ile Phe Ala Arg Lys Asp Thr Phe Phe Lys Asp Val Asp Tyr Val
 180 185 190

Cys Ile Ser Asp Asn Tyr Trp Leu Gly Lys Lys Lys Pro Cys Ile Thr
 195 200 205

Tyr Gly Leu Arg Gly Ile Cys Tyr Phe Phe Ile Glu Val Glu Cys Ser
 210 215 220

Asn Lys Asp Leu His Ser Gly Val Tyr Gly Gly Ser Val His Glu Ala
 225 230 235 240

Met Thr Asp Leu Ile Leu Leu Met Gly Ser Leu Val Asp Lys Arg Gly

1468

245	250	255
Asn Ile Leu Ile Pro Gly Ile Asn Glu Ala Val Ala Ala Val Thr Glu		
260	265	270
Glu Glu His Lys Leu Tyr Asp Asp Ile Asp Phe Asp Ile Glu Glu Phe		
275	280	285
Ala Lys Asp Val Gly Ala Gln Ile Leu Leu His Ser His Lys Lys Asp		
290	295	300
Ile Leu Met His Arg Trp Arg Tyr Pro Ser Leu Ser Leu His Gly Ile		
305	310	315
Glu Gly Ala Phe Ser Gly Ser Gly Ala Lys Thr Val Ile Pro Arg Lys		
325	330	335
Val Val Gly Lys Phe Ser Ile Arg Leu Val Pro Asn Met Thr Pro Glu		
340	345	350
Val Val Gly Glu Gln Val Thr Ser Tyr Leu Thr Lys Lys Phe Ala Glu		
355	360	365
Leu Arg Ser Pro Asn Glu Phe Lys Val Tyr Met Gly His Gly Gly Lys		
370	375	380
Pro Trp Val Ser Asp Phe Ser His Pro His Tyr Leu Ala Gly Arg Arg		
385	390	395
Ala Met Lys Thr Val Phe Gly Val Glu Pro Asp Leu Thr Arg Glu Gly		
405	410	415
Gly Ser Ile Pro Val Thr Leu Thr Phe Gln Glu Ala Thr Gly Lys Asn		
420	425	430
Val Met Leu Leu Pro Val Gly Ser Ala Asp Asp Gly Ala His Ser Gln		
435	440	445
Asn Glu Lys Leu Asn Arg Tyr Asn Tyr Ile Glu Gly Thr Lys Met Leu		
450	455	460
Ala Ala Tyr Leu Tyr Glu Val Ser Gln Leu Lys Asp		
465	470	475

<210> 1398

<211> 187

<212> PRT

<213> Homo sapiens

1469

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1398

Leu His Leu Xaa Pro Thr Ser Ile Ser Ser Ser Ser Ser Cys Ser Val
 1 5 10 15

Ser Ser Val Val Ser Gln Arg Leu Thr Glu Ser Pro Cys Ala Leu Val
 20 25 30

Ala Ser Gln Tyr Gly Trp Ser Gly Asn Met Glu Arg Ile Met Lys Ala
 35 40 45

Gln Ala Tyr Gln Thr Gly Lys Asp Ile Ser Thr Asn Tyr Tyr Ala Ser
 50 55 60

Gln Lys Lys Thr Phe Glu Ile Asn Pro Arg His Pro Leu Ile Arg Asp
 65 70 75 80

Met Leu Arg Arg Ile Lys Glu Asp Glu Asp Asp Lys Thr Val Leu Asp
 85 90 95

Leu Ala Val Val Leu Phe Glu Thr Ala Thr Leu Arg Ser Gly Tyr Leu
 100 105 110

Leu Pro Asp Thr Lys Ala Tyr Gly Asp Arg Ile Glu Arg Met Leu Arg
 115 120 125

Leu Ser Leu Asn Ile Asp Pro Asp Ala Lys Val Glu Glu Glu Pro Glu
 130 135 140

Glu Glu Pro Glu Glu Thr Ala Glu Asp Thr Thr Glu Asp Thr Glu Gln
 145 150 155 160

Asp Glu Asp Glu Glu Met Asp Val Gly Thr Asp Glu Glu Glu Glu Thr
 165 170 175

Ala Lys Glu Ser Thr Ala Glu Lys Asp Glu Leu
 180 185

<210> 1399

<211> 376

<212> PRT

<213> Homo sapiens

<400> 1399

Lys Ser Ser Thr Gly Val Ile Pro Asp Glu Ala Lys Ala Leu Ser Leu

1470

1	5	10	15												
Leu	Ala	Pro	Ala	Asn	Ala	Val	Ala	Gly	Leu	Leu	Pro	Gly	Gly	Gly	Leu
			20					25					30		
Leu	Pro	Thr	Pro	Asn	Pro	Leu	Thr	Gln	Ile	Gly	Ala	Val	Pro	Leu	Ala
		35					40					45			
Ala	Leu	Gly	Ala	Pro	Thr	Leu	Asp	Pro	Ala	Leu	Ala	Ala	Leu	Gly	Leu
	50					55					60				
Pro	Gly	Ala	Asn	Leu	Asn	Ser	Gln	Ser	Leu	Ala	Ala	Asp	Gln	Leu	Leu
65					70					75				80	
Lys	Leu	Met	Ser	Thr	Val	Asp	Pro	Lys	Leu	Asn	His	Val	Ala	Ala	Gly
					85				90					95	
Leu	Val	Ser	Pro	Ser	Leu	Lys	Ser	Asp	Thr	Ser	Ser	Lys	Glu	Ile	Glu
			100					105					110		
Glu	Ala	Met	Lys	Arg	Val	Arg	Glu	Ala	Gln	Ser	Leu	Ile	Ser	Ala	Ala
		115					120					125			
Ile	Glu	Pro	Asp	Lys	Lys	Glu	Glu	Lys	Arg	Arg	His	Ser	Arg	Ser	Arg
	130					135					140				
Ser	Arg	Ser	Arg	Arg	Arg	Arg	Thr	Pro	Ser	Ser	Ser	Arg	His	Arg	Arg
145					150					155				160	
Ser	Arg	Ser	Arg	Ser	Arg	Arg	Arg	Ser	His	Ser	Lys	Ser	Arg	Ser	Arg
				165					170				175		
Arg	Arg	Ser	Lys	Ser	Pro	Arg	Arg	Arg	Arg	Ser	His	Ser	Arg	Glu	Arg
			180					185					190		
Gly	Arg	Arg	Ser	Arg	Ser	Thr	Ser	Lys	Thr	Arg	Asp	Lys	Lys	Lys	Glu
		195					200					205			
Asp	Lys	Glu	Lys	Lys	Arg	Ser	Lys	Thr	Pro	Pro	Lys	Ser	Tyr	Ser	Thr
	210					215					220				
Ala	Arg	Arg	Ser	Arg	Ser	Ala	Ser	Arg	Glu	Arg	Arg	Arg	Arg	Arg	Ser
225					230					235				240	
Arg	Ser	Gly	Thr	Arg	Ser	Pro	Lys	Lys	Pro	Arg	Ser	Pro	Lys	Arg	Lys
			245						250				255		
Leu	Ser	Arg	Ser	Pro	Ser	Pro	Arg	Arg	His	Lys	Lys	Glu	Lys	Lys	Lys
			260					265				270			
Asp	Lys	Asp	Lys	Glu	Arg	Ser	Arg	Asp	Glu	Arg	Glu	Arg	Ser	Thr	Ser

1471

275 280 285
 Lys Lys Lys Lys Ser Lys Asp Lys Glu Lys Asp Arg Glu Arg Lys Ser
 290 295 300
 Glu Ser Asp Lys Asp Val Lys Gln Val Thr Arg Asp Tyr Asp Glu Glu
 305 310 315 320
 Glu Gln Gly Tyr Asp Ser Glu Lys Glu Lys Lys Glu Glu Lys Lys Pro
 325 330 335
 Ile Glu Thr Gly Ser Pro Lys Thr Lys Glu Cys Ser Val Glu Lys Gly
 340 345 350
 Thr Gly Asp Ser Leu Arg Glu Ser Lys Val Asn Gly Asp Asp His His
 355 360 365
 Glu Glu Asp Met Asp Met Ser Asp
 370 375

<210> 1400

<211> 112

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (21)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1400

Thr Ala Gly Leu Thr Ser Arg Gly Trp Gly Ser Leu Pro Pro Ser Leu
 1 5 10 15

Glu Thr Phe Leu Xaa Trp Leu Lys Ser Arg Lys Glu Asn Glu Cys Thr
 20 25 30

Ser Arg Leu Ala Gln Ser Leu Ser Pro Ser Ser Ser Leu Phe Pro Ala
 35 40 45

Gly Pro Ser Gly Leu Tyr Gly Pro Asp Gly Gly Leu Arg Lys Met Arg
 50 55 60

Gly Leu Trp Phe Ser Gly Ile Pro Ala Gly Ala Thr Pro Ser Cys Leu
 65 70 75 80

Gln Met Val His Val Pro Ile Pro Pro Ser Arg Pro Leu Leu Cys Leu
 85 90 95

1472

Leu Cys His Arg Asp Ser Gln Gln Arg Phe Phe Phe Val Leu Ala Val
100 105 110

<210> 1401

<211> 69

<212> PRT

<213> Homo sapiens

<400> 1401

Arg Arg Gln Val Gly Ala Ala Ala Val Ala Met Thr Arg Gly Asn Gln
1 5 10 15

Arg Glu Leu Ala Arg Gln Lys Asn Met Lys Lys Gln Ser Asp Ser Val
20 25 30

Lys Gly Lys Arg Arg Asp Asp Gly Leu Ser Ala Ala Ala Arg Lys Gln
35 40 45

Arg Asp Ser Glu Ile Met Gln Gln Lys Gln Lys Lys Ala Asn Glu Lys
50 55 60

Lys Glu Glu Pro Lys
65

<210> 1402

<211> 177

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (162)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (166)

<223> Xaa equals any of the naturally occurring L-amino acids

1473

<400> 1402

Arg Pro Pro Arg Arg Xaa Pro Met Asp Gly Pro Ala Ile Ile Thr Gln
 1 5 10 15

Val Thr Asn Pro Lys Glu Asp Glu Gly Arg Leu Pro Gly Ala Gly Glu
 20 25 30

Lys Ala Ser Gln Cys Asn Val Ser Leu Lys Lys Gln Arg Ser Arg Ser
 35 40 45

Ile Leu Ser Ser Phe Phe Cys Cys Phe Arg Asp Tyr Asn Val Glu Ala
 50 55 60

Pro Pro Pro Ser Ser Pro Ser Val Leu Pro Pro Leu Val Glu Glu Asn
 65 70 75 80

Gly Gly Leu Gln Lys Pro Pro Ala Lys Tyr Leu Leu Pro Glu Val Thr
 85 90 95

Val Leu Asp Tyr Gly Lys Lys Cys Val Val Ile Asp Leu Asp Glu Thr
 100 105 110

Leu Val His Ser Ser Phe Lys Pro Ile Ser Asn Ala Asp Phe Ile Val
 115 120 125

Pro Val Glu Ile Asp Gly Thr Ile His Gln Val Tyr Val Leu Lys Arg
 130 135 140

Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Gln Leu Leu Asn Val
 145 150 155 160

Cys Xaa Leu Leu Pro Xaa Gly Gln Val Cys Arg Pro Val Ala Asp Leu
 165 170 175

Leu

<210> 1403

<211> 82

<212> PRT

<213> Homo sapiens

<400> 1403

Lys His Ile Leu Ser Thr Phe Glu Thr Ser Val Leu Glu Gly Arg Leu
 1 5 10 15

His Lys Leu Ser Ser Pro Arg Leu Arg Arg Leu Gln Ser Gly Lys Leu
 20 25 30

1474

Thr Cys Arg Asn Gly Val Pro Phe Met Leu Tyr Leu Asp Lys Gly Asn
 35 40 45

Gln Lys Trp Asn Gln Cys Arg Gln Asn Leu Gly Phe Ala Ala Ser Ile
 50 55 60

Asn Gln Ser Met Thr Asn Arg Gly Ser Leu Lys Cys Lys Gly Thr Asn
 65 70 75 80

Phe Thr

<210> 1404

<211> 251

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (37)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (41)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1404

Thr Thr Lys Pro Ala Thr Thr Pro Ser Ser Thr Thr Arg Thr Cys Arg
 1 5 10 15

Arg Ser Pro Ser Thr Leu Pro Ser Ala Thr Trp Thr Pro Leu Ala Ser
 20 25 30

Arg Thr Ala His Xaa Leu Pro Arg Xaa Tyr Met Tyr Pro Ser Met Asp
 35 40 45

Gln Leu Ala Glu Met Leu Pro Gly Val Leu Gln Gln Phe Gly Leu Lys
 50 55 60

Ser Ile Ile Gly Met Gly Thr Gly Ala Gly Ala Tyr Ile Leu Thr Arg
 65 70 75 80

Phe Ala Leu Asn Asn Pro Glu Met Val Glu Gly Leu Val Leu Ile Asn
 85 90 95

Val Asn Pro Cys Ala Glu Gly Trp Met Asp Trp Ala Ala Ser Lys Ile
 100 105 110

1475

Ser Gly Trp Thr Gln Ala Leu Pro Asp Met Val Val Ser His Leu Phe
 115 120 125
 Gly Lys Glu Glu Met Gln Ser Asn Val Glu Val Val His Thr Tyr Arg
 130 135 140
 Gln His Ile Val Asn Asp Met Asn Pro Gly Asn Leu His Leu Phe Ile
 145 150 155 160
 Asn Ala Tyr Asn Ser Arg Arg Asp Leu Glu Ile Glu Arg Pro Met Pro
 165 170 175
 Gly Thr His Thr Val Thr Leu Gln Cys Pro Ala Leu Leu Val Val Gly
 180 185 190
 Asp Ser Ser Pro Ala Val Asp Ala Val Val Glu Cys Asn Ser Lys Leu
 195 200 205
 Asp Pro Thr Lys Thr Thr Leu Leu Lys Met Ala Asp Cys Gly Gly Leu
 210 215 220
 Pro Gln Ile Ser Gln Pro Ala Lys Leu Ala Glu Ala Phe Lys Tyr Phe
 225 230 235 240
 Val Gln Gly Met Gly Tyr Met Pro Arg Leu Ala
 245 250

<210> 1405
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 1405
 Phe Glu Gly Phe Tyr Ser Gly Arg Lys Asn Arg Thr Lys Val Tyr Val
 1 5 10 15
 Pro Ser Ser Val Val Leu Ile Asp Leu Phe Phe Leu Phe Glu Thr Lys
 20 25 30
 Val Val Ser Val Phe Trp Phe Ser Gly Asn Met Tyr Tyr Ile Val Leu
 35 40 45
 Lys Glu Cys Cys Pro Thr Asn Tyr Ser Ser Lys Gln Arg Ile Val Thr
 50 55 60
 Ile Asn Lys Val Ser Val Thr Leu Leu Pro Leu Ser His Asn Ile His
 65 70 75 80
 Cys Arg Ala Leu Cys Arg Ser Lys Asn Arg Ala Ala Gln Asn Leu Cys

1476

85

90

95

Gly Ser Phe Leu Ser Phe Cys Asn Leu Arg His Met Phe Gln Arg Thr
100 105 110

Gly Ile Phe Val Trp Ser Ser Asp Leu Gly Asp His Ser His Asn
115 120 125

<210> 1406

<211> 230

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (90)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (112)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (118)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (169)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (190)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (192)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (194)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1477

<221> SITE

<222> (217)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (218)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1406

Ala Glu Arg Pro Leu Gln Val Pro Arg Ser Ala Gly Glu Ala Ala Pro
 1 5 10 15

His Ser Arg Arg Pro Pro Gly Leu Leu Pro His Ala Pro Arg Ala Ala
 20 25 30

Ser Ala Gln Leu Glu Glu Arg Arg Asp Pro His Pro Gly Met Thr
 35 40 45

Leu Gln Glu Gly Asp Cys Arg Gly Ser Gln Thr Val Ser Leu Thr Met
 50 55 60

Gly Thr Ala Asp Ser Asp Glu Met Ala Pro Glu Ala Pro Gln His Thr
 65 70 75 80

His Ile Asp Val His Ile His Gln Glu Xaa Ala Leu Ala Lys Leu Leu
 85 90 95

Leu Thr Cys Cys Ser Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg Xaa
 100 105 110

Ser Ser Arg Leu Leu Xaa Ala Ser Trp Val Met Gln Ile Val Leu Gly
 115 120 125

Ile Leu Ser Ala Val Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr Thr
 130 135 140

Leu Leu Val Thr Ser Gly Ala Ala Ser Gly Gln Gly Leu Trp Leu Cys
 145 150 155 160

Cys Trp Ser Cys Cys Leu His Leu Xaa Glu Thr Gly Trp Tyr Ile Leu
 165 170 175

Gly Pro Ala Glu Asp Ser Ala Asn Ala Gly Lys Leu Ser Xaa Gln Xaa
 180 185 190

Ser Xaa Ala Ser Asn Phe Gly Asn Glu Glu Phe Arg Tyr Gly Leu Leu
 195 200 205

Leu Ile Thr Thr Ser Gly Trp Pro Xaa Xaa Gln Val Arg Val Asp Trp
 210 215 220

1478

Asn Thr Ser Ser Pro Gln
225 230

<210> 1407
<211> 79
<212> PRT
<213> Homo sapiens

<400> 1407
Arg Gly His Phe Leu Leu Pro Asp Leu Asp Ile Pro Ser Asn Pro Ser
1 5 10 15
Ser Tyr Ser Met Leu Lys Glu Lys Tyr Ser Gln Met His Tyr Val Asn
20 25 30
Gly Glu Lys Lys His Ser Ile Val Glu Thr Pro Ile Leu Ala Asn Val
35 40 45
Phe Trp Ser Val Phe His Phe Thr Val Tyr Ile Pro Ala Leu Lys Thr
50 55 60
Gln Gly Gln Val Leu Thr Lys Glu Val Cys Ser His Ser Lys Tyr
65 70 75

<210> 1408
<211> 289
<212> PRT
<213> Homo sapiens

<400> 1408
Val Arg Pro Pro Ser His Val Thr Ala Asp Ser Gly Arg Ser Pro Leu
1 5 10 15
Ser Leu Thr Tyr Leu Pro Leu Gln Glu Pro Gly Asp Met Ala Ala Ala
20 25 30
Val Pro Arg Ala Ala Phe Leu Ser Pro Leu Leu Pro Leu Leu Gly
35 40 45
Phe Leu Leu Leu Ser Ala Pro His Gly Gly Ser Gly Leu His Thr Lys
50 55 60
Gly Ala Leu Pro Leu Asp Thr Val Thr Phe Tyr Lys Val Ile Pro Lys
65 70 75 80
Ser Lys Phe Val Leu Val Lys Phe Asp Thr Gln Tyr Pro Tyr Gly Glu

1479

[illegible]

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<210> 1409
<211> 488
<212> PRT
<213> Homo sapiens
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<400> 1409
Pro Ala Ser Ala Gly Thr Val Ser Glu Gly Pro Pro Gly Thr Asp Gly
1 5 10 15

1480

Ser Ala Gly Arg Gly Gly Thr Ala Phe Ala Met Ala Ala Thr Val Asn
 20 25 30

Leu Glu Leu Asp Pro Ile Phe Leu Lys Ala Leu Gly Phe Leu His Ser
 35 40 45

Lys Ser Lys Asp Ser Ala Glu Lys Leu Lys Ala Leu Leu Asp Glu Ser
 50 55 60

Leu Ala Arg Gly Ile Asp Ser Ser Tyr Arg Pro Ser Gln Lys Asp Val
 65 70 75 80

Glu Pro Pro Lys Ile Ser Ser Thr Lys Asn Ile Ser Ile Lys Gln Glu
 85 90 95

Pro Lys Ile Ser Ser Ser Leu Pro Ser Gly Asn Asn Asn Gly Lys Val
 100 105 110

Leu Thr Thr Glu Lys Val Lys Lys Glu Ala Glu Lys Arg Pro Ala Asp
 115 120 125

Lys Met Lys Ser Asp Ile Thr Glu Gly Val Asp Ile Pro Lys Lys Pro
 130 135 140

Arg Leu Glu Lys Pro Glu Thr Gln Ser Ser Pro Ile Thr Val Gln Ser
 145 150 155 160

Ser Lys Asp Leu Pro Met Ala Asp Leu Ser Ser Phe Glu Glu Thr Ser
 165 170 175

Ala Asp Asp Phe Ala Met Glu Met Gly Leu Ala Cys Val Val Cys Arg
 180 185 190

Gln Met Met Val Ala Ser Gly Asn Gln Leu Val Glu Cys Gln Glu Cys
 195 200 205

His Asn Leu Tyr His Arg Asp Cys His Lys Pro Gln Val Thr Asp Lys
 210 215 220

Glu Ala Asn Asp Pro Arg Leu Val Trp Tyr Cys Ala Arg Cys Thr Arg
 225 230 235 240

Gln Met Lys Arg Met Ala Gln Lys Thr Gln Lys Pro Pro Gln Lys Pro
 245 250 255

Ala Pro Ala Val Val Ser Val Thr Pro Ala Val Lys Asp Pro Leu Val
 260 265 270

Lys Lys Pro Glu Thr Lys Leu Lys Gln Glu Thr Thr Phe Leu Ala Phe
 275 280 285

1481

Lys Arg Thr Glu Val Lys Thr Ser Thr Val Ile Ser Gly Asn Ser Ser
 290 295 300

Ser Ala Ser Val Ser Ser Ser Val Thr Ser Gly Leu Thr Gly Trp Ala
 305 310 315 320

Ala Phe Ala Ala Lys Thr Ser Ser Ala Gly Pro Ser Thr Ala Lys Leu
 325 330 335

Ser Ser Thr Thr Gln Asn Asn Thr Gly Lys Pro Ala Thr Ser Ser Ala
 340 345 350

Asn Gln Lys Pro Val Gly Leu Thr Gly Leu Ala Thr Ser Ser Lys Gly
 355 360 365

Gly Ile Gly Ser Lys Ile Gly Ser Asn Asn Ser Thr Thr Pro Thr Val
 370 375 380

Pro Leu Lys Pro Pro Pro Pro Leu Thr Leu Gly Lys Thr Gly Leu Ser
 385 390 395 400

Arg Ser Val Ser Cys Asp Asn Val Ser Lys Val Gly Leu Pro Ser Pro
 405 410 415

Ser Ser Leu Val Pro Gly Ser Ser Ser Gln Leu Ser Gly Asn Gly Asn
 420 425 430

Ser Gly Thr Ser Gly Pro Ser Gly Ser Thr Thr Ser Lys Thr Thr Ser
 435 440 445

Glu Ser Ser Ser Ser Pro Ser Ala Ser Leu Lys Gly Pro Thr Ser Gln
 450 455 460

Glu Ser Gln Leu Asn Ala Met Lys Arg Leu Gln Met Val Lys Lys Lys
 465 470 475 480

Ala Ala Gln Lys Lys Leu Lys Lys
 485

<210> 1410

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (53)

<223> Xaa equals any of the naturally occurring L-amino acids

1482

<400> 1410

His Tyr Gly Leu Lys Leu Ala Val Lys Met Pro Asn Thr Val Val Pro
1 5 10 15

Trp Asn Pro Val Tyr Ser Cys Ala Lys Gln Asn Cys Lys Ile Val Lys
20 25 30

Met Ser Tyr Gln Val Ile Arg Arg Leu Gln Arg His His Leu Phe Phe
35 40 45

Ile Ser Phe Phe Xaa Leu Thr His Val Val Val Ile Phe Asn Thr Phe
50 55 60

<210> 1411

<211> 129

<212> PRT

<213> Homo sapiens

<400> 1411

Ala Ala Cys Leu Ala Leu Arg Ile Ala Ala Ala Met Ala Ser Gln Ser
1 5 10 15

Gln Gly Ile Gln Gln Leu Leu Gln Ala Glu Lys Arg Ala Ala Glu Lys
20 25 30

Val Ser Glu Ala Arg Lys Arg Lys Asn Arg Arg Leu Lys Gln Ala Lys
35 40 45

Glu Glu Ala Gln Ala Glu Ile Glu Gln Tyr Arg Leu Gln Arg Glu Lys
50 55 60

Glu Phe Lys Ala Lys Glu Ala Ala Ala Leu Gly Ser Arg Gly Ser Cys
65 70 75 80

Ser Thr Glu Val Glu Lys Glu Thr Gln Glu Lys Met Thr Ile Leu Gln
85 90 95

Thr Tyr Phe Arg Gln Asn Arg Asp Glu Val Leu Asp Asn Leu Leu Ala
100 105 110

Phe Val Cys Asp Ile Arg Pro Glu Ile His Glu Asn Tyr Arg Ile Asn
115 120 125

Gly

1483

<210> 1412

<211> 177

<212> PRT

<213> Homo sapiens

<400> 1412

Val Thr Val Pro Ser Ser Ser Ala Ala Gly Thr Leu Phe Gln Gly Leu
1 5 10 15

Cys Gly Ala Pro Asp Ala Pro His Pro Leu Ser Lys Ile Pro Gly Gly
20 25 30

Arg Gly Gly Gly Arg Asp Pro Ser Leu Ser Ala Leu Ile Tyr Lys Asp
35 40 45

Glu Lys Leu Thr Val Thr Gln Asp Leu Pro Val Asn Asp Gly Lys Pro
50 55 60

His Ile Val His Phe Gln Tyr Glu Val Thr Glu Val Lys Val Ser Ser
65 70 75 80

Trp Asp Ala Val Leu Ser Ser Gln Ser Leu Phe Val Glu Ile Pro Asp
85 90 95

Gly Leu Leu Ala Asp Gly Ser Lys Glu Gly Leu Leu Ala Leu Leu Glu
100 105 110

Phe Ala Glu Glu Lys Met Lys Val Asn Tyr Val Phe Ile Cys Phe Arg
115 120 125

Lys Gly Arg Glu Asp Arg Ala Pro Leu Leu Lys Thr Phe Ser Phe Leu
130 135 140

Gly Phe Glu Ile Val Arg Pro Gly His Pro Cys Val Pro Ser Arg Pro
145 150 155 160

Asp Val Met Phe Met Val Tyr Pro Leu Asp Gln Asn Leu Ser Asp Glu
165 170 175

Asp

<210> 1413

<211> 112

<212> PRT

<213> Homo sapiens

1484

<400> 1413

Ser Gly Leu Arg Leu Ala Met Ser Thr Asn Asn Met Ser Asp Pro Arg
 1 5 10 15

Arg Pro Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn
 20 25 30

Pro Ala Leu Asp Asp Pro Thr Pro Asp Tyr Met Asn Leu Leu Gly Met
 35 40 45

Ile Phe Ser Met Cys Gly Leu Met Leu Lys Leu Lys Trp Cys Ala Trp
 50 55 60

Val Ala Val Tyr Cys Ser Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser
 65 70 75 80

Glu Asp Thr Lys Gln Met Met Ser Ser Phe Met Leu Ser Ile Ser Ala
 85 90 95

Val Val Met Ser Tyr Leu Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
 100 105 110

<210> 1414

<211> 186

<212> PRT

<213> Homo sapiens

<400> 1414

Cys Leu Gly Gly Arg Pro Arg Cys Val Leu Arg Leu Thr Ala Asn Leu
 1 5 10 15

Glu Gly Arg Arg Asp Ser Ala Thr His Ala Pro Pro His Pro Arg Leu
 20 25 30

Arg Val Lys Arg Ala Val Gly Pro Glu Ser Pro Pro Leu Trp Gln Trp
 35 40 45

Pro Pro Leu Tyr Ser Ile Leu Pro Ser Gly Arg Ser Ala Val Asn Lys
 50 55 60

Arg Trp Ala Pro Gln Ser Thr Cys Pro Pro Thr Ala Leu Ala Val Leu
 65 70 75 80

Gly Ser Ser Leu Gln Phe Thr Gly Asn Lys Pro Glu Ser Ala Arg Thr
 85 90 95

1485

Arg Gly Cys Ser Pro Gly Ser Ala Arg Pro Pro Leu Ser Pro Ala Thr
 100 105 110

Gly Trp Arg Cys Arg Ala Arg Ala Ala Ser Arg Arg Phe Pro Gly
 115 120 125

Ala Pro Gly Pro Glu Glu Arg Ser Pro Gln Ser Lys Gly Gly Asn Thr
 130 135 140

Cys Leu Arg Cys Lys Glu Ile Leu Phe Gln Ser Ile Pro Val Val Gln
 145 150 155 160

Thr Asp Thr Val Pro Asn Glu Arg Ser Asp Val Phe Ser Ser Pro Phe
 165 170 175

Leu Ile Cys Phe Leu Thr Gly Leu Arg Phe
 180 185

<210> 1415

<211> 108

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (46)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (68)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1415

Thr Lys Thr Thr Leu Phe Leu Glu Arg Pro Leu Phe Lys Lys Glu Ser
 1 5 10 15

Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys Met Lys Leu Gly Lys
 20 25 30

Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg Met Xaa Ser Thr
 35 40 45

Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr
 50 55 60

Pro Phe Pro Xaa Pro Pro Leu Leu Tyr Gln Val Glu Leu Ser Val Gly
 65 70 75 80

1486

Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln Ala Ala Lys His
 85 90 95

Asp Ala Ala Ala Lys Ala Val Glu Asp Pro Ala Glu
 100 105

<210> 1416

<211> 621

<212> PRT

<213> Homo sapiens

<400> 1416

Ala Gly His Arg Ala Gly Val Cys Ser Leu Ser Ala Thr Arg Leu Leu
 1 5 10 15

Leu Pro Lys Asp Arg Gly Val Gly Arg Arg Gln Thr Met Trp Thr Leu
 20 25 30

Val Ser Trp Val Ala Leu Thr Ala Gly Leu Val Ala Gly Thr Arg Cys
 35 40 45

Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu Asp Pro Gly Gly
 50 55 60

Ala Ser Tyr Ser Cys Cys Arg Pro Leu Leu Asp Lys Trp Pro Thr Thr
 65 70 75 80

Leu Ser Arg His Leu Gly Gly Pro Cys Gln Val Asp Ala His Cys Ser
 85 90 95

Ala Gly His Ser Cys Ile Phe Thr Val Ser Gly Thr Ser Ser Cys Cys
 100 105 110

Pro Phe Pro Glu Ala Val Ala Cys Gly Asp Gly His His Cys Cys Pro
 115 120 125

Arg Gly Phe His Cys Ser Ala Asp Gly Arg Ser Cys Phe Gln Arg Ser
 130 135 140

Gly Asn Asn Ser Val Gly Ala Ile Gln Cys Pro Asp Ser Gln Phe Glu
 145 150 155 160

Cys Pro Asp Phe Ser Thr Cys Cys Val Met Val Asp Gly Ser Trp Gly
 165 170 175

Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp Arg Val His Cys
 180 185 190

1487

Cys Pro His Gly Ala Phe Cys Asp Leu Val His Thr Arg Cys Ile Thr
 195 200 205
 Pro Thr Gly Thr His Pro Leu Ala Lys Lys Leu Pro Ala Gln Arg Thr
 210 215 220
 Asn Arg Ala Val Ala Leu Ser Ser Ser Val Met Cys Pro Asp Ala Arg
 225 230 235 240
 Ser Arg Cys Pro Asp Gly Ser Thr Cys Cys Glu Leu Pro Ser Gly Lys
 245 250 255
 Tyr Gly Cys Cys Pro Met Pro Asn Ala Thr Cys Cys Ser Asp His Leu
 260 265 270
 His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile Gln Ser Lys Cys
 275 280 285
 Leu Ser Lys Glu Asn Ala Thr Thr Asp Leu Leu Thr Lys Leu Pro Ala
 290 295 300
 His Thr Val Gly Asp Val Lys Cys Asp Met Glu Val Ser Cys Pro Asp
 305 310 315 320
 Gly Tyr Thr Cys Cys Arg Leu Gln Ser Gly Ala Trp Gly Cys Cys Pro
 325 330 335
 Phe Thr Gln Ala Val Cys Cys Glu Asp His Ile His Cys Cys Pro Ala
 340 345 350
 Gly Phe Thr Cys Asp Thr Gln Lys Gly Thr Cys Glu Gln Gly Pro His
 355 360 365
 Gln Val Pro Trp Met Glu Lys Ala Pro Ala His Leu Ser Leu Pro Asp
 370 375 380
 Pro Gln Ala Leu Lys Arg Asp Val Pro Cys Asp Asn Val Ser Ser Cys
 385 390 395 400
 Pro Ser Ser Asp Thr Cys Cys Gln Leu Thr Ser Gly Glu Trp Gly Cys
 405 410 415
 Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp His Gln His Cys Cys
 420 425 430
 Pro Gln Gly Tyr Thr Cys Val Ala Glu Gly Gln Cys Gln Arg Gly Ser
 435 440 445
 Glu Ile Val Ala Gly Leu Glu Lys Met Pro Ala Arg Arg Ala Ser Leu
 450 455 460

1488

Ser His Pro Arg Asp Ile Gly Cys Asp Gln His Thr Ser Cys Pro Val
465 470 475 480

Gly Gln Thr Cys Cys Pro Ser Leu Gly Gly Ser Trp Ala Cys Cys Gln
485 490 495

Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His Cys Cys Pro Ala
500 505 510

Gly Tyr Thr Cys Asn Val Lys Ala Arg Ser Cys Glu Lys Glu Val Val
515 520 525

Ser Ala Gln Pro Ala Thr Phe Leu Ala Arg Ser Pro His Val Gly Val
530 535 540

Lys Asp Val Glu Cys Gly Glu Gly His Phe Cys His Asp Asn Gln Thr
545 550 555 560

Cys Cys Arg Asp Asn Arg Gln Gly Trp Ala Cys Cys Pro Tyr Arg Gln
565 570 575

Gly Val Cys Cys Ala Asp Arg Arg His Cys Cys Pro Ala Gly Phe Arg
580 585 590

Cys Ala Ala Arg Gly Thr Lys Cys Leu Arg Arg Glu Ala Pro Arg Trp
595 600 605

Asp Ala Pro Leu Arg Asp Pro Ala Leu Arg Gln Leu Leu
610 615 620

<210> 1417

<211> 340

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (24)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1417

Ser Ala His Ala Ser Glu Arg Ile Ala Xaa Ser Gly Cys Gly Ala Pro
1 5 10 15

1489

Ala Ala Gly Ala Gly Pro Arg Xaa Arg Ser Leu Gly Ala Asp Pro Gly
 20 25 30

Arg Ala Ala Arg Arg His Glu Gly Gln Gly Gly Glu Gly Gly Arg Arg
 35 40 45

Thr Ala Gly Arg Trp Arg Arg Lys Pro Glu Lys Ser Pro Ser Ala Gln
 50 55 60

Glu Leu Lys Glu Gln Gly Asn Arg Leu Phe Val Gly Arg Lys Tyr Pro
 65 70 75 80

Glu Ala Ala Ala Cys Tyr Gly Arg Ala Ile Thr Arg Asn Pro Leu Val
 85 90 95

Ala Val Tyr Tyr Thr Asn Arg Ala Leu Cys Tyr Leu Lys Met Gln Gln
 100 105 110

His Glu Gln Ala Leu Ala Asp Cys Arg Arg Ala Leu Glu Leu Asp Gly
 115 120 125

Gln Ser Val Lys Ala His Phe Phe Leu Gly Gln Cys Gln Leu Glu Met
 130 135 140

Glu Ser Tyr Asp Glu Ala Ile Ala Asn Leu Gln Arg Ala Tyr Ser Leu
 145 150 155 160

Ala Lys Glu Gln Arg Leu Asn Phe Gly Asp Asp Ile Pro Ser Ala Leu
 165 170 175

Arg Ile Ala Lys Lys Lys Arg Trp Asn Ser Ile Glu Glu Arg Arg Ile
 180 185 190

His Gln Glu Ser Glu Leu His Ser Tyr Leu Ser Arg Leu Ile Ala Ala
 195 200 205

Glu Arg Glu Arg Glu Leu Glu Glu Cys Gln Arg Asn His Glu Gly Asp
 210 215 220

Glu Asp Asp Ser His Val Arg Ala Gln Gln Ala Cys Ile Glu Ala Lys
 225 230 235 240

His Asp Lys Tyr Met Ala Asp Met Asp Glu Leu Phe Ser Gln Val Asp
 245 250 255

Glu Lys Arg Lys Lys Arg Asp Ile Pro Asp Tyr Leu Cys Gly Lys Ile
 260 265 270

Ser Phe Glu Leu Met Arg Glu Pro Cys Ile Thr Pro Ser Gly Ile Thr
 275 280 285

1490

Tyr Asp Arg Lys Asp Ile Glu Glu His Leu Gln Arg Val Gly His Phe
290 295 300

Asp Pro Val Thr Arg Ser Pro Leu Thr Gln Glu Gln Leu Ile Pro Asn
305 310 315 320

Leu Ala Met Lys Glu Val Ile Asp Ala Phe Ile Ser Glu Asn Gly Trp
325 330 335

Val Glu Asp Tyr
340

<210> 1418

<211> 235

<212> PRT

<213> Homo sapiens

<400> 1418

Ser Pro Arg Pro Leu Arg Phe Cys Gly Gly Ala Arg Ala Arg Arg Pro
1 5 10 15

Leu Ser Ala Val Ala Arg Pro Ala Arg Ser Ser Asp Pro Leu Arg Ser
20 25 30

Ala Pro Leu Gly Pro Ala Pro Pro Val Asn Met Ile Arg Cys Gly Leu
35 40 45

Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro Leu Leu Leu Ser Ala
50 55 60

Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser
65 70 75 80

Ser Asp His Gly Gln Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu
85 90 95

Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu
100 105 110

Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile
115 120 125

Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro
130 135 140

Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala
145 150 155 160

Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr

1491

	165		170		175
Gln Thr Phe Thr Leu His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn					
	180		185		190
Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys					
	195		200		205
Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly					
	210		215		220
Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala					
	225		230		235

<210> 1419

<211> 86

<212> PRT

<213> Homo sapiens

<400> 1419

Arg Arg Gln Ala Leu Gln Glu Arg Cys Pro Phe Asn Pro Leu Ser Ala					
1	5		10		15
Leu Asp Arg Arg Cys Cys Val Lys Leu Leu Met Asp Ile Tyr Met Arg					
	20		25		30
Ser Ser Phe Leu Tyr Ala Ile Pro Ala Val Phe Phe Phe Leu Thr Gly					
	35		40		45
Pro Cys Leu Arg Ile Asn Lys Ser Val Met Ser Glu Thr Lys Val Tyr					
	50		55		60
Ser Ser Val Cys Arg Cys Val Ala Pro Pro Phe Ser Pro Ala Ala Pro					
	65		70		75
					80
His Ile Gln Ser Arg Ser					
					85

<210> 1420

<211> 351

<212> PRT

<213> Homo sapiens

<400> 1420

Thr Trp Cys Thr Thr Thr Met Leu Ala Ala Arg Leu Val Cys Leu Arg					
1	5		10		15

1492

Thr Leu Pro Ser Arg Val Phe His Pro Ala Phe Thr Lys Ala Ser Pro
20 25 30

Val Val Lys Asn Ser Ile Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser
35 40 45

Arg Glu Tyr Ala Thr Lys Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr
50 55 60

Gly Gln Glu Leu Lys Glu Ala Ala Leu Glu Pro Ser Met Glu Lys Ile
65 70 75 80

Phe Lys Ile Asp Gln Met Gly Arg Trp Phe Val Ala Gly Gly Ala Ala
85 90 95

Val Gly Leu Gly Ala Leu Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu
100 105 110

Ile Gly Ala Ile Glu Lys Ala Val Ile Trp Pro Gln Tyr Val Lys Asp
115 120 125

Arg Ile His Ser Thr Tyr Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr
130 135 140

Ala Leu Ser Ala Ile Ala Ile Ser Arg Thr Pro Val Leu Met Asn Phe
145 150 155 160

Met Met Arg Gly Ser Trp Val Thr Ile Gly Val Thr Phe Ala Ala Met
165 170 175

Val Gly Ala Gly Met Leu Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro
180 185 190

Gly Pro Lys His Leu Ala Trp Leu Leu His Ser Gly Val Met Gly Ala
195 200 205

Val Val Ala Pro Leu Thr Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala
210 215 220

Ala Trp Tyr Thr Ala Gly Ile Val Gly Gly Leu Ser Thr Val Ala Met
225 230 235 240

Cys Ala Pro Ser Glu Lys Phe Leu Asn Met Gly Ala Pro Leu Gly Val
245 250 255

Gly Leu Gly Leu Val Phe Val Ser Ser Leu Gly Ser Met Phe Leu Pro
260 265 270

Pro Thr Thr Val Ala Gly Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly
275 280 285

1493

Gly Leu Val Leu Phe Ser Met Phe Leu Leu Tyr Asp Thr Gln Lys Val
 290 295 300

Ile Lys Arg Ala Glu Val Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp
 305 310 315 320

Pro Ile Asn Ser Met Leu Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe
 325 330 335

Met Arg Val Ala Thr Met Leu Ala Thr Gly Gly Asn Arg Lys Lys
 340 345 350

<210> 1421

<211> 81

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1421

Cys Gly Xaa Leu Leu Met Ala Gln Gly Leu Ser Ala Ser Ala Leu Glu
 1 5 10 15

Gly Leu Lys Thr Glu Glu Gly Ser Val Arg Gly Ala Leu Pro Ala Val
 20 25 30

Ser Ser Pro Pro Ala Pro Val Ser Pro Ser Ser Pro Thr Thr His Asn
 35 40 45

Gly Glu Leu Glu Pro Ser Phe Ser Pro Leu Leu Gly Glu Gly Lys Thr
 50 55 60

Pro Glu Thr Leu Leu Pro Gln Lys Cys Trp Gly Gln Gly Gly Pro Gly
 65 70 75 80

Arg

<210> 1422

<211> 484

<212> PRT

<213> Homo sapiens

<400> 1422

1494

Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser Ala Gln Glu Arg
1 5 10 15
Arg Ala Leu Gly Pro Leu Pro Pro Cys Ser Phe Ala Leu Gln Leu Gly
20 25 30
Met Ala Gly Tyr Leu Arg Val Val Arg Ser Leu Cys Arg Ala Ser Gly
35 40 45
Ser Arg Pro Ala Trp Ala Pro Ala Ala Leu Thr Ala Pro Thr Ser Gln
50 55 60
Glu Gln Pro Arg Arg His Tyr Ala Asp Lys Arg Ile Lys Val Ala Lys
65 70 75 80
Pro Val Val Glu Met Asp Gly Asp Glu Met Thr Arg Ile Ile Trp Gln
85 90 95
Phe Ile Lys Glu Lys Leu Ile Leu Pro His Val Asp Ile Gln Leu Lys
100 105 110
Tyr Phe Asp Leu Gly Leu Pro Asn Arg Asp Gln Thr Asp Asp Gln Val
115 120 125
Thr Ile Asp Ser Ala Leu Ala Thr Gln Lys Tyr Ser Val Ala Val Lys
130 135 140
Cys Ala Thr Ile Thr Pro Asp Glu Ala Arg Val Glu Glu Phe Lys Leu
145 150 155 160
Lys Lys Met Trp Lys Ser Pro Asn Gly Thr Ile Arg Asn Ile Leu Gly
165 170 175
Gly Thr Val Phe Arg Glu Pro Ile Ile Cys Lys Asn Ile Pro Arg Leu
180 185 190
Val Pro Gly Trp Thr Lys Pro Ile Thr Ile Gly Arg His Ala His Gly
195 200 205
Asp Gln Tyr Lys Ala Thr Asp Phe Val Ala Asp Arg Ala Gly Thr Phe
210 215 220
Lys Met Val Phe Thr Pro Lys Asp Gly Ser Gly Val Lys Glu Trp Glu
225 230 235 240
Val Tyr Asn Phe Pro Ala Gly Gly Val Gly Met Gly Met Tyr Asn Thr
245 250 255
Asp Glu Ser Ile Ser Gly Phe Ala His Ser Cys Phe Gln Tyr Ala Ile
260 265 270

1495

Gln Lys Lys Trp Pro Leu Tyr Met Ser Thr Lys Asn Thr Ile Leu Lys
275 280 285

Ala Tyr Asp Gly Arg Phe Lys Asp Ile Phe Gln Glu Ile Phe Asp Lys
290 295 300

His Tyr Lys Thr Asp Phe Asp Lys Asn Lys Ile Trp Tyr Glu His Arg
305 310 315 320

Leu Ile Asp Asp Met Val Ala Gln Val Leu Lys Ser Ser Gly Gly Phe
325 330 335

Val Trp Ala Cys Lys Asn Tyr Asp Gly Asp Val Gln Ser Asp Ile Leu
340 345 350

Ala Gln Gly Phe Gly Ser Leu Gly Leu Met Thr Ser Val Leu Val Cys
355 360 365

Pro Asp Gly Lys Thr Ile Glu Ala Glu Ala Ala His Gly Thr Val Thr
370 375 380

Arg His Tyr Arg Glu His Gln Lys Gly Arg Pro Thr Ser Thr Asn Pro
385 390 395 400

Ile Ala Ser Ile Phe Ala Trp Thr Arg Gly Leu Glu His Arg Gly Lys
405 410 415

Leu Asp Gly Asn Gln Asp Leu Ile Arg Phe Ala Gln Met Leu Glu Lys
420 425 430

Val Cys Val Glu Thr Val Glu Ser Gly Ala Met Thr Lys Asp Leu Ala
435 440 445

Gly Cys Ile His Gly Leu Ser Asn Val Lys Leu Asn Glu His Phe Leu
450 455 460

Asn Thr Thr Asp Phe Leu Asp Thr Ile Lys Ser Asn Leu Asp Arg Ala
465 470 475 480

Leu Gly Arg Gln

<210> 1423

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

1496

<222> (153)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1423

Val	Arg	Ile	Pro	Gly	Ser	Thr	His	Ala	Ser	Gly	Gly	Gly	Asp	Gly	Asp
1				5					10					15	
Met	Glu	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe	Asp
			20					25					30		
Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala	Val	Cys
	35						40					45			
Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	Glu	Gly	Tyr
	50					55					60				
Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	Phe	Asn	Arg	Asn
65					70					75				80	
Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	Val	Leu	Ala	Phe	Leu
			85						90					95	
Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	Tyr	Phe	Pro	Gln	Ile	Ser
			100					105					110		
Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	Ile	Gly	Asp	Leu	Leu	Phe	Ser
		115					120					125			
Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn
	130					135					140				
Gln	Trp	Ala	Val	Thr	Asn	Pro	Lys	Xaa	Val	Leu	Val	Gly	Ala	Asp	Ser
145					150					155				160	
Val	Arg	Ala	Ala	Ile	Thr	Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly
				165					170					175	
Val	Leu	Ala	Ser	Leu	Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp
			180					185						190	
Phe	Ile	Gln	Asn	Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr
		195					200						205		
Ala	Ser	Tyr	Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe
		210					215					220			
Thr	Gln	Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr
225					230					235				240	

1497

<210> 1424

<211> 244

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (62)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (221)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1424

Arg	Val	Arg	Arg	Gln	Ser	Ser	Gly	Asn	Leu	Thr	Met	Ala	Trp	Thr	Pro
1				5					10					15	

Leu	Leu	Leu	Pro	Leu	Leu	Thr	Phe	Cys	Thr	Val	Ser	Glu	Ala	Ser	Tyr
			20					25						30	

Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ser	Pro	Gly	Gln	Thr	Ala
		35					40					45			

Arg	Ile	Thr	Cys	Ser	Gly	Asp	Ala	Leu	Pro	Xaa	Lys	Tyr	Xaa	Tyr	Trp
	50					55					60				

Tyr	Gln	Gln	Lys	Ser	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr	Glu	Asp
65					70					75				80	

Thr	Arg	Arg	Pro	Ser	Ala	Ile	Pro	Glu	Arg	Phe	Ser	Ala	Ser	Ser	Ser
				85					90					95	

Gly	Thr	Met	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Ala	Gln	Val	Glu	Asp	Glu
		100						105					110		

Ala	Asp	Tyr	Tyr	Cys	Tyr	Ser	Thr	Asp	Ser	Ser	Ser	Tyr	Tyr	Arg	Val
		115					120					125			

Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala
	130					135						140			

1498

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
165 170 175

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
180 185 190

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
195 200 205

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Xaa Ser Tyr Ser
210 215 220

Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
225 230 235 240

Thr Glu Cys Ser

<210> 1425

<211> 173

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (115)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (136)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (137)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (159)

1499

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1425

Xaa Val Arg Val Gln Thr Arg Gly Ser Ala Asp Pro Ala Gln Leu Arg
 1 5 10 15

Arg His Pro Gly Tyr Lys Arg Thr Ala Ser Ala Thr Leu Ser Asp Pro
 20 25 30

Ala Ala Ala Ala Met Gln Pro Ser Ser Leu Leu Pro Leu Ala Leu Cys
 35 40 45

Leu Leu Ala Ala Pro Ala Ser Ala Leu Val Arg Ile Pro Leu His Lys
 50 55 60

Phe Thr Ser Ile Arg Arg Thr Met Ser Glu Val Gly Gly Ser Val Glu
 65 70 75 80

Asp Leu Ile Ala Lys Gly Pro Val Ser Lys Tyr Ser Gln Ala Val Pro
 85 90 95

Ala Val Thr Glu Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp
 100 105 110

Ala Gln Xaa Tyr Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Cys Phe
 115 120 125

Thr Val Val Phe Asp Thr Gly Xaa Xaa Asn Leu Trp Val Pro Ser Ile
 130 135 140

His Cys Lys Leu Leu Asp Ile Ala Cys Trp Ile His His Lys Xaa Asn
 145 150 155 160

Ser Asp Lys Ser Ser Asn Tyr Val Lys Asn Gly Asn Ser
 165 170

<210> 1426

<211> 351

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (35)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1426

Ile Arg His Glu Ile Leu Trp Leu Leu Cys Ser His Arg Pro Ala Pro
 1 5 10 15

1500

Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly Gln Ala
 20 25 30
 Pro Ala Xaa Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro Gln Arg
 35 40 45
 Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp Leu Asp
 50 55 60
 Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr Leu Lys
 65 70 75 80
 Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala Val Glu
 85 90 95
 Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu Lys Gly
 100 105 110
 Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys Leu Tyr
 115 120 125
 Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly Ser Lys
 130 135 140
 Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val Glu Lys
 145 150 155 160
 Gly Phe Lys Ala Glu Trp Leu Ala Val Lys Asp Glu Arg Leu Tyr Val
 165 170 175
 Gly Gly Leu Gly Lys Glu Trp Thr Thr Thr Thr Gly Asp Val Val Asn
 180 185 190
 Glu Asn Pro Glu Trp Val Lys Val Val Gly Tyr Lys Gly Ser Val Asp
 195 200 205
 His Glu Asn Trp Val Ser Asn Tyr Asn Ala Leu Arg Ala Ala Ala Gly
 210 215 220
 Ile Gln Pro Pro Gly Tyr Leu Ile His Glu Ser Ala Cys Trp Ser Asp
 225 230 235 240
 Thr Leu Gln Arg Trp Phe Phe Leu Pro Arg Arg Ala Ser Gln Glu Arg
 245 250 255
 Tyr Ser Glu Lys Asp Asp Glu Arg Lys Gly Ala Asn Leu Leu Leu Ser
 260 265 270
 Ala Ser Pro Asp Phe Gly Asp Ile Ala Val Ser His Val Gly Ala Val
 275 280 285

1501

Val Pro Thr His Gly Phe Ser Ser Phe Lys Phe Ile Pro Asn Thr Asp
 290 295 300

Asp Gln Ile Ile Val Ala Leu Lys Ser Glu Glu Asp Ser Gly Arg Val
 305 310 315 320

Ala Ser Tyr Ile Met Ala Phe Thr Leu Asp Gly Arg Phe Leu Leu Pro
 325 330 335

Glu Thr Lys Ile Gly Ser Val Lys Tyr Glu Gly Ile Glu Phe Ile
 340 345 350

<210> 1427

<211> 510

<212> PRT

<213> Homo sapiens

<400> 1427

Glu Arg Ser Trp Phe Ala Gln Val Arg Arg Leu Gly Pro His Gly Ala
 1 5 10 15

Val Ala Arg Leu Arg Val Arg Gly Leu Pro Gly Ala Gly Arg Gly Leu
 20 25 30

Arg Leu Pro Ala Gly Ala Arg Ala Ala Arg Leu Gly Ala Ala Leu Ser
 35 40 45

Leu Glu Leu Ala Val Ser Gly Ala Arg Ala Cys Ala Pro Gly Thr Arg
 50 55 60

Leu Pro Arg Gly Pro Val Gly Gly Ser Trp Asp Ala Leu Ile Val Arg
 65 70 75 80

Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn Ala Cys Val
 85 90 95

Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu Gly Leu Ser
 100 105 110

Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg Asn Asp Leu
 115 120 125

Glu Glu Ala Phe Ile His Phe Met Gly Lys Gly Ala Ala Ala Glu Arg
 130 135 140

Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln Val Ala Ser
 145 150 155 160

1502

Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala Ala Leu Ile
 165 170 175

Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu Leu Cys Gly
 180 185 190

Pro Val Gly Pro Lys Leu His Glu Leu Leu Asp Asp Asn Val Phe Val
 195 200 205

Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu Ile Leu Glu
 210 215 220

Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro His Ala Asn
 225 230 235 240

Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met Asn Met Leu
 245 250 255

Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp Leu Val Val
 260 265 270

Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu Leu Gln Arg
 275 280 285

Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile Pro Thr Gly
 290 295 300

Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg Glu Leu Met
 305 310 315 320

Ser Ser Ile Val His Gln Gln Val Phe Pro Ala Val Thr Ser Leu Gly
 325 330 335

Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser Gly Pro
 340 345 350

His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly Met Val
 355 360 365

Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser Lys Ser
 370 375 380

Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val Tyr His
 385 390 395 400

Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala Ala Val
 405 410 415

Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr Glu Thr
 420 425 430

1503

Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe Met Thr
 435 440 445

Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn Lys Pro
 450 455 460

Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr Pro Val
 465 470 475 480

Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp Ala Ile
 485 490 495

Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr
 500 505 510

<210> 1428
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 1428
 Pro Pro Leu Pro Pro Arg Ser Phe Pro Asn Leu Phe Ser Arg Pro Glu
 1 5 10 15

Pro Leu Pro Glu Pro Gly Arg Arg Gly Cys Asn Arg Ser Arg Glu Pro
 20 25 30

Ala Ala Arg Ala Pro Ser Pro Pro Pro Phe Glu Gly Ala Pro Gly
 35 40 45

Arg Ala Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu
 50 55 60

Ala Lys Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro
 65 70 75 80

Pro Asp Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro
 85 90 95

Val Gly Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala
 100 105 110

Phe Met Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr
 115 120 125

Phe Ala Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile
 130 135 140

Lys Asp Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala

1504

145 150 155 160
 Leu Tyr Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu
 165 170 175
 Val Glu Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro
 180 185 190
 Ala Asn Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp
 195 200 205
 Leu Asn Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val
 210 215 220
 Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly
 225 230 235 240
 Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr
 245 250 255
 Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu
 260 265 270
 Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys
 275 280 285
 Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe
 290 295 300
 Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
 305 310 315

<210> 1429

<211> 398

<212> PRT

<213> Homo sapiens

<400> 1429

His Thr Arg Val Asp Phe Asn Val Pro Met Lys Asn Asn Gln Ile Thr
 1 5 10 15
 Asn Asn Gln Arg Ile Lys Ala Ala Val Pro Ser Ile Lys Phe Cys Leu
 20 25 30
 Asp Asn Gly Ala Lys Ser Val Val Leu Met Ser His Leu Gly Arg Pro
 35 40 45
 Asp Gly Val Pro Met Pro Asp Lys Tyr Ser Leu Glu Pro Val Ala Val
 50 55 60

1505

Glu Leu Lys Ser Leu Leu Gly Lys Asp Val Leu Phe Leu Lys Asp Cys
65 70 75 80

Val Gly Pro Glu Val Glu Lys Ala Cys Ala Asn Pro Ala Ala Gly Ser
85 90 95

Val Ile Leu Leu Glu Asn Leu Arg Phe His Val Glu Glu Glu Gly Lys
100 105 110

Gly Lys Asp Ala Ser Gly Asn Lys Val Lys Ala Glu Pro Ala Lys Ile
115 120 125

Glu Ala Phe Arg Ala Ser Leu Ser Lys Leu Gly Asp Val Tyr Val Asn
130 135 140

Asp Ala Phe Gly Thr Ala His Arg Ala His Ser Ser Met Val Gly Val
145 150 155 160

Asn Leu Pro Gln Lys Ala Gly Gly Phe Leu Met Lys Lys Glu Leu Asn
165 170 175

Tyr Phe Ala Lys Ala Leu Glu Ser Pro Glu Arg Pro Phe Leu Ala Ile
180 185 190

Leu Gly Gly Ala Lys Val Ala Asp Lys Ile Gln Leu Ile Asn Asn Met
195 200 205

Leu Asp Lys Val Asn Glu Met Ile Ile Gly Gly Gly Met Ala Phe Thr
210 215 220

Phe Leu Lys Val Leu Asn Asn Met Glu Ile Gly Thr Ser Leu Phe Asp
225 230 235 240

Glu Glu Gly Ala Lys Ile Val Lys Asp Leu Met Ser Lys Ala Glu Lys
245 250 255

Asn Gly Val Lys Ile Thr Leu Pro Val Asp Phe Val Thr Ala Asp Lys
260 265 270

Phe Asp Glu Asn Ala Lys Thr Gly Gln Ala Thr Val Ala Ser Gly Ile
275 280 285

Pro Ala Gly Trp Met Gly Leu Asp Cys Gly Pro Glu Ser Ser Lys Lys
290 295 300

Tyr Ala Glu Ala Val Thr Arg Ala Lys Gln Ile Val Trp Asn Gly Pro
305 310 315 320

Val Gly Val Phe Glu Trp Glu Ala Phe Ala Arg Gly Thr Lys Ala Leu
325 330 335

1506

Met Asp Glu Val Val Lys Ala Thr Ser Arg Gly Cys Ile Thr Ile Ile
340 345 350

Gly Gly Gly Asp Thr Ala Thr Cys Cys Ala Lys Trp Asn Thr Glu Asp
355 360 365

Lys Val Ser His Val Ser Thr Gly Gly Gly Ala Ser Leu Glu Leu Leu
370 375 380

Glu Gly Lys Val Leu Pro Gly Val Asp Ala Leu Ser Asn Ile
385 390 395

<210> 1430

<211> 249

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (245)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1430

Pro Ala Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe
1 5 10 15

Gly Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu
20 25 30

Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu
35 40 45

Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg
50 55 60

Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val
65 70 75 80

Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu
85 90 95

Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser
100 105 110

Pro Ile Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly
115 120 125

Ile Ile Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu

1507

130 135 140
 Gly Pro Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu
 145 150 155 160
 Thr Ser Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp
 165 170 175
 Gly Val Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu
 180 185 190
 Gly Leu Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu
 195 200 205
 Asn Pro Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val
 210 215 220
 Ser Met Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser
 225 230 235 240
 Ile Gln Arg Ser Xaa Leu Cys Lys Asp
 245

<210> 1431
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 1431
 Arg Pro Thr Arg Pro Val Met Ala Pro Arg Ser Leu Leu Leu Leu
 1 5 10 15
 Ser Gly Ala Leu Ala Leu Thr Asp Thr Trp Ala Gly Ser His Ser Leu
 20 25 30
 Arg Tyr Phe Ser Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro Arg
 35 40 45
 Tyr Ile Ala Val Glu Tyr Val Asp Asp Thr Gln Phe Leu Arg Phe Asp
 50 55 60
 Ser Asp Ala Ala Ile Pro Arg Met Glu Pro Arg Glu Pro Trp Val Glu
 65 70 75 80
 Gln Glu Gly Pro Gln Tyr Trp Glu Trp Thr Thr Gly Tyr Ala Lys Ala
 85 90 95
 Asn Ala Gln Thr Asp Arg Val Ala Leu Arg Asn Leu Leu Arg Arg Tyr
 100 105 110

1508

Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln Gly Met Asn Gly Cys
 115 120 125

Asp Met Gly Pro Asp Gly Arg Leu Leu Arg Gly Tyr His Gln His Ala
 130 135 140

Tyr Asp Gly Lys Asp Tyr Ile Ser Leu Asn Glu Asp Leu Arg Ser Trp
 145 150 155 160

Thr Ala Ala Asp Thr Val Ala Gln Ile Thr Gln Arg Phe Tyr Glu Ala
 165 170 175

Glu Glu Tyr Ala Glu Glu Phe Arg Thr Tyr Leu Glu Gly Glu Cys Leu
 180 185 190

Glu Leu Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg
 195 200 205

Ala Asp Pro Pro Lys Ala His Val Ala His His Pro Ile Ser Asp His
 210 215 220

Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile
 225 230 235 240

Thr Leu Thr Trp Gln Arg Asp Gly Glu Glu Gln Thr Gln Asp Thr Glu
 245 250 255

Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Arg Ser Gly
 260 265 270

<210> 1432

<211> 455

<212> PRT

<213> Homo sapiens

<400> 1432

Ala His Ala Ser Gly Ala Pro Glu Gln Arg Pro Arg Pro Pro Arg Leu
 1 5 10 15

Leu Arg Arg Asp Leu Glu Arg Lys Thr Pro Ala Arg Arg Pro Ala Leu
 20 25 30

Ala Ser Leu Pro Thr Gly His Thr Ala Pro Pro Pro Arg Pro Arg Cys
 35 40 45

Ala Arg Pro Val Arg Cys Thr Pro Ala Cys Trp Arg Leu Arg Arg Arg
 50 55 60

1509

Ala Arg Pro Gly Leu Leu Leu Arg Ala Thr Met Ser Ser Arg Ile Ala
65 70 75 80

Arg Ala Leu Ala Leu Val Val Thr Leu Leu His Leu Thr Arg Leu Ala
85 90 95

Leu Ser Thr Cys Pro Ala Ala Cys His Cys Pro Leu Glu Ala Pro Lys
100 105 110

Cys Ala Pro Gly Val Gly Leu Val Arg Asp Gly Cys Gly Cys Cys Lys
115 120 125

Val Cys Ala Lys Gln Leu Asn Glu Asp Cys Ser Lys Thr Gln Pro Cys
130 135 140

Asp His Thr Lys Gly Leu Glu Cys Asn Phe Gly Ala Ser Ser Thr Ala
145 150 155 160

Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu Gly Arg Pro Cys Glu Tyr
165 170 175

Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser Phe Gln Pro Asn Cys Lys
180 185 190

His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Ile Pro Leu Cys
195 200 205

Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly Cys Pro Asn Pro Arg Leu
210 215 220

Val Lys Val Thr Gly Gln Cys Cys Glu Glu Trp Val Cys Asp Glu Asp
225 230 235 240

Ser Ile Lys Asp Pro Met Glu Asp Gln Asp Gly Leu Leu Gly Lys Glu
245 250 255

Leu Gly Phe Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn Glu Leu
260 265 270

Ile Ala Val Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val Phe Gly
275 280 285

Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu Gln Gly Gln Lys Cys Ile
290 295 300

Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr Gly
305 310 315 320

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys
325 330 335

1510

Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Val Tyr Ser
 340 345 350

Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys Lys Ser Pro Glu
 355 360 365

Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu Ser Val Lys Lys Tyr Arg
 370 375 380

Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Gln
 385 390 395 400

Leu Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu Asp Gly Glu Thr
 405 410 415

Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys Cys Asn Tyr Asn
 420 425 430

Cys Pro His Ala Asn Glu Ala Ala Phe Pro Phe Tyr Arg Leu Phe Asn
 435 440 445

Asp Ile His Lys Phe Arg Asp
 450 455

<210> 1433

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1433

Thr Glu Gly Glu Thr Trp Arg Ser Asp Ser Glu Val Arg Leu Gln Leu
 1 5 10 15

Ala His His Leu Arg Pro Gly Pro Asp Glu Pro Pro Val Ala Ser Ala
 20 25 30

Gly Ala Ala Ala Ala Ser Arg Gly Ala Cys Gly Pro Ser His Ser Arg
 35 40 45

His Cys Leu Pro Ala Gly Leu Glu Pro Ser Glu Arg Pro Asn Pro Arg
 50 55 60

Pro Gly Arg Asp Leu Arg Gly Met Thr Ala Glu Pro Pro Lys Gly Gly
 65 70 75 80

Glu Phe Glu Gly Arg Gly Pro
 85

1511

<210> 1434

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1434

Val Trp Arg Ala Gly Ala Gly Met Ala Ser Leu Arg Ser Gln His Gly
 1 5 10 15

Pro Gly Ala Pro Glu Ser Leu Arg Lys Val Leu Met Pro Ser Ser Met
 20 25 30

Gly Leu Leu Leu Ile Leu Tyr Ala Arg Leu Pro Pro Ser Leu Val Gly
 35 40 45

Gln Ala Gly Arg Trp Ile Gly Trp Ala Gly Arg Ala Gly Gly Gln Ala
 50 55 60

Val Arg Gln Pro Ser Pro Thr Val Leu Ile Asp Gly Val Glu Cys Ser
 65 70 75 80

Asp Val Lys Phe Phe Gln Leu Ala Ala Gln Trp Ser Ser His Val Lys
 85 90 95

His Phe Pro Ile Cys Ile Phe Gly His Ser Lys Ala Thr Phe
 100 105 110

<210> 1435

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1435

Gly Ser Gln Asp Ala Arg Arg Gly Ser Gly Leu Gly Val Ser Ser Phe
 1 5 10 15

Leu Arg Gly Ser Gly Gly Ser Gly Pro Leu Trp Val Gln His Gly Lys
 20 25 30

Arg Gly Arg Tyr Phe Ser Ser Trp Ala Phe Ile Lys Glu Lys Thr Met
 35 40 45

Leu Ala Gly Arg Gly Gly Ser Arg Leu Gln Ser Gln His Phe Gly Arg
 50 55 60

Pro Arg Arg Val Asp His Leu Arg Ser Gly Val Gln Asp Gln Pro Gly
 65 70 75 80

1512

Gln His Gly Glu Thr Pro Ser Leu Leu Lys Asn Thr Lys Ile Ser Gln
 85 90 95

Val Trp Trp Leu Thr Leu Met
 100

<210> 1436

<211> 413

<212> PRT

<213> Homo sapiens

<400> 1436

Asn Glu Cys Thr Gly Pro Glu Phe Arg Val Asp Pro Arg Val Ala Ser
 1 5 10 15

Ala Pro Arg Ala Gln Ser Leu Ala Phe Ala Asp Pro Pro Pro Val His
 20 25 30

Thr Arg Arg Gln Leu Thr Met Asp Asp Asp Ile Ala Ala Leu Val Val
 35 40 45

Asp Asn Gly Ser Gly Met Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala
 50 55 60

Pro Arg Ala Val Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly
 65 70 75 80

Val Met Val Gly Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala
 85 90 95

Gln Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly
 100 105 110

Ile Val Thr Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe
 115 120 125

Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Val Leu Leu Thr
 130 135 140

Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile
 145 150 155 160

Met Phe Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile Gln Ala
 165 170 175

Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Met Asp
 180 185 190

Ser Gly Asp Gly Val Thr His Thr Val Pro Ile Tyr Glu Gly Tyr Ala

1513

195	200	205
Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr		
210	215	220
Asp Tyr Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr		
225	230	235 240
Thr Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr		
	245	250 255
Val Ala Leu Asp Phe Glu Gln Glu Met Ala Thr Ala Ala Ser Ser Ser		
	260	265 270
Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile		
	275	280 285
Gly Asn Glu Arg Phe Arg Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe		
	290	295 300
Leu Gly Met Glu Ser Cys Gly Ile His Glu Thr Thr Phe Asn Ser Ile		
305	310	315 320
Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val		
	325	330 335
Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln		
	340	345 350
Lys Glu Ile Thr Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile		
	355	360 365
Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu		
	370	375 380
Ala Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr		
385	390	395 400
Asp Glu Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe		
	405	410

<210> 1437

<211> 97

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (28)

1514

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1437

Val Val Pro Ser Thr Lys Asp Phe Leu Val Gly Val Lys Gly Ser Gly
 1 5 10 15

Gly His Arg Gly Gly Gly Glu Met Ala Phe Ser Xaa Ser Gln Ala Pro
 20 25 30

Tyr Leu Ser Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu
 35 40 45

Gln Asp Gly Leu Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser
 50 55 60

Gly Thr Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro Arg Phe Glu
 65 70 75 80

Asp Gly Gly Tyr Val Val Cys Thr Ala Gly Arg Thr Glu Ala Gly Gly
 85 90 95

Pro

<210> 1438

<211> 153

<212> PRT

<213> Homo sapiens

<400> 1438

Leu Ala Pro Leu Arg Cys Gln Pro Gly Thr Arg Thr Gln Pro Arg Ser
 1 5 10 15

His Pro Ala Ala Asn Asp Pro Ser Ala Ala Met Ser Ala Ala Gly Ala
 20 25 30

Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
 35 40 45

Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
 50 55 60

Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
 65 70 75 80

Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
 85 90 95

Gln Ser Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser

1515

100	105	110
Leu Val Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe		
115	120	125
Val Gly Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn		
130	135	140
Gln Glu Leu Lys Ala Lys Ala His Lys		
145	150	

<210> 1439
 <211> 343
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (244)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (305)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (325)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (328)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (340)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1439
 Trp Ile Gln Arg Ile Arg Ala Arg Gly Lys Thr Asn Leu Arg Arg Thr
 1 5 10 15

Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met Gly Phe
 20 25 30

Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp Arg Gln

1516

35	40	45
Thr Leu Met Trp Ser Ala	Thr Trp Pro Lys Glu Val Arg Gln Leu Ala	
50	55	60
Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala Leu Glu		
65	70	75 80
Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys His Asp		
	85	90 95
Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile Met Ser		
100	105	110
Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg Arg Cys		
115	120	125
Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala Met Gly		
130	135	140
Ile His Gly Asp Lys Ser Gln Gln Glu Arg Asp Trp Val Leu Asn Glu		
145	150	155 160
Phe Lys His Gly Lys Ala Pro Ile Leu Ile Ala Thr Asp Val Ala Ser		
	165	170 175
Arg Gly Leu Asp Val Glu Asp Val Lys Phe Val Ile Asn Tyr Asp Tyr		
180	185	190
Pro Asn Ser Ser Glu Asp Tyr Ile His Arg Ile Gly Arg Thr Ala Arg		
195	200	205
Ser Thr Lys Thr Gly Thr Ala Tyr Thr Phe Phe Thr Pro Asn Asn Ile		
210	215	220
Lys Gln Val Ser Asp Leu Ile Ser Val Leu Arg Glu Ala Asn Gln Ala		
225	230	235 240
Ile Asn Pro Xaa Leu Leu Gln Leu Val Glu Asp Arg Gly Ser Gly Arg		
	245	250 255
Ser Arg Gly Arg Gly Gly Met Lys Asp Asp Arg Arg Asp Arg Tyr Ser		
260	265	270
Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Arg Glu Asn Tyr		
275	280	285
Asp Arg Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala Lys Thr		
290	295	300
Xaa Asn Gly Gly Tyr Ser Ala Cys Lys Phe Thr Asn Gly Ser Phe Gly		

1517

305 310 315 320
Ser Asn Phe Gly Xaa Cys Trp Xaa Ser Gly Pro Val Leu Gly Leu Gly
 325 330 335

Ile Pro Thr Xaa Ala Leu Pro
 340

<210> 1440

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1440

Ile Cys Val Ser Ala Arg Arg Ala Leu Ser Gly Leu Glu His Gly Leu
1 5 10 15

Gly Trp Glu Arg Val Trp Glu Lys Met Gly Asn Lys Glu Pro Gly Ser
 20 25 30

His Gly His Arg Ser Asp Ala Asp Pro Ser Arg Phe Ser Pro Val Leu
 35 40 45

Pro Pro Ala Val Gln Leu Gly Val Trp Arg Glu Glu Gly Arg Gly Gly
 50 55 60

Ser Cys Pro Phe Ser Trp Gly Arg Gly Pro Val Ser Ser Thr Trp Leu
65 70 75 80

Phe Pro Lys Gly Ser Lys Arg Glu Gly Leu Gly Glu Lys Thr Met Glu
 85 90 95

Arg Gly Pro Ala Lys Glu Asn Arg Glu Glu Val Ser Gly Leu Ile Ser
 100 105 110

Leu Leu Ser Arg Cys Ser Gly Ser Leu Ile
 115 120

<210> 1441

<211> 74

<212> PRT

<213> Homo sapiens

<400> 1441

Gly His Arg His Thr Pro Pro His Leu Ala Asn Phe Tyr Tyr Phe Phe
1 5 10 15

1518

Cys Arg Asp Glu Val Ser Leu Cys Pro Gly Trp Ser Gln Thr Pro Val
 20 25 30
 Leu Lys Gln Ser Ser His Leu Gly Ser Leu Ser Ala Gly Ile Ile Gly
 35 40 45
 Met Ser His Arg Ala Arg Pro His Val Cys Met Leu Lys Val Leu Arg
 50 55 60
 Ile Pro Met Glu Asn Lys Phe Asp Phe Ala
 65 70

<210> 1442
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (2)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (3)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1442
 Ala Xaa Xaa His Gln Pro Ser Leu Lys Gly Thr Lys Ala Gly Ala Pro
 1 5 10 15
 Pro Arg Cys Gly Arg Ser Arg Thr Ser Gly Ser Pro Gly Leu Gln Glu
 20 25 30
 Phe Gly Thr Arg Glu Ala Glu Ala Gly Val Gln Trp Cys Asp Leu Gly
 35 40 45
 Ser Leu Gln Pro Leu Pro Pro Arg Phe Gln Gln Phe Ser Cys Leu Ser
 50 55 60
 Leu Pro Ser Gly Trp Asp Asp Arg Arg Leu Pro Ser Cys Leu Thr Ser
 65 70 75 80
 Phe Cys Ile Phe Ser Arg Asp Gly Val Ser Pro Cys Trp Pro Gly Trp
 85 90 95
 Ser Gln Thr Pro Asp Leu Arg
 100

1519

<210> 1443
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (48)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (57)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (58)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (63)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (66)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (70)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (83)
<223> Xaa equals any of the naturally occurring L-amino acids

1520

<220>

<221> SITE

<222> (99)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (100)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (102)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1443

Leu His Ala Ala Ala Cys Ala Ala Ala Met Ser Leu Val Ile Pro Glu
1 5 10 15

Lys Phe Gln His Ile Leu Arg Val Leu Asn Thr Asn Ile Asp Gly Arg
20 25 30

Arg Lys Ile Ala Phe Ala Ile Thr Ala Ile Lys Gly Val Gly Arg Xaa
35 40 45

Tyr Ala His Val Xaa Leu Arg Lys Xaa Xaa Ile Asp Leu Thr Xaa Arg
50 55 60

Ala Xaa Glu Leu Thr Xaa Asp Xaa Val Glu Arg Val Ile Thr Ile Met
65 70 75 80

Gln Asn Xaa Arg Gln Tyr Lys Ile Pro Asp Trp Phe Leu Asn Arg Gln
85 90 95

Asn Asp Xaa Xaa Asp Xaa Ser Thr Ser Ser
100 105

<210> 1444

<211> 14

<212> PRT

<213> Homo sapiens

<400> 1444

Pro Val Trp Pro Lys Trp Ser Gly Trp Pro Leu Ala Leu Pro
1 5 10

1521

<210> 1445
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (104)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (119)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (123)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (124)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1445
 Phe Leu Arg Leu Val Leu Gly Leu Leu Ile Gly Arg Cys Leu Gln Glu
 1 5 10 15

Met Leu Lys Leu Gly Thr Leu Pro Pro Thr Ser Lys Pro Gln Leu Leu
 20 25 30

Cys Gln Met Val Ser Leu Lys Ile Ser Ala Cys Leu Thr Thr Lys Gly
 35 40 45

Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys
 50 55 60

Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu Glu Phe Lys Lys
 65 70 75 80

Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser His Phe Cys His
 85 90 95

Leu Ala Trp Val Asn Thr Pro Xaa Lys Gln Gly Gly Leu Gly Pro Met
 100 105 110

Asn Ile Pro Leu Val Ser Xaa Pro Thr His Xaa Xaa Ser Gly
 115 120 125

1522

<210> 1446
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (92)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1446
 Cys Asp Lys Glu Lys Asn Leu Leu His Val Thr Asp Thr Gly Val Gly
 1 5 10 15

Met Thr Arg Glu Glu Leu Val Lys Asn Leu Gly Thr Ile Ala Lys Ser
 20 25 30

Gly Thr Ser Glu Phe Leu Asn Lys Met Thr Glu Ala Gln Glu Asp Gly
 35 40 45

Gln Ser Thr Ser Asp Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser
 50 55 60

Ala Phe Leu Val Ala Asp Lys Val Ile Val Thr Ser Lys His Asn Asn
 65 70 75 80

Asp Thr Gln His Ile Trp Glu Ser Asp Ser Asn Xaa Phe Ser Val Asn
 85 90 95

Cys

<210> 1447
 <211> 47
 <212> PRT
 <213> Homo sapiens

<400> 1447
 His Ser Arg His Arg Gly Val Phe Leu Thr Pro Leu Leu Ala Met Ser
 1 5 10 15

Ser His Lys Thr Phe Arg Ile Lys Arg Phe Leu Ala Lys Lys Gln Lys
 20 25 30

Gln Asn Arg Pro Ile Pro Gln Trp Ile Arg Met Lys Thr Gly Lys
 35 40 45

1523

<210> 1448
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (85)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1448
Val Phe Arg Val Glu Ala Trp Arg Thr Ser Gly Glu Thr Pro Ala Ile
1 5 10 15
Ser Pro Ser Lys Arg Ala Arg Pro Ala Glu Val Gly Gly Met Gln Leu
20 25 30
Arg Phe Ala Arg Leu Ser Glu His Ala Thr Ala Pro Thr Arg Gly Ser
35 40 45
Ala Arg Ala Ala Gly Tyr Asp Leu Tyr Ser Ala Tyr Asp Tyr Thr Ile
50 55 60
Pro Pro Met Glu Lys Ala Val Val Lys Thr Asp Ile Gln Ile Ala Leu
65 70 75 80
Pro Ser Gly Cys Xaa Gly Arg Val Ala Pro Arg Ser Gly Leu Ala Ala
85 90 95
Lys His Phe Ile Asp Val Gly Xaa Val Ser
100 105

<210> 1449
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (41)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1524

<221> SITE

<222> (44)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1449

Thr Met Ala Val Gly Lys Asn Lys Arg Leu Thr Lys Gly Gly Lys Lys
 1 5 10 15

Gly Ala Lys Lys Lys Val Val Asp Pro Phe Phe Lys Lys Asp Trp Tyr
 20 25 30

Asp Val Lys Ala Pro Ala Met Phe Xaa Ile Arg Xaa Ile Gly Lys Thr
 35 40 45

Leu Val Thr Arg Thr Gln Gly Thr Lys Ile Ala Ser
 50 55 60

<210> 1450

<211> 45

<212> PRT

<213> Homo sapiens

<400> 1450

Asn Phe Gly Ser Leu Leu Gly Ala Cys Leu Ile Leu Gln Ile Thr Thr
 1 5 10 15

Gly Leu Phe Leu Ala Met His Tyr Ser Pro Asp Ala Ser Thr Ala Phe
 20 25 30

Ser Ser Ile Ala His Ile Thr Arg Asp Val Asn Tyr Gly
 35 40 45

<210> 1451

<211> 34

<212> PRT

<213> Homo sapiens

<400> 1451

Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu
 1 5 10 15

Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys Leu Glu
 20 25 30

Arg Ile

1525

<210> 1452
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1452
Pro Arg Val Arg Leu Xaa Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro
1 5 10 15
Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg
20 25 30
Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala
35 40 45
Arg Arg Ile Thr Glu Val Leu Gly Asn Pro Phe Pro His
50 55 60

<210> 1453
<211> 44
<212> PRT
<213> Homo sapiens

<400> 1453
Arg Glu Gln Lys Leu Glu Leu His Arg Gly Ala Ala Ala Leu Glu Leu
1 5 10 15
Val Asp Pro Pro Gly Cys Arg Asn Ser Ala Arg Gly Cys Ser Glu Pro
20 25 30
Arg Ser His His Cys Thr Pro Val Trp Ala Thr Glu
35 40

<210> 1454
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

1526

<222> (76)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (84)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (98)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (99)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (106)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (111)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1454

Thr	Arg	Val	Ala	Pro	Ser	Val	Leu	Arg	Leu	Ala	Met	Thr	Ser	Tyr	Ser
1				5					10					15	

Tyr	Arg	Gln	Ser	Ser	Ala	Thr	Ser	Ser	Phe	Gly	Gly	Leu	Gly	Gly	Gly
		20						25					30		

Ser	Val	Arg	Ile	Gly	Pro	Gly	Val	Ala	Phe	Arg	Ala	Pro	Ser	Ile	His
		35					40						45		

Gly	Gly	Ser	Gly	Gly	Arg	Gly	Val	Ser	Val	Ser	Ser	Ala	Arg	Phe	Val
		50				55						60			

Ser	Ser	Ser	Ser	Ser	Gly	Gly	Tyr	Gly	Gly	Gly	Xaa	Gly	Gly	Val	Leu
65					70					75				80	

Thr	Ala	Ser	Xaa	Gly	Leu	Leu	Ala	Gly	Asn	Glu	Lys	Leu	Thr	Met	Gln
				85					90					95	

Asn	Xaa	Xaa	Thr	Ala	Trp	Leu	Leu	Leu	Xaa	Lys	Phe	Ala	Pro	Xaa	Gly
			100					105						110	

Ala Lys Gly Thr Lys Ser

1527

115

<210> 1455
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (34)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (43)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1455
Ala Xaa Glu Asn Ser Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu
1 5 10 15
Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu Thr Glu Gln Ala Leu Arg
20 25 30
Met Xaa Val Glu Ala Asp Ile Asn Gly Leu Xaa Arg Cys Trp Met Ser
35 40 45

<210> 1456
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (131)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

1528

<222> (137)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1456

Gly	Asp	Tyr	Ser	His	Tyr	Tyr	Thr	Thr	Ile	Gln	Asp	Leu	Arg	Asp	Lys
1				5					10					15	

Ile	Leu	Gly	Ala	Thr	Ile	Glu	Asn	Ser	Arg	Ile	Val	Leu	Gln	Ile	Asp
			20					25					30		

Asn	Ala	Arg	Leu	Ala	Ala	Asp	Asp	Phe	Arg	Thr	Lys	Phe	Glu	Thr	Glu
		35					40					45			

Gln	Ala	Leu	Arg	Met	Ser	Val	Glu	Ala	Asp	Ile	Asn	Gly	Leu	Arg	Arg
	50					55					60				

Val	Leu	Asp	Glu	Leu	Thr	Leu	Ala	Arg	Thr	Asp	Leu	Glu	Met	Gln	Ile
65					70					75					80

Glu	Gly	Leu	Lys	Glu	Glu	Leu	Ala	Tyr	Leu	Lys	Lys	Asn	His	Glu	Glu
			85						90					95	

Glu	Ile	Ser	Thr	Leu	Arg	Gly	Gln	Val	Gly	Gly	Gln	Val	Ser	Val	Glu
			100				105						110		

Val	Asp	Ser	Ala	Pro	Gly	Thr	Asp	Leu	Ala	Lys	Ile	Leu	Ser	Asp	Met
		115					120					125			

Arg	Ser	Xaa	Tyr	Glu	Val	Met	Ala	Xaa	Gln	Asn	Arg	Lys	Asp	Ala	
	130					135						140			

<210> 1457

<211> 116

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (21)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1457

Gly	Cys	Val	Gly	Val	Arg	Pro	Ser	Leu	His	Pro	Ala	Thr	Ser	Thr	Ala
1				5					10					15	

Ser	Gly	Ser	Ala	Xaa	Pro	Thr	Leu	Ala	Arg	Ala	Met	Ala	Ser	Val	Ser
			20					25						30	

Glu	Leu	Ala	Cys	Ile	Tyr	Ser	Ala	Leu	Ile	Leu	His	Asp	Asp	Glu	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1529

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          35          40          45
Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile Lys Ala Ala Gly Val
   50          55          60
Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala Lys Ala Leu Ala Asn
   65          70          75          80
Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly Ala Gly Gly Pro Ala
          85          90          95
Pro Ala Ala Gly Ala Ala Thr Ser Arg Arg Ser Cys Pro Leu His Cys
          100          105          110
Cys Cys Ser Ser
          115

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<210> 1458

<211> 115

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (47)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1458

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Leu Val Pro Asn Ser Ala Arg Ala Ala Ala Ser Ala Ala Asp Ala Ala
   1          5          10          15
Ala Met Arg Tyr Val Ala Ser Tyr Leu Leu Ala Ala Leu Gly Gly Asn
          20          25          30
Ser Ser Pro Ser Ala Lys Gly Ile Lys Lys Ile Leu Asp Asn Xaa Gly
          35          40          45
Ile Glu Ala Asp Asp Asp Arg Leu Asn Lys Val Ile Ser Glu Leu Asn
          50          55          60
Gly Lys Asn Ile Glu Asp Val Ile Ala Gln Gly Ile Gly Lys Leu Ala
          65          70          75          80
Ser Val Pro Ala Gly Gly Ala Val Ala Val Ser Ala Ala Pro Gly Ser
          85          90          95
Ala Ala Pro Ala Ala Gly Ser Ala Pro Ala Ala Ala Glu Glu Lys Lys
          100          105          110

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1530

Asp Glu Lys
115

<210> 1459
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (115)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (126)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (129)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1459
Ala Ser Asp Ala Leu His Ser Leu Ser Ala Pro Val Leu Arg Leu Ser
1 5 10 15

Ser Arg Ser Ala Ala Arg Pro Ala Thr Met Thr Glu Gln Ala Ile Ser
20 25 30

Phe Ala Lys Asp Phe Leu Ala Gly Gly Ile Ala Ala Ala Ile Ser Lys
35 40 45

Thr Ala Val Ala Pro Ile Glu Arg Val Lys Leu Leu Leu Gln Val Gln
50 55 60

His Ala Ser Lys Gln Ile Ala Ala Asp Lys Gln Tyr Lys Gly Ile Val
65 70 75 80

Asp Cys Ile Val Arg Ile Pro Lys Glu Gln Gly Val Leu Ser Phe Trp
85 90 95

Arg Gly Asn Leu Ala Asn Val Ile Arg Tyr Phe Pro Thr Gln Ala Leu
100 105 110

1531

Asn Phe Xaa Phe Lys Asp Lys Tyr Lys Gln Xaa Phe Leu Xaa Gly Val
115 120 125

Xaa Lys His Thr
130

<210> 1460

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (80)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (85)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (107)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (112)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1532

<222> (117)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (119)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (120)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (121)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1460

Xaa	Ser	Xaa	Lys	Thr	Gly	Phe	Xaa	Asp	Trp	Ile	Ser	Val	Ala	Tyr	Tyr
1				5					10					15	

Gly	Cys	Phe	Arg	Glu	Gly	Ala	Thr	Ile	Ile	Gln	Val	Gly	Lys	Leu	Ile
			20					25					30		

Lys	Glu	Ala	Ala	Gly	Lys	Ser	Asn	Leu	Lys	Arg	Val	Thr	Leu	Glu	Leu
	35						40					45			

Gly	Gly	Lys	Ser	Pro	Cys	Ile	Val	Leu	Ala	Asp	Ala	Asp	Leu	Asp	Asn
	50					55						60			

Ala	Val	Glu	Phe	Ala	His	His	Gly	Val	Phe	Tyr	His	Gln	Gly	Gln	Xaa
65					70					75					80

Cys	Ile	Ala	Ala	Xaa	Arg	Ile	Phe	Val	Glu	Glu	Ser	Ile	Tyr	Asp	Glu
				85					90					95	

Phe	Val	Arg	Arg	Ser	Val	Glu	Arg	Val	Lys	Xaa	Ile	Ser	Leu	Gly	Xaa
		100						105					110		

Pro	Leu	Thr	Pro	Xaa	Val	Xaa	Xaa	Xaa	Pro	Ser	Asp
	115						120				

<210> 1461

<211> 179

<212> PRT

<213> Homo sapiens

<220>

1533

<221> SITE
 <222> (102)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (125)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (142)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (145)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (157)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (163)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (173)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (174)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (176)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1461

Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu Val Val Pro Leu Ala
 1 5 10 15

Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu Asp Gly Leu Ser Glu
 20 25 30

1534

Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp Phe Ala Lys Trp Arg
 35 40 45
 Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser Ala Leu Ala Ile Met
 50 55 60
 Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser Ile Cys Gln Gln Asn
 65 70 75 80
 Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu Pro Asp Gly Asp His
 85 90 95
 Asp Leu Lys Arg Leu Xaa Val Cys Asp Arg Lys Gly Ala Trp Leu Ala
 100 105 110
 Ala Thr Arg Leu Leu Ser Asp His His Ile Tyr Leu Xaa Gly Thr Leu
 115 120 125
 Leu Lys Pro Asn Met Val Pro Gln Ala Met Leu Ala Leu Xaa Ser Phe
 130 135 140
 Xaa Met Lys Glu Ile Ala His Gly Glu Pro Val Ser Xaa Ala Val Pro
 145 150 155 160
 Ala Gln Xaa Pro Pro Arg Leu Ser Leu Gly Ile Asn Xaa Xaa Cys Xaa
 165 170 175
 Gly Arg Pro

<210> 1462

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (13)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1462

Ala Asn Ser Leu Ala Cys Gln Gly Lys Tyr Thr Pro Xaa Gly Gln Ala
 1 5 10 15
 Gly Ala Ala Ala Ser Glu Ser Leu Phe Val Ser Asn His Ala Tyr
 20 25 30

1535

<210> 1463
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (65)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (69)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1463
Asp Asp Cys Glu Phe Lys Ala Glu Gly Asn Ser Lys Phe Thr Tyr Thr
1 5 10 15

Val Leu Glu Asp Gly Cys Thr Lys His Thr Gly Glu Trp Ser Lys Thr
20 25 30

Val Phe Glu Tyr Arg Thr Arg Lys Ala Val Arg Leu Pro Ile Val Asp
35 40 45

Ile Ala Pro Tyr Asp Ile Gly Gly Pro Asp Gln Glu Phe Gly Val Asp
50 55 60

Xaa Gly Pro Val Xaa Phe Leu
65 70

<210> 1464
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (10)

1536

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1464

Xaa Gly Thr Arg His Xaa Leu Arg Thr Xaa Asn Gln Ser Ser Asp Glu
1 5 10 15

Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys Glu Gln Leu Ser
20 25 30

Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu Tyr Gly Ser Glu
35 40 45

Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala Lys Lys Leu Ile
50 55 60

Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Thr Ile Thr
65 70 75

<210> 1465

<211> 105

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (83)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (98)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (103)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (104)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1465

Leu Lys Gly Arg Pro Gly Phe Pro Gly Ser Lys Gly Glu Ala Gly Phe
1 5 10 15

Phe Gly Ile Pro Gly Leu Lys Gly Leu Ala Gly Glu Pro Gly Phe Lys
20 25 30

1537

Gly Ser Arg Gly Asp Pro Gly Pro Pro Gly Pro Pro Pro Val Ile Leu
35 40 45

Pro Gly Met Lys Asp Ile Lys Gly Glu Lys Gly Asp Glu Gly Pro Met
50 55 60

Gly Leu Lys Gly Tyr Leu Gly Ala Lys Gly Ile Gln Gly Met Pro Gly
65 70 75 80

Ile Pro Xaa Leu Ser Gly Ile Pro Gly Leu Pro Gly Arg Pro Gly His
85 90 95

Ile Xaa Gly Ile Lys Gly Xaa Xaa Gly
100 105

<210> 1466

<211> 36

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1466

Arg Pro Gly Leu Cys Ala Lys Thr Val Phe Lys Ala Leu Gln Ala Pro
1 5 10 15

Ala Leu Xaa Glu Glu His Gly Glu Gly Trp Arg Leu His Pro Trp Gly
20 25 30

Val Trp Glu Thr
35

<210> 1467

<211> 82

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (76)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1538

<221> SITE
<222> (79)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (80)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (82)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1467
Arg Val Pro Ala Met Ala Ala Lys Gly Gly Thr Val Lys Ala Ala Ser
1 5 10 15
Ala Phe Asn Ala Thr Glu Asp Ala Gln Thr Leu Arg Lys Ala Met Lys
20 25 30
Gly Leu Gly Thr Asp Glu Asp Ala Ile Ile Ser Val Leu Ala Tyr Arg
35 40 45
Asn Thr Ala Gln Arg Gln Glu Ile Arg Thr Ala Leu Gln Glu His His
50 55 60
Ser Ala Gly Asp Leu Val Leu Arg Asn Gly Pro Xaa Phe Val Xaa Xaa
65 70 75 80
Trp Xaa

<210> 1468
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (24)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1539

<221> SITE
 <222> (35)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (61)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
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 <222> (66)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (79)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (82)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (83)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <400> 1468
 Gly Trp His Leu Gly Pro Pro Gly Ser Trp Cys Trp Trp Ser Xaa Cys
 1 5 10 15
 Ile Thr Gly Pro Asn Thr Ser Xaa Cys Cys Trp Thr His Phe Glu Lys
 20 25 30
 Pro Arg Xaa Ile Asp Asn Val Leu Val Ile Phe Ser His Asp Phe Trp
 35 40 45
 Ser Thr Glu Ile Asn Gln Leu Ile Ala Gly Val Asn Xaa Cys Pro Val
 50 55 60
 Leu Xaa Val Phe Phe Pro Phe Ser Ile Gln Leu Phe Pro Asn Xaa Phe
 65 70 75 80
 Pro Xaa Xaa

<210> 1469

1540

<211> 26
<212> PRT
<213> Homo sapiens

<400> 1469
Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln
1 5 10 15

Pro Lys Ile Val Lys Trp Asp Arg Asp Met
20 25

<210> 1470
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (139)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (141)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (143)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (146)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
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1541

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (152)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (153)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (158)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1470

Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Gly	Gly	Arg	Ser
1			5					10					15	

Xaa	Gly	Ser	Lys	Leu	Thr	Tyr	Ala	Cys	Met	Arg	Arg	His	Ser	Ser	Ser
			20					25					30		

Ile	Val	Ser	Pro	Lys	Phe	Asn	Ser	Leu	Ala	Val	Val	Leu	Gln	Arg	Arg
		35					40						45		

Asp	Trp	Glu	Asn	Pro	Gly	Val	Thr	Gln	Leu	Asn	Arg	Leu	Ala	Ala	His
		50					55				60				

Pro	Pro	Phe	Ala	Ser	Trp	Arg	Asn	Ser	Glu	Glu	Ala	Arg	Thr	Asp	Arg
	65				70					75				80	

Pro	Ser	Gln	Gln	Leu	Arg	Ser	Leu	Asn	Gly	Lys	Trp	Asp	Ala	Pro	Cys
				85					90					95	

Ser	Gly	Ala	Leu	Ser	Ala	Ala	Gly	Val	Val	Val	Thr	Arg	Ser	Val	Thr
		100						105					110		

Ala	Thr	Leu	Ala	Ser	Ala	Leu	Arg	Pro	Val	Leu	Ser	Phe	Leu	Pro	Phe
		115					120					125			

Leu	Ser	Arg	His	Val	Arg	Arg	Xaa	Ser	Pro	Xaa	Ser	Xaa	Lys	Xaa	Gly
		130					135				140				

Ala	Xaa	Phe	Xaa	Val	Pro	Ile	Xaa	Xaa	Leu	Arg	Asp	Leu	Xaa	Pro	Lys
	145				150					155				160	

Asn	Leu	Ile	Arg	Val	Met	Val	Thr
					165		

1542

<210> 1471
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (22)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (88)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (111)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (116)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (119)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1471
 Cys His Leu Asn Ser Ile His Trp Pro Ser Phe Tyr Asn Val Val Thr
 1 5 10 15

Gly Lys Thr Leu Ala Xaa Pro Asn Leu Ile Ala Leu Gln His Ile Pro
 20 25 30

Leu Ser Pro Ala Gly Ser Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro
 35 40 45

Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Asp Ala Pro Cys Ser
 50 55 60

Gly Ala Leu Ser Ala Ala Gly Val Val Val Thr Arg Ser Val Thr Ala
 65 70 75 80

Thr Leu Ala Ser Ala Leu Ala Xaa Ala Pro Phe Ala Phe Phe Pro Ser
 85 90 95

1543

Phe Leu Ala Thr Phe Ala Gly Phe Pro Arg Gln Ala Leu Asn Xaa Gly
100 105 110

Leu Pro Leu Xaa Phe Arg Xaa Ser Ala Val Arg His Leu Asp Pro Lys
115 120 125

Lys Leu Asp
130

<210> 1472
<211> 179
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 <400> 1472
 Lys Lys Lys Lys Xaa Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 1 5 10 15

 Lys Lys Lys Lys Gly Gly Arg Xaa Xaa Gly Ser Lys Leu Thr Tyr Ala
 20 25 30

 Cys Met Xaa Arg His Ser Ser Xaa Ile Gly Ser Pro Lys Phe Asn Ser
 35 40 45

 Leu Ala Xaa Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr
 50 55 60

 Gln Leu Asn Arg Leu Ala Xaa His Pro Xaa Phe Ala Ser Trp Arg Asn
 65 70 75 80

 Ser Xaa Lys Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu
 85 90 95

 Asn Gly Lys Trp Asp Xaa Pro Cys Xaa Gly Ala Leu Xaa Xaa Ala Gly
 100 105 110

1546

Val Xaa Val Thr Xaa Xaa Xaa Thr Ala Thr Leu Ala Xaa Ala Leu Ala
115 120 125

Pro Ala Pro Phe Ala Phe Phe Pro Ser Phe Xaa Ala Thr Phe Ala Gly
130 135 140

Phe Pro Arg Gln Ala Xaa Asn Arg Gly Leu Pro Leu Gly Phe Arg Leu
145 150 155 160

Xaa Ala Leu Arg Asp Leu Xaa Pro Gln Lys Asn Leu Ile Arg Gly Asp
165 170 175

Gly Ser Xaa

<210> 1473
<211> 58
<212> PRT
<213> Homo sapiens

<400> 1473
Ile Ala Ser Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala
50 55

<210> 1474
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1474
Ile Ala Ser Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

1547

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
50 55 60

Glu Ala Arg Thr Asp Arg
65 70

<210> 1475

<211> 62

<212> PRT

<213> Homo sapiens

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<400> 1475

Leu Pro Xaa Ala Xaa Tyr Thr Xaa Xaa Gly Thr Thr Pro His Tyr Arg

1548

1 5 10 15
Glu Ser Trp Tyr Ala Cys Arg Tyr Arg Ser Gly Ile Pro Gly Ser Thr
 20 25 30
His Ala Ser Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Xaa
 35 40 45
Asp Asp Leu Glu Asp Pro Lys Leu Thr Tyr Xaa Xaa Met Gln
 50 55 60

<210> 1476
<211> 80
<212> PRT
<213> Homo sapiens

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1549

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1476

Ile Arg Xaa Xaa Xaa Leu Arg Xaa Asp Thr Thr His Tyr Arg Glu Ser
1 5 10 15

Trp Tyr Ala Cys Arg Tyr Arg Ser Gly Ile Pro Gly Xaa Thr His Ala
20 25 30

Ser Val Glu Ile Cys Pro Pro Xaa Ser Arg Pro Xaa Ser Ser Gln Ser
35 40 45

Asn Gly Glu Gly Tyr Ser Xaa Cys Arg Arg Pro Gln Ala Leu Glu Ala
50 55 60

Ala Thr Tyr Leu Asn Pro Val Pro Xaa Arg Ile Leu Leu Lys Pro Phe
65 70 75 80

<210> 1477

<211> 52

<212> PRT

<213> Homo sapiens

<400> 1477

Arg Gln Val Pro His Glu Arg Ala Val Arg Asp Gly Arg Gly Gly Gly
1 5 10 15

Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met Arg Arg His Ser
20 25 30

Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala Val Val Leu Gln
35 40 45

Arg Arg Asp Trp
50

1550

<210> 1478

<211> 154

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (140)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1478

Ile Ala Ser Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
50 55 60

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
65 70 75 80

Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
85 90 95

Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ser Ala Leu Ala Pro Ala
100 105 110

Pro Phe Ala Phe Phe Pro Ser Phe Leu Ala Thr Phe Ala Gly Phe Pro
115 120 125

Arg Gln Ala Leu Asn Arg Gly Leu Pro Leu Gly Xaa Arg Phe Lys Cys
130 135 140

Phe Thr Asp Leu Asp Pro Lys Lys Leu Asp
145 150

<210> 1479

<211> 130

<212> PRT

<213> Homo sapiens

<220>

1551

<221> SITE

<222> (122)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1479

Ile Ala Gly Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
50 55 60

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
65 70 75 80

Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
85 90 95

Val Thr Arg Ser Val Thr Ala Thr Leu Ala Lys Arg Pro Lys Arg Pro
100 105 110

Phe Leu Ser Leu Ser Ser Phe Leu Phe Xaa Pro Arg Ser Ala Gly Phe
115 120 125

Ser Pro
130

<210> 1480

<211> 131

<212> PRT

<213> Homo sapiens

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<222> (103)

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1552

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<220>

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<222> (129)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1480

Ile Ala Ser Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
50 55 60

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
65 70 75 80

Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
85 90 95

Val Thr Arg Ser Val Thr Xaa Thr Leu Ala Ser Ala Leu Ala Pro Xaa
100 105 110

Pro Phe Ala Phe Phe Leu Leu Ser Arg His Gly Arg Pro Ala Xaa Pro
115 120 125

Xaa Lys Leu
130

<210> 1481

<211> 112

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (88)

1553

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1481

Xaa Ser Ser Arg Ser Arg Ala Ala Arg Ser Arg Gly Ser Lys Leu Thr
1 5 10 15

Tyr Ala Cys Met Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe
20 25 30

Asn Ser Leu Ala Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly
35 40 45

Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp
50 55 60

His Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg
65 70 75 80

Ser Leu Asn Gly Glu Trp Asp Xaa Pro Cys Ser Gly Ala Leu Ser Ala
85 90 95

Ala Gly Val Val Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ala Pro
100 105 110

<210> 1482

<211> 53

<212> PRT

<213> Homo sapiens

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<222> (17)

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<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (50)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1482

Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Glu

1554

1 5 10 15
Xaa Ser Arg Glu Leu Asn Leu Cys Leu Xaa Lys Gln Leu Gly Arg Met
20 25 30
Gly Arg Tyr Phe Val Leu Asn Leu Gln Tyr Phe Lys Arg Gly Ser Tyr
35 40 45
Phe Xaa Ile Leu Cys
50

<210> 1483
<211> 61
<212> PRT
<213> Homo sapiens

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<222> (59)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1483
Ala Asn Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
1 5 10 15
Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile
20 25 30
Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
35 40 45
Gly Lys Gln Leu Glu Gly Trp Xaa Gln Leu Xaa Gln Thr
50 55 60

<210> 1484
<211> 27
<212> PRT
<213> Homo sapiens

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1555

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<221> SITE

<222> (23)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1484

Gly	Glu	Gly	Pro	Thr	Xaa	Pro	Leu	Pro	Ser	Glu	Thr	Xaa	Gly	Asp	Val
1					5				10					15	

Ala	Pro	Leu	Xaa	Cys	Xaa	Xaa	Gly	Leu	Asn	Met
			20					25		

<210> 1485

<211> 45

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

1556

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<222> (34)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1485

Phe Leu Ala Ala Gly Asn Pro Leu Arg Trp Pro Xaa Ile Leu Thr Ser
 1 5 10 15

Arg Trp Lys Ser Asp Ile Tyr Xaa Arg Lys Ser Asp Gly Xaa Tyr Ile
 20 25 30

Ile Xaa Leu Lys Arg Thr Trp Glu Lys Leu Leu Leu Gly
 35 40 45

<210> 1486

<211> 140

<212> PRT

<213> Homo sapiens

<400> 1486

Pro Arg Val Arg Arg Ala Glu Trp Leu Cys Gly Arg Val Ser Glu Thr
 1 5 10 15

Gly Ser Ala Cys Ser Met Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala
 20 25 30

Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr
 35 40 45

Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn
 50 55 60

Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp
 65 70 75 80

Gly Asn Gly Thr Ile Asp Phe Pro Glu Phe Leu Thr Met Met Ala Arg
 85 90 95

Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg
 100 105 110

Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg
 115 120 125

His Val Met Thr Asn Leu Gly Arg Glu Val Asn Arg
 130 135 140

1557

<210> 1487
 <211> 36
 <212> PRT
 <213> Homo sapiens

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<220>
 <221> SITE
 <222> (35)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1487
 Xaa Leu Gly Arg Asn Trp Ala Xaa Phe Thr Gly Lys Xaa Val Gly Xaa
 1 5 10 15

Ala Ser Xaa Asn Val Tyr Val His Ile Pro His Leu Arg Asn Ser His
 20 25 30

Glu Lys Xaa Ser
 35

<210> 1488
 <211> 34
 <212> PRT

1558

<213> Homo sapiens

<400> 1488

Ser Gly Pro Leu Trp Ile Leu Gly Asp Val Phe Ile Gly Arg Tyr Tyr
1 5 10 15

Thr Val Phe Asp Arg Asp Asn Asn Arg Val Gly Phe Ala Glu Ala Ala
20 25 30

Arg Leu

<210> 1489

<211> 160

<212> PRT

<213> Homo sapiens

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<222> (4)

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<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (160)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1489

Pro Thr Asn Xaa Xaa Lys Ser Xaa Glu Leu His Arg Gly Gly Gly Arg
1 5 10 15

Ser Arg Thr Ser Gly Ser Pro Gly Leu Gln Glu Phe Gly Thr Ser Thr
20 25 30

Gln Arg Pro Val Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu
35 40 45

Gly Glu Gln Asn Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala
50 55 60

1559

Arg Arg Leu Thr Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg
65 70 75 80

Val Ala Leu Leu Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe
85 90 95

Pro Leu Ser His Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr
100 105 110

Gln Tyr Leu Asn Ser Phe Ser His Val Gly Ala Gly Val Val His Ala
115 120 125

Ile Asn Ala Ile Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala
130 135 140

Glu Leu Pro Ser Trp Ser Ser Arg Thr Ala Ser Arg Ala Thr Thr Xaa
145 150 155 160

<210> 1490

<211> 105

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1490

Ala	Gln	Met	Gly	Met	Leu	Lys	Gly	Pro	Leu	Leu	Asn	Lys	Phe	Leu	Thr
1				5					10					15	

Thr	Ala	Lys	Asp	Lys	Asn	Arg	Trp	Glu	Asp	Xaa	Gly	Lys	Gln	Leu	Tyr
		20						25					30		

Asn	Val	Glu	Ala	Thr	Ser	Tyr	Xaa	Leu	Xaa	Ala	Leu	Leu	Gln	Leu	Lys
		35						40				45			

Xaa	Phe	Asp	Phe	Val	Pro	Pro	Val	Val	Xaa	Xaa	Leu	Asn	Xaa	Gln	Arg
		50					55					60			

1561

Xaa Tyr Gly Gly Gly Tyr Gly Ser Thr Gln Ala Thr Phe Met Val Phe
65 70 75 80

Gln Xaa Leu Ala Gln Xaa Gln Lys Asp Gly Pro Asp His Gln Ala Leu
85 90 95

Asn Leu Xaa Val Xaa Leu Gln Met Leu
100 105

<210> 1491

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1491

Arg Asn Thr Leu Ile Ile Tyr Leu Asp Lys Val Ser His Ser Glu Asp
1 5 10 15

Asp Cys Leu Ala Phe Lys Val His Gln Tyr Phe Asn Val Glu Leu Ile
20 25 30

Gln Pro Gly Ala Val Lys Val Tyr Ala Tyr Tyr Asn Leu Glu Glu Ser
35 40 45

Cys Thr Arg Phe Tyr His Pro Glu Lys Glu Asp Gly Lys Leu Asn Lys
50 55 60

Leu Cys Arg Asp Glu Leu Cys Arg Cys Ala Glu Glu Asn Cys Phe Ile
65 70 75 80

Gln Lys Ser Asp Asp Lys Val Thr Leu Glu Glu Arg Leu Asp Lys Ala
85 90 95

Cys Glu Pro Gly Val Asp Tyr Val Tyr Lys Thr Arg Leu Ala Arg Phe
100 105 110

Lys Leu Ser Asn Asp Phe Asp Arg Val His His Gly His
115 120 125

<210> 1492

<211> 68

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (62)

1562

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1492

Arg Pro Thr Arg Pro Ala Leu Ser Ile Ile Ala Leu Glu Ile Gln Ala
1 5 10 15

Gln Lys Cys Val Glu Leu Thr Glu Gly Ile Glu Cys Leu Gln Thr His
20 25 30

Ser Lys Ile Asn Gly Arg Asp Leu Thr Phe Trp Gln Glu Leu Val Ser
35 40 45

Lys Cys Leu Thr Glu Tyr Ser Ser Lys Gln Ser Gly Ser Xaa Pro Asn
50 55 60

Val Pro Glu Val
65

<210> 1493

<211> 74

<212> PRT

<213> Homo sapiens

<220>

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<222> (14)

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (52)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

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<222> (55)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1563

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 <223> Xaa equals any of the naturally occurring L-amino acids

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 <223> Xaa equals any of the naturally occurring L-amino acids

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 <223> Xaa equals any of the naturally occurring L-amino acids

 <400> 1493
 Glu Glu Ile Gln Lys His Asn His Ser Lys Ser Thr Trp Xaa Asp Pro
 1 5 10 15

 Xaa Thr Thr Arg Cys Thr Asn Leu Thr Lys Phe Leu Xaa Glu Ala Ser
 20 25 30

 Leu Val Gly Glu Glu Val Leu Arg Gly Thr Ser Leu Glu Val Thr Leu
 35 40 45

 Leu Glu Glu Xaa Leu Arg Xaa Val Arg Gly Thr Phe Thr Xaa Xaa Pro
 50 55 60

 Lys Gly Lys Leu Phe Pro Lys Thr Phe Xaa
 65 70

<210> 1494
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (46)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (49)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1494
 Asp Ala Thr Ser Pro Ile Ile Glu Glu Leu Ile Thr Phe His Asp His
 1 5 10 15

1564

Ala Leu Ile Ile Ile Phe Leu Ile Cys Phe Leu Val Leu Tyr Ala Leu
20 25 30

Phe Leu Thr Leu Thr Thr Lys Leu Thr Asn Thr Asn Ile Xaa Asp Ala
35 40 45

Xaa Glu Ile Glu Thr Val
50

<210> 1495

<211> 38

<212> PRT

<213> Homo sapiens

<400> 1495

Phe Phe Gly His Pro Glu Val Tyr Ile Leu Ile Leu Pro Gly Phe Gly
1 5 10 15

Ile Ile Ser His Ile Val Thr Tyr Tyr Ser Gly Lys Lys Glu Pro Phe
20 25 30

Gly Tyr Ile Gly Met Val
35

<210> 1496

<211> 46

<212> PRT

<213> Homo sapiens

<400> 1496

Ala Phe Tyr His Ser Ser Leu Ala Pro Thr Pro Gln Leu Gly Gly His
1 5 10 15

Trp Pro Pro Thr Gly Ile Thr Pro Leu Asn Pro Leu Glu Val Pro Leu
20 25 30

Leu Asn Thr Ser Val Leu Leu Ala Ser Gly Val Ser Ile Thr
35 40 45

<210> 1497

<211> 60

<212> PRT

<213> Homo sapiens

<400> 1497

1565

Ala Gln Val Gly Leu Gln Asp Ala Thr Ser Pro Ile Ile Glu Glu Leu
1 5 10 15

Ile Thr Phe His Asp His Ala Leu Ile Ile Ile Phe Leu Ile Cys Phe
20 25 30

Leu Val Leu Tyr Ala Leu Phe Leu Thr Leu Thr Thr Lys Leu Thr Asn
35 40 45

Thr Asn Ile Ser Asp Ala Gln Glu Ile Glu Thr Val
50 55 60

<210> 1498

<211> 45

<212> PRT

<213> Homo sapiens

<400> 1498

Thr Tyr Glu Tyr Thr Asp Tyr Gly Gly Leu Ile Phe Asn Ser Tyr Ile
1 5 10 15

Leu Pro Pro Leu Phe Leu Glu Pro Gly Asp Leu Arg Leu Leu Asp Gly
20 25 30

Asp Asn Arg Val Val Leu Pro Ile Glu Ala Pro Phe Val
35 40 45

<210> 1499

<211> 69

<212> PRT

<213> Homo sapiens

<220>

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<222> (63)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1499

His Arg Leu Asp Phe Leu Gln Leu Met Ile Asp Ser Gln Asn Ser Lys
1 5 10 15

Glu Thr Glu Ser His Lys Ala Leu Ser Asp Leu Glu Leu Ala Ala Gln
20 25 30

Ser Ile Ile Phe Ile Phe Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu
35 40 45

1566

Ser Phe Thr Leu Tyr Glu Leu Ala Thr His Pro Asp Val Gln Xaa Lys
 50 55 60

Leu Gln Lys Gly Asp
 65

<210> 1500

<211> 35

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1500

Arg Leu Thr Ser Thr Ala Cys Ala Glu Ser Trp Asp Glu Leu Thr Leu
 1 5 10 15

Ala Arg Xaa Asp Leu Glu Xaa Gln Ile Glu Gly Leu Asn Glu Xaa Ala
 20 25 30

Ser Leu Thr
 35

<210> 1501

<211> 126

<212> PRT

<213> Homo sapiens

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<222> (117)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1501

Phe	Xaa	Ala	Pro	Ser	Arg	Ile	Ser	Ala	Trp	Xaa	Gly	Pro	Pro	Ala	Ser
1				5					10					15	

Thr	Pro	Ala	Ser	Thr	Met	Ser	Ile	Lys	Val	Thr	Gln	Lys	Ser	Tyr	Lys
			20					25						30	

Xaa	Ser	Thr	Ser	Ser	Pro	Arg	Ala	Phe	Ser	Ser	Arg	Ser	Tyr	Thr	Asn
			35				40					45			

Xaa	Pro	Gly	Ser	Arg	Ile	Asn	Xaa	Ser	Xaa	Phe	Ser	Arg	Ile	Gly	Ser
	50					55						60			

Ser	Asn	Xaa	Xaa	Ser	Gly	Leu	Gly	Gly	Gly	Tyr	Xaa	Gly	Ala	Ser	Xaa
65					70					75					80

Met	Xaa	Gly	Ile	Thr	Ala	Val	Thr	Val	Asn	Gln	Ser	Leu	Leu	Xaa	Pro
					85					90				95	

Leu	Xaa	Leu	Glu	Val	Asp	Pro	Asn	Ile	Gln	Ala	Val	Arg	Thr	Gln	Glu
			100						105					110	

Lys	Glu	Gln	Ile	Xaa	Thr	Leu	Asn	Asn	Lys	Phe	Ala	Ser	Ser
			115					120				125	

<210> 1502

<211> 84

<212> PRT

<213> Homo sapiens

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<222> (76)
<223> Xaa equals any of the naturally occurring L-amino acids

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<400> 1502
Gln Arg Asn Ser Xaa Gly Ser Arg Thr Xaa Xaa Ser Arg Xaa Xaa Cys
1 5 10 15
Lys Xaa Val Ala Met Phe Ser Trp Asp Pro Xaa Leu Val Xaa Gly Gly
20 25 30
Gly Ala Ser Lys Met Ala Val Ala His Ala Leu Xaa Glu Lys Ser Xaa
35 40 45
Ala Met Asp Trp Cys Gly Asn Asn Gly His Thr Gly Leu Leu Xaa Arg
50 55 60
Ala Leu Xaa Val His Ser Ser Xaa Pro Trp Ile Xaa Lys Leu Trp Gly
65 70 75 80
Xaa Ser His His

<210> 1503
<211> 70
<212> PRT
<213> Homo sapiens

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<220>
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1571

<222> (70)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1503

Val Gly Val Leu Gly Leu Asp Leu Trp Gln Val Lys Ser Gly Thr Ile
1 5 10 15

Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu Ala Tyr Ala Glu Glu Phe
20 25 30

Gly Asn Glu Thr Trp Gly Val Thr Lys Ala Ala Glu Lys Gln Met Lys
35 40 45

Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys Glu Glu Glu Glu Asp Lys
50 55 60

Lys Arg Lys Glu Xaa Xaa
65 70

<210> 1504

<211> 42

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (41)

<223> Xaa equals any of the naturally occurring L-amino acids

1572

<400> 1504

Asn Thr Leu Xaa Tyr Xaa Met Lys Ala Thr Xaa Ile Leu Leu Leu Xaa
1 5 10 15

Ala Gln Leu Ser Trp Ala Gly Pro Phe His Gln Thr Gly Leu Leu Asp
20 25 30

Ser Met Leu Glu His Glu Ala Tyr Xaa Ile
35 40

<210> 1505

<211> 72

<212> PRT

<213> Homo sapiens

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<220>

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (72)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1505

Xaa His Xaa Asp Cys Ser Xaa Pro Ile Val Ala Ala Gly Val Gly Glu
1 5 10 15

1573

Phe Glu Ala Gly Ile Ser Lys Asn Gly Gln Thr Arg Glu His Ala Leu
20 25 30

Leu Ala Tyr Thr Leu Gly Val Lys Gln Leu Ile Val Gly Xaa Asn Lys
35 40 45

Met Asp Ser Thr Glu Pro Pro Tyr Ser Gln Lys Arg Tyr Glu Glu Ile
50 55 60

Xaa Lys Glu Val Ser Thr Tyr Xaa
65 70

<210> 1506
<211> 23
<212> PRT
<213> Homo sapiens

<400> 1506
Ala Glu Thr Arg Lys Arg Lys Gly Leu Lys Glu Gly Ile Pro Ala Leu
1 5 10 15

Asp Asn Phe Leu Asp Lys Leu
20

<210> 1507
<211> 87
<212> PRT
<213> Homo sapiens

<220>
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<400> 1507
Lys Leu Pro Leu Lys Ala Lys Met Gly Lys Glu Lys Thr His Ile Asn
1 5 10 15

Ile Val Val Ile Gly His Val Asp Ser Gly Lys Ser Thr Thr Thr Gly
20 25 30

His Leu Ile Tyr Lys Cys Gly Gly Ile Asp Lys Arg Thr Ile Glu Lys
35 40 45

Phe Glu Lys Glu Ala Ala Glu Met Gly Lys Gly Ser Phe Lys Tyr Ala
50 55 60

1574

Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile Xaa Ile
 65 70 75 80

Gly Tyr Leu Leu Val Glu Ile
 85

<210> 1508

<211> 110

<212> PRT

<213> Homo sapiens

<220>

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<222> (4)

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1508

Pro Asp Pro Xaa Ile Phe Ala Pro Pro Ile Ser Ala Pro Pro Pro Ser
 1 5 10 15

Ser Gly Thr Arg Asp Arg Ser Gln Arg Ser Leu Asp His Tyr Glu Pro
 20 25 30

Pro Val Gln Pro Arg Gly Pro Cys Pro Arg Ser Phe Glu Leu Leu Val
 35 40 45

Arg Ala Val Gly Ala Ala Ala Ala Asp Ala Ala Arg Ala His Arg
 50 55 60

1575

Gln Arg Trp Ser Cys Arg Cys Cys Val Xaa Arg Ala Ala Leu Pro Phe
65 70 75 80

Val Tyr Arg Pro Arg Lys Glu Ser Ile Pro Lys Met Ile Ser Asn Xaa
85 90 95

Gln Val Xaa Ala Ile Gly Pro Thr Val Leu Gln Xaa Gly Lys
100 105 110

<210> 1509

<211> 60

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

1576

<400> 1509

Ser Phe Val Glu Leu Pro Leu Ala Ser Ile Val Ser Leu His Ala Ser
 1 5 10 15

Ser Xaa Gly Gly Arg Leu Gln Thr Ser Pro Xaa Pro Ile Gln Xaa Thr
 20 25 30

Pro Pro Lys Asp Thr Cys Ser Pro Xaa Leu Xaa Met Ser Leu Xaa Pro
 35 40 45

Xaa Lys Leu Cys Arg Arg Arg His Gly Pro Trp Tyr
 50 55 60

<210> 1510

<211> 116

<212> PRT

<213> Homo sapiens

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<222> (108)

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<400> 1510

Gly Thr Ser Ser Ser Gln Arg Phe Tyr Lys Glu Asn Leu Gly Gln Gly
 1 5 10 15

Trp Met Thr Gln Lys His Glu Arg Met Lys Val Tyr Val Pro Thr Gly
 20 25 30

Phe Ser Ala Phe Pro Phe Glu Leu Leu His Thr Pro Glu Lys Trp Val
 35 40 45

Arg Phe Lys Tyr Pro Lys Leu Ile Ser Tyr Ser Tyr Met Val Arg Gly

1577

50 55 60
 Gly His Phe Ala Ala Phe Glu Glu Pro Glu Leu Leu Ala Gln Asp Ile
 65 70 75 80
 Arg Lys Phe Leu Ser Val Leu Glu Arg His Xaa Xaa Thr Pro Leu Pro
 85 90 95
 Pro Leu Ala Thr Ser Pro His Asn Ala Leu Gln Xaa Phe Leu Gly Glu
 100 105 110
 Asp Asn Xaa Phe
 115

<210> 1511
 <211> 156
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<400> 1511
 Arg Glu Gln Lys Leu Glu Leu His Arg Gly Xaa Gly Arg Ser Arg Thr
 1 5 10 15
 Ser Gly Ser Pro Gly Leu Gln Glu Phe Gly Thr Arg Asp Arg Gly Gly
 20 25 30
 Phe Pro Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly
 35 40 45
 Gly Asn Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Ser
 50 55 60
 Ile Gly Asp Phe Cys Cys Asp Val Ile Val Cys Arg Gly Cys Gly Asn
 65 70 75 80

1578

Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Gly Asp Arg Gly
85 90 95

Arg Gly Gly Pro Gly Gly Met Xaa Gly Gly Arg Gly Gly Leu Met Asp
100 105 110

Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg Gly Gly Asp Arg
115 120 125

Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly Gly Phe Xaa Gly
130 135 140

Gly Arg Arg Gly Gly Pro Gly Gly Pro Leu Asp Leu
145 150 155

<210> 1512

<211> 102

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<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (101)

1579

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Pro	Met	Arg	Arg	Pro	Arg	Gly	Glu	Pro	Ala	Pro	Gly	Pro	Arg	Asp	Arg
1				5				10					15		

Leu	Arg	Glu	Arg	Pro	Ala	Gln	Gly	Pro	Gly	Ser	His	Val	Arg	Val	Ala
			20					25					30		

Pro	Leu	Ala	Thr	Val	Asn	Ile	Leu	Xaa	Ser	Leu	Cys	Gln	Leu	Arg	Cys
		35					40					45			

Leu	Pro	Phe	Xaa	Ala	Leu	His	Phe	Val	Xaa	Ser	Pro	Gly	Phe	Ile	Xaa
	50					55					60				

Tyr	Ile	Ser	Gly	Thr	Pro	His	Ala	Leu	Ile	Val	Arg	Arg	Tyr	Leu	Ser
	65				70					75				80	

Leu	Leu	Asp	Thr	Ala	Val	Glu	Leu	Xaa	Leu	Pro	Arg	Tyr	Arg	Gly	Pro
			85						90					95	

Arg	Leu	Pro	Arg	Xaa	Gln
					100

<210> 1513

<211> 139

<212> PRT

<213> Homo sapiens

<220>

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1513

Glu	Thr	Glu	Arg	Gly	Phe	Glu	Glu	Leu	Pro	Leu	Cys	Ser	Cys	Arg	Met
1				5				10					15		

Glu	Ala	Pro	Lys	Ile	Asp	Ser	Ile	Ser	Glu	Arg	Ala	Gly	His	Lys	Cys
			20					25					30		

Met	Ala	Thr	Glu	Ser	Val	Asp	Gly	Glu	Leu	Ser	Gly	Cys	Asn	Ala	Ala
		35					40					45			

Ile	Leu	Lys	Arg	Glu	Thr	Met	Arg	Pro	Ser	Ser	Arg	Val	Ala	Leu	Met
	50					55					60				

Val	Leu	Cys	Glu	Thr	His	Arg	Ala	Arg	Met	Val	Lys	His	His	Cys	Cys
	65					70				75				80	

1580

Pro Gly Cys Gly Tyr Phe Cys Thr Ala Gly Thr Phe Leu Glu Cys His
85 90 95

Pro Asp Phe Arg Val Ala His Arg Phe His Lys Ala Cys Val Ser Gln
100 105 110

Leu Asn Gly Met Val Phe Cys Pro His Cys Gly Glu Asp Thr Ser Glu
115 120 125

Ala Gln Xaa Val Thr Ile Pro Gly Val Thr Gly
130 135

<210> 1514

<211> 72

<212> PRT

<213> Homo sapiens

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1581

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 <400> 1514
 Ile Arg His Glu Ser Ile Ser Gly Ala Ser Xaa Lys Asp Ile Val His
 1 5 10 15

 Ser Gly Xaa Ala Tyr Thr Xaa Glu Xaa Ser Ala Arg Gln Xaa Met Arg
 20 25 30

 Thr Ala Met Lys Xaa Asn Leu Gly Xaa Asp Leu Arg Thr Ala Ser Tyr
 35 40 45

 Xaa Asn Ala Ile Xaa Xaa Val Phe Lys Val Tyr Xaa Glu Ala Gly Val
 50 55 60

 Thr Phe Thr Xaa Met Xaa His Gly
 65 70

1582

<210> 1515

<211> 88

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1515

Leu Tyr Pro Pro Ala Cys Ser Ala Thr Arg Thr Pro Ser Thr Met Thr
1 5 10 15

Thr Ser Ala Ser Ser His Leu Asn Lys Gly Ile Lys Gln Val Tyr Met
20 25 30

Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp Ile Asp
35 40 45

Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp Ser Glu
50 55 60

Pro Lys Cys Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly Ser Ser
65 70 75 80

Thr Xaa Gln Ser Xaa Gly Ser Ser
85

<210> 1516

<211> 105

<212> PRT

<213> Homo sapiens

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1583

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<400> 1516
Gly Arg Glu Ser Gln Asp Thr Xaa Phe Xaa Xaa Leu Val Glu Arg Val
1 5 10 15
Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Xaa Phe Lys Ser Val His
20 25 30
Phe Pro Gly Gln Ala Xaa Gly Thr Arg Arg Gly Ser Pro Leu Leu Ile
35 40 45
Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile Leu
50 55 60
Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg Val
65 70 75 80

1584

Asp Ser Thr Thr Cys Leu Xaa Pro Xaa Glu Glu Lys Ala Xaa Glu Tyr
85 90 95

Tyr Phe Ala Ser Asp Ala Xaa Ala Ala
100 105

<210> 1517

<211> 121

<212> PRT

<213> Homo sapiens

<220>

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1585

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<222> (110)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1517

Gly	Xaa	Glu	Lys	Arg	Glu	Arg	Glu	Arg	Leu	Val	Ile	Arg	Gln
1				5				10				15	

Xaa	Pro	Xaa	Val	Gln	Xaa	Leu	Gln	Ala	Tyr	Lys	Pro	Arg	Glu	Asn	Asp
			20					25					30		

Xaa	Leu	Ala	Leu	Glu	Lys	Ala	Asp	Val	Val	Met	Val	Thr	His	Gln	Ser
	35						40					45			

Ser	Ala	Arg	Leu	Ala	Gly	Gly	Arg	Glu	Ala	Leu	Arg	Arg	Gly	Ala	Arg
	50					55					60				

Leu	Val	Ser	Cys	Asp	Ser	Xaa	Xaa	Ser	Ser	Phe	Pro	Thr	Gln	Arg	Ser
	65					70				75				80	

Val	Thr	Gln	Asn	Leu	Lys	Gly	Ser	Phe	Ile	Glu	Cys	Lys	Thr	Cys	Gln
			85						90					95	

Thr	Thr	Ala	Xaa	Gly	Asn	Ser	Lys	Pro	Xaa	Phe	Ser	Xaa	Xaa	Glu	Gly
		100						105						110	

Val	Phe	Val	Ser	Trp	Lys	Asn	Lys	Leu
	115						120	

<210> 1518

<211> 146

<212> PRT

<213> Homo sapiens

<220>

1586

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<222> (71)
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1518
Arg Gly Pro Ala Gln Arg Gly Glu Gly Ala Arg Glu Ala Asn Lys Lys
1 5 10 15
Ile Glu Lys Gln Leu Gln Lys Asp Lys Gln Val Tyr Arg Ala Thr His
20 25 30
Arg Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val
35 40 45
Lys Gln Met Arg Ile Leu His Val Asn Gly Phe Asn Gly Asp Ser Glu
50 55 60
Lys Ala Thr Lys Val Gln Xaa Ile Lys Asn Asn Leu Lys Glu Ala Ile
65 70 75 80
Glu Thr Ile Val Ala Ala Met Ser Asn Leu Val Pro Pro Val Glu Leu
85 90 95
Ala Asn Pro Glu Asn Gln Phe Arg Val Asp Tyr Ile Leu Ser Val Met
100 105 110
Asn Val Pro Asp Phe Xaa Phe Pro Pro Glu Phe Tyr Glu His Ala Lys
115 120 125
Ala Leu Trp Xaa Asp Glu Xaa Val Arg Xaa Cys Tyr Glu Arg Ser Asn
130 135 140

1587

Glu Tyr
145

<210> 1519

<211> 137

<212> PRT

<213> Homo sapiens

<220>

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<222> (72)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1519

Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly Val Ile Ala Gly Leu
1 5 10 15

Asn Val Leu Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr
20 25 30

Gly Leu Asp Arg Thr Gly Lys Gly Glu Arg Asn Val Leu Ile Phe Asp
35 40 45

Leu Gly Gly Gly Thr Phe Asp Val Ser Ile Leu Thr Ile Asp Asp Gly
50 55 60

Ile Phe Glu Val Lys Ala Thr Xaa Gly Asp Thr His Leu Gly Gly Glu
65 70 75 80

Asp Phe Asp Asn Arg Leu Val Asn His Phe Val Glu Glu Phe Lys Arg
85 90 95

Lys His Lys Lys Asp Ile Ser Gln Asn Lys Arg Ala Val Arg Arg Leu
100 105 110

Arg Thr Ala Ala Arg Gly Pro Arg Gly Pro Cys Arg Pro Ala Pro Arg
115 120 125

Pro Ala Trp Arg Ser Thr Ser Leu Phe
130 135

<210> 1520

<211> 100

<212> PRT

<213> Homo sapiens

1588

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 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1520
 Cys Arg Lys Ser Ser Trp Lys Arg Trp Trp Pro Gln Ser Lys Leu Xaa
 1 5 10 15
 Thr Arg Xaa Ile Val Thr Ile Gly Ile Lys Ala Met Ala Thr Met Asp
 20 25 30
 Ile Thr Ala Lys Val Thr Val Val Met Glu Asp Met Xaa Tyr Thr Gly
 35 40 45
 Tyr Asn Asn Tyr Tyr Gly Tyr Gly Asp Tyr Ser Asn Gln Gln Ser Gly
 50 55 60
 Tyr Gly Lys Val Ser Arg Arg Gly Gly His Gln Asn Ser Tyr Lys Pro
 65 70 75 80
 Tyr Leu Asn Tyr Ser Ile Cys Asn Leu Ser Pro Thr Gly Gly Glu Ala
 85 90 95
 Tyr Phe Xaa Ile
 100

<210> 1521
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
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1589

<222> (72)

<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (95)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (110)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (123)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1521

Asp	Ala	Trp	Ala	Leu	Ala	Pro	Gly	Pro	Val	Leu	Phe	Ser	Asn	Met	Val
1				5					10					15	

Cys	Leu	Lys	Phe	Pro	Gly	Ser	Ser	Cys	Met	Ala	Ala	Leu	Thr	Val	Thr
		20					25						30		

Leu	Met	Val	Leu	Asn	Ser	Pro	Leu	Ala	Leu	Ala	Gly	Asp	Thr	Arg	Pro
		35					40					45			

Arg	Phe	Leu	Glu	Gln	Val	Lys	His	Glu	Cys	His	Phe	Phe	Asn	Gly	Thr
	50					55					60				

Glu	Arg	Val	Arg	Phe	Leu	Asp	Xaa	Tyr	Phe	Tyr	His	Gln	Glu	Glu	Tyr
65					70					75					80

Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Xaa	Leu
			85						90					95	

Gly	Arg	Pro	Asn	Ser	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Xaa	Xaa	Asp
		100						105					110		

Arg	Ser	Gly	Pro	Arg	Trp	Thr	Pro	Thr	Ala	Xaa	Thr	Leu	Arg	Gly	Trp
		115				120						125			

Val

1590

<210> 1522
<211> 113
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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1591

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<222> (74)

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<220>

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<223> Xaa equals any of the naturally occurring L-amino acids

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<220>

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<222> (97)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (110)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1522

Xaa	Xaa	Thr	Asp	Ser	Xaa	Arg	Pro	Asp	Ser	Arg	Val	Asp	Pro	Arg	Val
1				5					10					15	

Arg	Glu	Val	Thr	Asp	Tyr	Ala	Ile	Ala	Arg	Arg	Ile	Val	Asp	Leu	His
			20					25					30		

Ser	Arg	Ile	Glu	Glu	Ser	Ile	Xaa	Asn	Ile	Tyr	Xaa	Leu	Asp	Asp	Ile
		35					40					45			

Arg	Arg	Tyr	Leu	Xaa	Tyr	Ala	Arg	Lys	Xaa	Lys	Pro	Lys	Asn	Ser	Lys
		50				55					60				

Xaa	Ser	Xaa	Asp	Phe	Ile	Val	Glu	Gln	Xaa	Lys	His	Leu	Arg	Pro	Xaa
65					70					75					80

Asp	Gly	Phe	Trp	Ser	Ser	Pro	Val	Phe	Xaa	Glu	Gly	Xaa	Ser	Cys	Gly
				85					90					95	

Xaa	Ile	Glu	Gly	Leu	Gly	Ser	Val	Ser	Leu	Gly	Ser	Gln	Xaa	Leu	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1592

100

105

110

Val

<210> 1523

<211> 32

<212> PRT

<213> Homo sapiens

<220>

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<222> (16)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (31)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1523

Pro	Cys	Lys	Gly	Ser	Ile	Ile	Thr	Trp	Ser	Leu	Ile	Arg	Asp	Leu	Xaa
1				5					10					15	

Glu	Trp	Leu	His	Glu	Gly	Gln	Leu	Ala	Leu	Thr	Phe	Asn	Gln	Xaa	Asn
			20				25							30	

<210> 1524

<211> 28

<212> PRT

<213> Homo sapiens

<400> 1524

Pro	Cys	Lys	Gly	Ser	Ile	Ile	Thr	Cys	Ser	Leu	Asn	Arg	Asp	Leu	Tyr
1				5					10					15	

Glu	Trp	Leu	His	Glu	Gly	Ser	Ala	Val	Ser	Tyr	Phe
			20				25				

<210> 1525

<211> 92

<212> PRT

1593

<213> Homo sapiens

<220>

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<222> (1)

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<221> SITE

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1525

Xaa Glu Gln Lys Leu Xaa Leu His Arg Gly Gly Gly Arg Ser Arg Thr
1 5 10 15

1594

Ser Gly Ser Pro Xaa Leu Xaa Glu Phe Gly Thr Ser Gly Thr Arg Pro
 20 25 30
 Cys Gly Val Tyr Thr Pro Arg Cys Gly Ser Gly Leu Leu Cys Tyr Pro
 35 40 45
 Pro Arg Gly Val Glu Lys Pro Leu His Thr Leu Met His Gly Gln Gly
 50 55 60
 Val Cys Met Glu Leu Ala Xaa Ile Glu Ala Xaa Xaa Glu Ser Leu Xaa
 65 70 75 80
 Pro Ser Asp Lys Asp Glu Gly Asp His Pro Asn Xaa
 85 90

<210> 1526

<211> 154

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (118)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1526

Xaa Glu Pro Ser Pro Gly Ile Phe Arg Trp Phe His Leu Val Asn Arg
 1 5 10 15
 Thr Glu Gln Arg Glu Leu Thr Met Glu Phe Gly Leu Ser Trp Leu Phe
 20 25 30
 Leu Val Ala Ile Leu Lys Gly Val Gln Cys Glu Val Gln Leu Val Glu
 35 40 45
 Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
 50 55 60
 Thr Val Ser Gly Phe Thr Phe Arg Asn Tyr Ala Met Ser Trp Val Arg
 65 70 75 80
 Gln Gly Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Asp Gly Ser
 85 90 95

1595

Gly Tyr Asn Thr Tyr Tyr Glu Arg Ser Leu Gln Gly Arg Phe Ser Val
 100 105 110
 Ser Arg Asp Asn Ser Xaa Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
 115 120 125
 Gly Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys Thr Glu Arg Met
 130 135 140
 Gly Thr Gly Trp Tyr Gly Arg Asn Asp Tyr
 145 150

<210> 1527
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
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<400> 1527
 Gly Lys Leu Val Arg Leu Gln Val Pro Val Arg Asn Ser Arg Val Asp
 1 5 10 15
 Pro Arg Val Arg Thr Val Thr Pro Gly Glu Thr Ala Ser Ile Ser Cys
 20 25 30
 Arg Ser Ser Gln Thr Leu Leu His Val Asn Gly His Asn Tyr Leu Asp
 35 40 45
 Trp Tyr Met Gln Lys Pro Gly Gln Pro Pro Gln Leu Val Val Tyr Arg
 50 55 60

1596

Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Gly Gly
 65 70 75 80
 Ser Gly Thr Asp Phe Thr Leu Arg Ile Thr Thr Val Glu Ala Xaa Asp
 85 90 95
 Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Ser Pro Tyr Thr Phe
 100 105 110
 Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Gly Cys Thr Ile
 115 120 125
 Xaa Leu His Leu Xaa Xaa Ile
 130 135

<210> 1528

<211> 139

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (117)

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<220>

<221> SITE

<222> (137)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1528

Arg Glu Gln Lys Leu Glu Leu His Arg Gly Gly Gly Arg Ser Arg Thr
 1 5 10 15
 Ser Gly Ser Pro Gly Leu Gln Glu Phe Gly Thr Ser Gly Trp Ala Leu
 20 25 30
 Arg Ile Ser Arg Phe Leu Pro Gly Phe His Ser Phe Ala Pro Cys Thr
 35 40 45
 Val Ala Pro Ser Leu Arg Ala Gln Pro Ala Lys Gln Arg Ala Pro Val
 50 55 60
 Ala Gly Val Met Gln Arg Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu
 65 70 75 80
 Thr Leu Leu Val Leu Leu Arg Gly Pro Pro Val Ala Arg Ala Gly Ala
 85 90 95

1597

Ser Ser Gly Gly Leu Gly Pro Val Val Arg Cys Glu Pro Cys Asp Ala
100 105 110

Arg Ala Leu Ala Xaa Cys Ala Pro Ser Ala Arg Arg Val Arg Arg Asn
115 120 125

Leu Val Arg Gln Ala Gly Leu Ala Xaa Ala Ala
130 135

<210> 1529

<211> 135

<212> PRT

<213> Homo sapiens

<400> 1529

Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu Ile Asp Asp Thr Asn
1 5 10 15

Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu
20 25 30

Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln
35 40 45

Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys
50 55 60

Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp
65 70 75 80

Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln
85 90 95

Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val
100 105 110

Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser
115 120 125

Leu Glu Ile Asp Leu Gly Leu
130 135

<210> 1530

<211> 132

<212> PRT

<213> Homo sapiens

1598

<400> 1530

Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu Gln Val Pro Ala Arg
1 5 10 15

Lys Lys Arg Pro Lys Arg Leu Arg Thr Gly Asn Met Val Arg Ser Gly
20 25 30

Asn Lys Ala Ala Val Val Leu Cys Met Asp Val Gly Phe Thr Met Ser
35 40 45

Asn Ser Ile Pro Gly Ile Glu Ser Pro Phe Glu Gln Ala Lys Lys Val
50 55 60

Ile Thr Met Phe Val Gln Arg Gln Val Phe Ala Glu Asn Lys Asp Glu
65 70 75 80

Ile Ala Leu Val Leu Phe Gly Thr Asp Gly Thr Asp Asn Pro Leu Ser
85 90 95

Gly Gly Asp Gln Tyr Gln Asn Ile Thr Val His Arg His Leu Met Leu
100 105 110

Pro Asp Phe Asp Leu Leu Glu Asp Ile Glu Lys Gln Asn Pro Thr Arg
115 120 125

Phe Ser Thr Gly
130

<210> 1531

<211> 94

<212> PRT

<213> Homo sapiens

<220>

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<222> (18)

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1599

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<220>
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<400> 1531
 Arg Lys Arg Leu Lys Gly Glu Glu Gln Lys Leu Leu Arg Asn Ala Arg
 1 5 10 15
 Arg Xaa Gln Lys Met Ala Cys Gln Met Thr Xaa Asn His Ser Ser Val
 20 25 30
 Ser Xaa Leu Lys Gly Ser Ser Leu Gln Asp Arg Arg Ala Ser Arg Phe
 35 40 45
 Leu Ile Lys Ser Val Gln Lys Ser Ser Gly Val Gln Xaa Asp Pro Ser
 50 55 60
 Ser Ser Ile Ser Xaa Pro Ser Leu Thr Ala Xaa Trp Ser Xaa Leu Pro
 65 70 75 80
 Trp His Leu Arg Gly Pro Lys Ala Ala Lys Thr Leu Lys Xaa
 85 90

<210> 1532
 <211> 153
 <212> PRT
 <213> Homo sapiens

1600

<400> 1532

Gln Thr Thr Met Cys Tyr Gly Lys Cys Ala Arg Cys Ile Gly His Ser
 1 5 10 15

Leu Val Gly Leu Ala Leu Leu Cys Ile Ala Ala Asn Ile Leu Leu Tyr
 20 25 30

Phe Pro Asn Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg
 35 40 45

Phe Val Trp Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu
 50 55 60

Leu Pro Ala Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly
 65 70 75 80

Cys Cys Gly His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser
 85 90 95

Val Leu Ala Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile
 100 105 110

Val Ala Ala Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu
 115 120 125

Gly Gln Trp Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Val Pro Ser
 130 135 140

Gly Tyr Leu His Met Val Arg Val His
 145 150

<210> 1533

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1533

Leu Cys Leu Leu Arg Thr Thr Val Thr Glu Val Ser Arg Ala Phe Ser
 1 5 10 15

Leu Leu Cys Lys Met Ala Thr Leu Lys Glu Lys Leu Ile Ala Pro Val
 20 25 30

Ala Glu Glu Glu Ala Thr Val Pro Asn Asn Lys Ile Thr Val Val Gly
 35 40 45

Val Gly Gln Val Gly Met Ala Cys Ala Ile Ser Ile Leu Gly Lys Ser
 50 55 60

1601

Leu Ala Asp Glu Leu Ala Leu Val Asp Val Leu Glu Asp Lys Leu Lys
 65 70 75 80

Gly Glu Met Met Asp Leu Gln His Gly Ser Leu Phe Leu Gln Thr Pro
 85 90 95

Lys Ile Leu Ala Asp Lys Asp Tyr Ser Val Thr Ala Asn Ser Lys Ile
 100 105 110

Val Val Val Thr Ala Gly Val Arg Gln Gln Glu Gly Glu Ser Arg Leu
 115 120 125

Asn Leu Val Gln Arg Asn Val Asn Val Phe Lys Phe Ile Ile
 130 135 140

<210> 1534

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

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<220>

<221> SITE

<222> (48)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (54)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (61)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1534

Ala His Cys His Ala Pro Pro Thr Thr Ala Arg Arg Ala Phe Pro Ile
 1 5 10 15

Pro Phe Gly Ser Lys Ser Asn Met Ala Thr Leu Lys Asp Gln Leu Ile
 20 25 30

Tyr Asn Leu Leu Lys Glu Glu Gln Thr Xaa Gln Asn Lys Ile Thr Xaa
 35 40 45

1602

Val Gly Val Gly Ala Xaa Gly Met Ala Cys Ala Ile Xaa Ile Leu Met
 50 55 60

Lys Asp Leu
 65

<210> 1535

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1535

Xaa Lys Lys Tyr Leu Gly Asp Xaa Ile Glu Gly Thr Pro Ala Gly Thr
 1 5 10 15

Gly Pro Glu Phe Pro Gly Leu Leu Thr Cys Leu Leu Gln Leu Ile Met
 20 25 30

Val Thr Asn Lys Ala Ile Ala Ser Gln Ile Ser Gln Ile Lys His Phe
 35 40 45

Phe His Cys Ile Leu Val Val Val Cys Pro Asn Ser Ser Met Tyr Leu
 50 55 60

Ile Met Ser Gly Ser Ile Leu His
 65 70

<210> 1536

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

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1603

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<220>
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 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (58)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (68)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1536
 Gly Lys Ala Trp Gly Ser Glu Cys Glu Lys Cys Pro Leu Pro Gly Thr
 1 5 10 15
 Glu Ala Phe Xaa Glu Ile Cys Pro Ala Gly His Gly Tyr Thr Tyr Ala
 20 25 30
 Ser Ser Asp Ile Arg Leu Ser Met Arg Lys Ala Glu Xaa Glu Glu Leu
 35 40 45
 Ala Xaa Pro Pro Arg Glu Gln Gly Gln Xaa Ser Ser Trp Ala Leu Pro
 50 55 60
 Gly Pro Thr Xaa Lys Gln Pro Leu Arg Val Arg His Gly His Leu Ala
 65 70 75 80

<210> 1537
 <211> 137
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (58)
 <223> Xaa equals any of the naturally occurring L-amino acids

1604

<220>

<221> SITE

<222> (74)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (122)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (134)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (136)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (137)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1537

Arg Lys Gln Cys Gln Asp Ser Lys Asp Ser Asn His Leu Pro Lys Met
1 5 10 15

Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr Ser
20 25 30

Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln Ser
35 40 45

Ser Pro Asn Cys Ala Pro Glu Cys Asn Xaa Pro Glu Ser Tyr Pro Ser
50 55 60

Ala Met Tyr Cys Asp Glu Leu Lys Leu Xaa Ser Val Pro Met Val Pro
65 70 75 80

Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His Ile
85 90 95

Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile Leu
100 105 110

Asp His Asn Leu Leu Glu Asn Ser Lys Xaa Lys Gly Arg Val Phe Ser
115 120 125

1605

Lys Leu Lys Gln Leu Xaa Lys Xaa Xaa
 130 135

<210> 1538
 <211> 144
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (134)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (137)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1538
 Tyr Gln Val Tyr Ser Lys Ile Gln Ala Thr Asn Thr Trp Leu Phe Leu
 1 5 10 15
 Ser Ser Cys Asn Gly Asn Glu Thr Ser Leu Trp Asp Cys Lys Asn Trp
 20 25 30
 Gln Trp Gly Gly Leu Thr Cys Asp His Tyr Glu Glu Ala Lys Ile Thr
 35 40 45
 Cys Ser Ala His Arg Glu Pro Arg Leu Val Gly Gly Asp Ile Pro Cys
 50 55 60
 Ser Gly Arg Val Glu Val Lys His Gly Asp Thr Trp Gly Ser Ile Cys
 65 70 75 80
 Asp Ser Asp Phe Ser Leu Glu Ala Ala Ser Val Leu Cys Arg Glu Leu
 85 90 95
 Gln Cys Gly Thr Val Val Ser Ile Leu Gly Gly Ala His Phe Gly Glu
 100 105 110
 Gly Met Asp Arg Ser Gly Leu Lys Asn Ser Ser Val Glu Gly His Glu
 115 120 125
 Ser Pro Ser Phe Ile Xaa Pro Val Xaa Thr Pro Pro Lys Arg Asn Leu
 130 135 140

1606

<210> 1539
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1539
Asn Met Ala Gly Val Glu Glu Val Ala Ala Ser Gly Ser His Leu Asn
1 5 10 15
Gly Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Ala Ala Ser Thr Ala
20 25 30
Glu Glu Xaa Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Ser Lys Gly
35 40 45
Pro Ser Ala Gly Lys Glu Ser Phe Met Phe Ser Gln Ser Pro Pro Gly
50 55 60
Thr Ala Glu Leu Phe Gly Ser Gly Pro Leu Arg Gly Pro Gly Pro Gly
65 70 75 80
Pro Gln Ser Pro Asp
85

<210> 1540
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (18)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (22)

1607

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (27)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1540

Gly Val Gly Phe Arg Glu Gly Thr Xaa Gly Ala Gln Thr Gln Arg Ile
1 5 10 15

Arg Xaa Arg Val Pro Xaa Asn Trp Lys Met Xaa Phe Glu Pro Ile Ser
20 25 30

Ser Thr Lys Phe
35

<210> 1541

<211> 144

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (21)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (107)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1608

<222> (123)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (131)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (132)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (143)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1541

Arg	Thr	Xaa	Ala	Xaa	Gly	Glu	Arg	Ala	Cys	Arg	Ser	Thr	Leu	Val	Asp
1				5					10					15	

Pro	Lys	Xaa	Val	Xaa	Thr	Val	Phe	Ser	Leu	Gly	Ala	Cys	Met	Glu	Gly
			20					25					30		

Leu	Asn	Ile	Leu	Leu	Asn	Arg	Leu	Leu	Gly	Ile	Ser	Leu	Tyr	Ala	Glu
	35					40						45			

Gln	Pro	Ala	Lys	Gly	Glu	Val	Trp	Ser	Glu	Asp	Val	Arg	Lys	Leu	Ala
	50					55						60			

Val	Val	His	Glu	Ser	Glu	Gly	Leu	Leu	Gly	Tyr	Ile	Tyr	Cys	Asp	Phe
65					70					75					80

Phe	Gln	Arg	Ala	Asp	Lys	Pro	His	Gln	Asp	Cys	His	Phe	Thr	Ile	Arg
			85						90					95	

Gly	Gly	Arg	Leu	Lys	Gly	Arg	Trp	Glu	Thr	Xaa	Gln	Leu	Pro	Val	Val
			100				105					110			

Ser	Ser	Tyr	Ala	Gly	Ile	Phe	Pro	Val	Pro	Xaa	Arg	Glu	Phe	Ser	Asn
		115					120					125			

Phe	Gly	Xaa	Xaa	Leu	Gly	Met	Met	Gly	Lys	Pro	Phe	Pro	Gly	Xaa	Gly
	130					135					140				

1609

<210> 1542
 <211> 145
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (40)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1542
 Ala Glu Arg Thr Pro Cys Arg Arg Pro Ala Glu Met Leu Arg Leu Pro
 1 5 10 15
 Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg Val Leu Ala Pro His
 20 25 30
 Leu Thr Arg Ala Tyr Ala Lys Xaa Val Lys Phe Gly Ala Asp Ala Arg
 35 40 45
 Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala Asp Ala Val Ala Val
 50 55 60
 Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile Glu Gln Ser Trp Gly
 65 70 75 80
 Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Asp
 85 90 95
 Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val
 100 105 110
 Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala Thr
 115 120 125
 Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys
 130 135 140
 Gly
 145

<210> 1543
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 1543
 Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu
 1 5 10 15

1610

Leu Ala Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val
20 25 30

Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val
35 40 45

Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly
50 55 60

Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly
65 70 75 80

Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu
85 90 95

Gly Phe Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg
100 105 110

Gly Val Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln
115 120 125

Ser Lys Pro Val Thr Thr Pro
130 135

<210> 1544

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (68)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (72)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (77)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (80)

<223> Xaa equals any of the naturally occurring L-amino acids

1611

<400> 1544

Cys Glu Phe Lys Arg Val Pro Gln Cys Pro Ser Gly Arg Val Tyr Val
1 5 10 15

Leu Lys Phe Lys Ala Gly Ser Lys Arg Leu Phe Phe Trp Met Gln Glu
20 25 30

Pro Lys Thr Asp Gln Asp Glu Glu His Cys Arg Lys Val Asn Glu Leu
35 40 45

Ser Gly Thr Thr Pro Arg Cys Leu Gly His Trp Gly Pro Ala Glu Gln
50 55 60

Arg Pro Arg Xaa Leu Cys Ala Xaa Arg Leu Arg Trp Xaa Ala Glu Xaa
65 70 75 80

Ala Gly Glu Thr

<210> 1545

<211> 22

<212> PRT

<213> Homo sapiens

<400> 1545

Tyr Leu Arg Leu Ile Tyr Ser Thr Ser Ile Thr Leu Leu Pro Ile Ser
1 5 10 15

Asn Asn Val Lys Ile Lys
20

<210> 1546

<211> 112

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (29)

<223> xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (49)

<223> Xaa equals any of the naturally occurring L-amino acids

1612

<220>
<221> SITE
<222> (51)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (57)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (58)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (64)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (70)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (82)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (85)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (100)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1613

<221> SITE
<222> (102)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (107)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (110)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (111)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1546
Pro Ser Ala Ala Ala Gly Asp Leu Gln Arg Thr Ala Ala Met Gly Ala
1 5 10 15
His Leu Val Arg Arg Tyr Leu Gly Asp Ala Ser Val Xaa Pro Asp Pro
20 25 30
Leu Gln Met Pro Thr Phe Pro Pro Asp Tyr Gly Phe Pro Glu Arg Lys
35 40 45
Xaa Arg Xaa Met Val Ala Thr Xaa Xaa Xaa Met Met Asp Ala His Xaa
50 55 60
Ser Ser Xaa Cys Gly Xaa Thr Ala Pro Thr Asn Ser Ser Gly Cys Ser
65 70 75 80
Ile Xaa Thr Leu Xaa Leu Pro Pro Leu Pro Trp Leu Ala Asn Gln Glu
85 90 95
Arg Asp Lys Xaa Glu Xaa Xaa Gln Thr Pro Xaa Xaa Phe Xaa Xaa Pro
100 105 110

1614

<210> 1547

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1547

Lys Val Ser Ala Val Met Ala Phe Leu Ala Ser Gly Pro Tyr Leu Thr
1 5 10 15

His Gln Gln Lys Val Leu Arg Leu Tyr Lys Arg Ala Leu Arg His Leu
20 25 30

Glu Ser Trp Cys Val Gln Arg Asp Lys Tyr Arg Tyr Phe Ala Cys Leu
35 40 45

Met Arg Ala Arg Phe Glu Glu His Lys Asn Glu Lys Asp Met Ala Lys
50 55 60

Ala Thr Gln Leu Leu Lys Glu Ala Glu Glu Phe Trp Tyr Arg Gln
65 70 75 80

His Pro Gln Pro Tyr Ile Phe Pro Asp Ser Pro Gly Gly Thr Ser Tyr
85 90 95

Glu Arg Tyr Asp Cys Tyr Lys Val Pro Glu Trp Cys Leu Asp Asp Trp
100 105 110

His Pro Ser Glu Lys Ala Met Tyr Pro Asp Tyr Phe Ala Lys Arg Glu
115 120 125

Gln Trp Lys Lys Leu Arg Glu Gly Lys Leu Gly Thr Arg Gly
130 135 140

<210> 1548

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1615

<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (12)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (32)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (62)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (65)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (66)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

1616

<222> (82)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (84)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (92)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (95)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (97)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1548

Leu	Tyr	Tyr	Xaa	Leu	Gly	Phe	Leu	Xaa	Leu	Xaa	Xaa	Arg	Leu	Pro	Leu
1				5					10					15	

Asp	Ala	Ala	Lys	Arg	Xaa	His	Asp	Glu	Leu	Gly	Asn	Glu	Arg	Pro	Xaa
			20					25					30		

Ala	Tyr	Met	Xaa	Glu	His	Asn	Gln	Leu	Asn	Gly	Trp	Xaa	Ser	Asp	Glu
		35					40					45			

Asn	Asp	Trp	Asn	Glu	Lys	Leu	Tyr	Pro	Val	Trp	Lys	Arg	Xaa	Asp	Met
		50				55					60				

Xaa	Xaa	Glu	Lys	Leu	Leu	Glu	Gly	Arg	Pro	Val	Cys	Lys	Ala	Val	Leu
65					70					75					80

Thr	Xaa	Asp	Xaa	Pro	Thr	Leu	Gly	Gly	Leu	Lys	Xaa	Asn	Ile	Xaa	Arg
				85					90						95

Xaa Thr

<210> 1549

<211> 138

<212> PRT

<213> Homo sapiens

1617

<220>
 <221> SITE
 <222> (60)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (72)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (73)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (122)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (123)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (128)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (136)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1549

Gly Cys Ser Leu Glu Gln Arg Ser Phe Ile Ser Val Arg Leu Leu Ser
 1 5 10 15

Tyr Leu Ser Ala Cys Arg His Pro Met Glu Asp Ser Met Asp Met Asp
 20 25 30

Met Ser Pro Leu Arg Pro Gln Asn Tyr Leu Phe Gly Cys Glu Leu Lys
 35 40 45

Ala Asp Lys Asp Tyr His Phe Lys Val Asp Asn Xaa Glu Asn Glu His
 50 55 60

Gln Leu Ser Leu Arg Thr Val Xaa Xaa Gly Ala Gly Ala Lys Asp Glu
 65 70 75 80

1618

Leu His Ile Val Glu Ala Glu Ala Met Asn Tyr Glu Gly Ser Pro Ile
85 90 95

Lys Val Thr Leu Ala Thr Leu Lys Met Ser Val Gln Pro Thr Val Phe
100 105 110

Pro Leu Gly Ala Leu Asn Asn Thr Thr Xaa Xaa Leu Lys Val Glu Xaa
115 120 125

Trp Phe Arg Ala Met Pro Ile Xaa Gly Gln
130 135

<210> 1550

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1550

Thr Leu Ala Phe Phe Leu Ile Pro Cys Ile Gly Ser Pro Ala Cys Pro
1 5 10 15

Thr Met Ser Asp Ala Ala Val Asp Thr Ser Ser Glu Ile Thr Thr Lys
20 25 30

Asp Leu Lys Glu Lys Lys Glu Val Val Glu Glu Ala Glu Met Glu Glu
35 40 45

Thr Pro Cys
50

<210> 1551

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1619

<221> SITE
 <222> (27)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (37)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (63)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (67)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1551
 Lys Ala Xaa Ser Val Xaa Leu Tyr Lys Val Arg Leu Gln Val Pro Val
 1 5 10 15
 Arg Asn Ser Arg Val Asp Pro Arg Val Arg Xaa Gly Gly Glu Gln Val
 20 25 30
 Ser Ser Thr Ile Xaa Gly Leu Ser Gly Pro Pro Ser Arg Arg Gly Pro
 35 40 45
 Phe Pro Leu Ala Trp Val Ile Leu Phe Leu Leu Glu Ala Gln Xaa Gly
 50 55 60
 Pro Trp Xaa Leu Leu Pro Ser Ala His
 65 70

<210> 1552
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (4)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (5)
 <223> Xaa equals any of the naturally occurring L-amino acids

1620

<220>
<221> SITE
<222> (96)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (114)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (115)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (119)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (124)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (129)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1552
Asn Ser Ala Xaa Xaa Glu Leu Leu Thr Gln Pro Gly Asp Trp Thr Leu
1 5 10 15
Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met Thr Ser Glu Glu Lys
20 25 30
Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln Asn Ile Ile Leu Tyr
35 40 45
His Leu His Gln Glu Phe Ser Leu Glu Lys Asp Leu Asn Leu Val Leu
50 55 60
Leu Thr Phe Leu Lys Thr Thr Gln Gly Ser Lys Ile Phe Leu Glu Gly
65 70 75 80

1621

Ser Glu Met Val Thr Leu Leu Val Asn Gly Phe Gly Asn Pro Lys Xaa
 85 90 95

Ser Asp Ile His Gly Pro Pro Xaa Val Val Ile Ser Cys Cys Arg Leu
 100 105 110

Asn Xaa Xaa Phe Pro Ala Xaa Thr Pro Phe Gly Xaa Gly Ser Thr Gly
 115 120 125

Xaa Asp Thr
 130

<210> 1553
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (3)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (55)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (94)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (103)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1553
 Trp Ile Xaa Arg Ala Ala Gly Ile Arg His Glu Val Ala Asp Thr Met
 1 5 10 15

Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu Ser Cys
 20 25 30

Leu Met Leu Leu Ser Gln Val Gln Gly Glu Glu Pro Gln Arg Glu Leu
 35 40 45

Pro Ser Ala Arg Ile Arg Xaa Pro Lys Gly Ser Lys Ala Tyr Gly Ser

1622

50 55 60
His Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser Trp Thr Asp Ala Asp
65 70 75 80
Leu Ala Cys Gln Lys Arg Pro Ser Gly Asn Leu Val Ser Xaa Leu Ser
85 90 95
Gly Ala Glu Gly Ser Phe Xaa Pro Pro Trp
100 105

<210> 1554

<211> 117

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (109)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1554

Ala Thr Phe Pro Arg Glu Trp Leu Cys Asp Arg His Leu Arg Glu Lys
1 5 10 15
Met Phe Ser Ser Val Ala His Leu Ala Arg Ala Asn Pro Phe Asn Thr
20 25 30
Pro His Leu Gln Leu Val His Asp Gly Leu Gly Asp Leu Arg Ser Ser
35 40 45
Ser Pro Gly Pro Thr Gly Gln Pro Arg Arg Pro Arg Asn Leu Ala Ala
50 55 60
Ala Ala Val Glu Glu Gln Tyr Ser Cys Asp Tyr Gly Ser Gly Arg Phe
65 70 75 80
Phe Ile Leu Cys Gly Leu Gly Gly Ile Ile Ser Cys Gly Thr Thr His
85 90 95
Thr Ala Leu Val Pro Leu Asp Leu Val Lys Cys Arg Xaa Arg Phe Val
100 105 110
Phe Ala Cys Trp Thr
115

<210> 1555

1623

<211> 164
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (79)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (86)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (125)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1555

Glu Lys Lys Val Glu Arg Gln Thr Glu Leu Lys Arg Lys Phe Glu Gln
 1 5 10 15

Met Lys Gln Asp Arg Ile Thr Arg Tyr Gln Gly Val Asn Leu Tyr Val
 20 25 30

Lys Asn Leu Asp Asp Gly Ile Asp Asp Glu Arg Leu Arg Lys Glu Phe
 35 40 45

Ser Pro Phe Gly Thr Ile Thr Ser Ala Lys Val Met Met Glu Gly Gly
 50 55 60

Arg Ser Lys Gly Phe Gly Phe Val Cys Phe Ser Ser Pro Glu Xaa Ala
 65 70 75 80

Thr Lys Ala Val Thr Xaa Met Asn Gly Arg Ile Val Ala Thr Lys Pro
 85 90 95

Leu Tyr Val Ala Leu Ala Gln Arg Lys Glu Glu Arg Gln Ala His Leu
 100 105 110

Thr Asn Gln Tyr Met Gln Arg Met Ala Ser Val Arg Xaa Val Pro Asn
 115 120 125

Pro Val Ile Asn Pro Tyr Gln Pro Ala Pro Pro Ser Gly Tyr Phe Met
 130 135 140

Ala Ala Ile Pro Gln Thr Gln Asn Val Leu His Thr Ile Leu Leu Ala
 145 150 155 160

Lys Leu Leu Asn

1624

<210> 1556
<211> 166
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<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1556

Xaa Xaa Leu Thr Leu Thr Xaa Gly Xaa Lys Xaa Xaa Xaa Xaa Thr Ala
1 5 10 15

Val Ala Ala Ala Leu Ala Thr Ser Gly Ser Pro Gly Pro Val Arg Asn
20 25 30

Ser Ala Arg Ala Gly Thr Ser Glu Phe Leu Asn Lys Val Thr Glu Ala
35 40 45

Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile Gly Gln Phe Gly Val
50 55 60

Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys Val Ile Val Thr Ser
65 70 75 80

Lys His Asn Asn Asp Thr Gln His Ile Trp Glu Ser Asp Ser Asn Glu
85 90 95

Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr Leu Gly Arg Gly Thr
100 105 110

Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser Asp Tyr Leu Glu Leu
115 120 125

Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser Gln Phe Ile Asn Phe
130 135 140

Pro Ile Tyr Val Trp Xaa Ser Lys Thr Glu Thr Val Xaa Glu Pro Met
145 150 155 160

Glu Glu Glu Gly Ala Ala
165

<210> 1557

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<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (120)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1557

Xaa Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr Gly
1 5 10 15

His Ser Xaa Xaa Xaa Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp Thr
20 25 30

Gln Gln Val Ala Thr Xaa Asn Pro Ala Leu Ile Ser Arg Ser Val Ile
35 40 45

Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly Lys
50 55 60

Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe Pro Met
65 70 75 80

Pro Xaa Xaa Trp Ile Ser Pro Cys Ile Xaa Pro Val Gly Phe Xaa Lys
85 90 95

1628

Xaa Ala Val Pro Phe Leu Xaa Thr Phe Xaa Xaa Xaa Leu Thr Asn Phe
 100 105 110

Xaa Asn Asn Leu Xaa Phe Tyr Xaa Pro Ala Leu Trp Pro Gln Tyr
 115 120 125

<210> 1558

<211> 109

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (108)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1558

Lys Ala Gly Ala Ala Ala Gly Gly Pro Gly Val Ser Gly Val Cys Val
 1 5 10 15

Cys Lys Ser Arg Tyr Pro Val Cys Gly Ser Asp Gly Thr Thr Tyr Pro
 20 25 30

Ser Gly Cys Gln Leu Arg Ala Ala Ser Gln Arg Ala Glu Ser Arg Gly
 35 40 45

Glu Lys Ala Ile Thr Gln Val Ser Lys Gly Thr Cys Glu Gln Gly Pro
 50 55 60

Ser Ile Val Thr Pro Pro Lys Asp Ile Trp Asn Val Thr Gly Ala Xaa
 65 70 75 80

Val Tyr Leu Ser Cys Glu Val Ile Gly Ile Pro Thr Pro Val Leu Ile
 85 90 95

1629

Trp Asn Lys Val Xaa Arg Gly His Tyr Gly Xaa Xaa Arg
 100 105

<210> 1559

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1559

Gly Leu Arg Gly His Leu Arg Ser Ser Gly Ser Ser Ile Trp Asn Tyr
 1 5 10 15

Ile Lys Phe Arg Lys His Val Ser Arg Tyr Asp Ser Arg Thr Thr Ile
 20 25 30

Phe Ser Pro Glu Gly Arg Leu Tyr Gln Val Glu Tyr Ala Met Glu Ala
 35 40 45

Ile Gly His Ala Gly Thr Cys Leu Gly Ile Leu Ala Asn Asp Gly Val
 50 55 60

Leu Leu Ala Ala Glu Arg Arg Asn Ile His Lys Leu Leu Asp Glu Val
 65 70 75 80

Phe Phe Ser Glu Lys Ile Tyr Lys Leu Asn Glu Asp Met Ala Cys Ser
 85 90 95

Val Ala Gly Ile Thr Phe
 100

<210> 1560

<211> 159

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (146)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1560

Ser Thr His Ala Ser Ala Ala His Pro Ser Thr Leu Thr His Pro Gln
 1 5 10 15

Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr Thr Pro Glu Pro Asp
 20 25 30

1630

Lys Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr
 35 40 45
 Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp
 50 55 60
 Asn Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser
 65 70 75 80
 Val Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala
 85 90 95
 Ile Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met
 100 105 110
 Met Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val
 115 120 125
 Arg Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu
 130 135 140
 Met Xaa Gly Ala Gly Ala Ala Gln Val Pro Gly Arg Gln Glu Gly
 145 150 155

<210> 1561

<211> 155

<212> PRT

<213> Homo sapiens

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<222> (139)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (140)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1561

Arg Ala His Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn
 1 5 10 15

Gly Leu Asn Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys
 20 25 30

Ser Ser Gly Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser
 35 40 45

1631

Tyr Ile Arg Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu
 50 55 60
 Pro Pro Ser Leu Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg
 65 70 75 80
 Val Asp Ala Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly
 85 90 95
 Leu Ser Phe Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn
 100 105 110
 Thr Pro His Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg
 115 120 125
 Val Pro Gly Gly Leu Gln Ser Ile Lys Tyr Xaa Xaa Gly Gly Tyr Leu
 130 135 140
 His Asn Asn His Ile Ser Val Val Gly Ser Lys
 145 150 155

<210> 1562

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1562

Xaa Asn Gln Asn Ser Asn Gly Leu Val Phe Leu Leu Trp Gly Ser Tyr
 1 5 10 15
 Ala Gln Lys Lys Gly Ser Ala Ile Asp Arg Lys Arg His His Val Leu
 20 25 30
 Gln Thr Ala His Pro Ser Pro Leu Ser Val Tyr Arg Gly Phe Phe Gly
 35 40 45
 Cys Arg His Phe Ser Lys Thr Asn Glu Leu Leu Gln Lys Ser Gly Lys
 50 55 60
 Lys Pro Ile Asp Trp Lys Glu Leu
 65 70

1632

<210> 1563
<211> 110
<212> PRT
<213> Homo sapiens

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<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1563
Arg Thr Arg Gly Arg Leu Leu Gly His Leu Lys Glu Thr Trp Gly His
1 5 10 15
Pro Arg Arg Ala Ser Trp Val Val Arg Ser Arg Arg Cys Arg His Cys
20 25 30
Leu Cys Phe Met Arg Lys Met Leu Ala Ala Val Ser Arg Val Leu Ser
35 40 45
Gly Ala Ser Gln Lys Pro Ala Ser Arg Val Leu Val Ala Ser Arg Asn
50 55 60
Phe Ala Asn Asp Ala Thr Phe Glu Ile Xaa Lys Cys Asp Leu His Arg
65 70 75 80
Leu Glu Glu Ala Leu Leu Ser Gln Gln Cys Ser Pro Arg Glu Asp Gly
85 90 95
Leu Lys Tyr Tyr Arg Met Met Xaa Thr Val Pro Glu Trp Asn
100 105 110

<210> 1564
<211> 95
<212> PRT
<213> Homo sapiens

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<222> (61)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (94)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1564
Leu His Ser Xaa Cys Thr Arg Arg Gly Ser Gly Ser Leu Arg Leu Cys
1 5 10 15
Ser Val Ala Arg Val Gly Gln Arg Arg Met Thr Ser Ala Ala Met Ser
20 25 30
Lys Pro His Ser Glu Xaa Gly Thr Ala Phe Ile Gln Thr Gln Xaa Leu
35 40 45
His Ala Xaa Met Ala Asp Thr Phe Leu Glu His Met Xaa Arg Leu Asp
50 55 60

1634

Ile Asp Ser Pro Pro Xaa Thr Gly Arg Asn Thr Gly Ile Ile Cys Thr
65 70 75 80

Ile Gly Pro Ala Ser Arg Ser Xaa Gly Asp Gly Xaa Gly Xaa Asp
85 90 95

<210> 1565

<211> 50

<212> PRT

<213> Homo sapiens

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<222> (29)

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<222> (37)

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<222> (42)

<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (49)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1565

Pro Thr Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
1 5 10 15

Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Xaa Asp Gln Phe
20 25 30

Pro Glu Val Tyr Xaa Pro Thr Val Leu Xaa Glu Leu Tyr Cys Ala His
35 40 45

Xaa Gly
50

<210> 1566

<211> 161

1635

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (155)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1566

Ala Ala Met Phe Asn Ile Arg Asn Ile Gly Lys Thr Leu Val Thr Arg
 1 5 10 15

Thr Gln Gly Thr Lys Ile Ala Ser Asp Gly Leu Lys Gly Arg Val Phe
 20 25 30

Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Val Ala Phe Arg Lys
 35 40 45

Phe Lys Leu Ile Thr Glu Asp Val Gln Gly Lys Asn Cys Leu Thr Asn
 50 55 60

Phe His Gly Met Asp Leu Thr Arg Asp Lys Met Cys Ser Met Val Lys
 65 70 75 80

Lys Trp Gln Thr Met Ile Glu Ala His Val Asp Val Lys Thr Thr Asp
 85 90 95

Gly Tyr Leu Leu Arg Leu Phe Cys Val Gly Phe Thr Lys Lys Arg Asn
 100 105 110

Asn Gln Ile Arg Lys Thr Ser Tyr Ala Gln His Gln Gln Val Arg Gln
 115 120 125

Ile Arg Lys Lys Met Met Glu Ile Met Thr Arg Glu Val Gln Thr Asn
 130 135 140

Asp Leu Lys Glu Val Val Asn Lys Leu Ile Xaa Asp Ala Leu Glu Lys
 145 150 155 160

Thr

<210> 1567

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1567

Pro Ser Leu Lys Gly Thr Lys Ala Gly Ala Pro Pro Arg Cys Gly Arg

1636

1 5 10 15
 Ser Arg Thr Ser Gly Ser Pro Gly Leu Gln Glu Phe Gly Thr Ser Pro
 20 25 30
 Gly Pro Arg Gln Ser Pro Ala Arg Leu Val Ala Met Pro Arg Lys Ile
 35 40 45
 Glu Glu Ile Lys Asp Phe Leu Leu Thr Ala Arg Arg Lys Asp Ala Lys
 50 55 60
 Ser Val Lys Ile Lys Lys Asn Lys Asp Asn Val Lys Phe Lys Val Arg
 65 70 75 80
 Cys Ser Arg Tyr Leu Tyr Thr Leu Val Ile Thr Asp Lys Glu Lys Ala
 85 90 95
 Glu Lys Leu Lys Gln Ser Leu Pro Pro Gly Leu Ala Val Lys Glu Leu
 100 105 110
 Lys

<210> 1568

<211> 48

<212> PRT

<213> Homo sapiens

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<222> (8)

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<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (33)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1568

Gly Cys Asn Tyr Gly Lys Pro Xaa His His Gly Val Asn Gln Leu Lys
 1 5 10 15
 Phe Ala Arg Ser Leu Gln Ser Xaa Ala Glu Glu Arg Ala Gly Arg His
 20 25 30

1637

Xaa Gly Ala Leu Arg Val Leu Asn Ser Tyr Trp Val Gly Glu Asp Ser
 35 40 45

<210> 1569

<211> 120

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (106)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1569

Gly Thr Ser Glu Arg Xaa Glu His Ala Met Lys Ala Ser Gly Thr Leu
 1 5 10 15

Arg Glu Tyr Lys Val Val Gly Arg Cys Leu Pro Thr Pro Lys Cys His
 20 25 30

Thr Pro Pro Leu Tyr Arg Met Arg Ile Phe Ala Pro Asn His Val Val
 35 40 45

Ala Lys Ser Arg Phe Trp Tyr Phe Val Ser Gln Leu Lys Lys Met Lys
 50 55 60

Lys Ser Ser Gly Glu Ile Val Tyr Cys Gly Gln Val Phe Glu Lys Ser
 65 70 75 80

Pro Leu Arg Val Lys Asn Phe Gly Ile Trp Leu Arg Tyr Asp Ser Arg
 85 90 95

Ser Gly Thr His Asn Met Xaa Arg Glu Xaa Arg Asp Leu Thr Asn Ala
 100 105 110

1638

Gly Ala Val Asn Gln Cys Asn Gly
 115 120

<210> 1570
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Xaa equals any of the naturally occurring L-amino acids

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 <221> SITE
 <222> (78)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1570
 Cys Pro Pro Leu Trp Gln Glu Glu Val Trp Leu Asp Pro Asn Glu Thr
 1 5 10 15

Asn Glu Ile Ala Asn Ala Asn Ser Arg Gln Gln Ile Arg Lys Leu Ile
 20 25 30

Lys Asp Gly Leu Ile Ile Arg Lys Pro Val Thr Val His Ser Arg Ala
 35 40 45

Arg Cys Arg Lys Asn Thr Leu Ala Arg Arg Lys Gly Xaa His Met Gly
 50 55 60

Ile Val Ser Gly Lys Val Gln Pro Met Pro Glu Cys Gln Xaa Arg Ser
 65 70 75 80

His Gly Leu Arg Lys
 85

<210> 1571
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (134)
 <223> Xaa equals any of the naturally occurring L-amino acids

1639

<400> 1571

Phe Ala Lys Met Thr Asn Thr Lys Gly Lys Arg Arg Gly Thr Arg Tyr
1 5 10 15

Met Phe Ser Arg Pro Phe Arg Lys His Gly Val Val Pro Leu Ala Thr
20 25 30

Tyr Met Arg Ile Tyr Lys Lys Gly Asp Ile Val Asp Ile Lys Gly Met
35 40 45

Gly Thr Val Gln Lys Gly Met Pro His Lys Cys Tyr His Gly Lys Thr
50 55 60

Gly Arg Val Tyr Asn Val Thr Gln His Ala Val Gly Ile Val Val Asn
65 70 75 80

Lys Gln Val Lys Gly Lys Ile Leu Ala Lys Arg Ile Asn Val Arg Ile
85 90 95

Glu His Ile Lys His Ser Lys Ser Arg Asp Ser Phe Leu Lys Arg Val
100 105 110

Lys Glu Asn Asp Gln Lys Lys Lys Glu Ala Lys Glu Lys Gly Thr Trp
115 120 125

Val Gln Leu Lys Arg Xaa Pro
130 135

<210> 1572

<211> 71

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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 <222> (65)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (69)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1572
 Thr Ala Thr Pro Ala Asn Xaa Xaa Leu Pro Trp Gly Xaa Lys Lys Xaa
 1 5 10 15

Ala Arg Arg Ser Lys Ile Xaa Ser Phe Val Xaa Val Cys Xaa Tyr Asn
 20 25 30

1641

His Leu Met Pro Xaa Arg Tyr Ser Val Xaa Tyr Ser Pro Trp Gly Lys
 35 40 45

Ala Val Arg Ser Leu Gly Cys Leu Pro Xaa Phe Leu Ala Leu Lys Arg
 50 55 60

Xaa Ala Arg Arg Xaa Pro Arg
 65 70

<210> 1573

<211> 68

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (62)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (67)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1573

Ala Ala Ala Lys Gly Ala Ala Ala Met Ser Ala His Leu Gln Trp Met
 1 5 10 15

Val Val Arg Asn Cys Ser Ser Phe Leu Ile Lys Arg Asn Lys Gln Thr
 20 25 30

Tyr Ser Thr Glu Pro Asn Asn Leu Lys Ala Arg Asn Ser Phe Arg Tyr
 35 40 45

Asn Gly Leu Ile His Arg Lys Thr Val Gly Xaa Glu Pro Xaa Ala Asp
 50 55 60

Gly Lys Xaa Val
 65

<210> 1574

<211> 127

1642

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1574

Gly	Arg	Met	Xaa	Pro	Ala	Lys	Lys	Gly	Gly	Glu	Lys	Lys	Lys	Gly	Arg
1				5				10						15	

Ser	Ala	Ile	Asn	Glu	Val	Val	Thr	Arg	Glu	Tyr	Thr	Ile	Asn	Ile	His
		20						25					30		

Lys	Arg	Ile	His	Gly	Val	Gly	Phe	Lys	Lys	Arg	Ala	Pro	Arg	Ala	Leu
		35					40						45		

Lys	Glu	Ile	Arg	Lys	Phe	Ala	Met	Lys	Glu	Met	Gly	Thr	Pro	Asp	Val
	50					55					60				

Arg	Ile	Asp	Thr	Arg	Leu	Asn	Lys	Ala	Val	Trp	Ala	Lys	Gly	Ile	Arg
65					70					75				80	

Asn	Val	Pro	Tyr	Arg	Ile	Arg	Val	Arg	Leu	Ser	Arg	Lys	Arg	Asn	Glu
			85						90					95	

Asp	Glu	Asp	Ser	Pro	Asn	Lys	Leu	Tyr	Thr	Leu	Val	Thr	Tyr	Val	Pro
			100					105					110		

Val	Thr	Thr	Phe	Lys	Asn	Leu	Gln	Thr	Val	Asn	Val	Asp	Glu	Asn	
		115					120						125		

<210> 1575

<211> 115

<212> PRT

<213> Homo sapiens

<220>

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<222> (11)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE
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 <223> Xaa equals any of the naturally occurring L-amino acids

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 <223> Xaa equals any of the naturally occurring L-amino acids

 <400> 1575
 Trp Phe Pro Arg Ala Ala Gly Phe Arg His Xaa Xaa Val Gln Ile Arg
 1 5 10 15

 Ala Xaa Glu Arg Lys Gly Thr Ser Ser Phe Gly Lys Xaa Arg Asn Lys
 20 25 30

 Thr His Thr Leu Cys Arg Arg Xaa Gly Ser Lys Ala Tyr His Leu Gln
 35 40 45

 Xaa Ser Thr Cys Gly Lys Phe Gly Tyr Pro Ala Lys Arg Lys Arg Lys
 50 55 60

 Xaa Asn Trp Ser Ala Lys Ala Lys Arg Arg Asn Thr Thr Gly Thr Gly
 65 70 75 80

 Arg Xaa Arg His Leu Lys Phe Val Tyr Arg Arg Phe Arg His Gly Phe

1644

85 90 95

Xaa Glu Gly Thr Thr Pro Lys Pro Lys Arg Ala Ala Val Ala Ala Ser
100 105 110

Ser Ser Ser
115

<210> 1576
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (114)
<223> Xaa equals any of the naturally occurring E-amino acids

<220>
<221> SITE
<222> (116)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1576
Gly Arg Arg Ser Glu Met Thr Lys Gly Thr Ser Ser Phe Gly Lys Arg
1 5 10 15

Arg Asn Lys Thr His Thr Leu Cys Arg Arg Cys Gly Ser Lys Ala Tyr
20 25 30

His Leu Gln Lys Ser Thr Cys Gly Lys Cys Gly Tyr Pro Ala Lys Arg
35 40 45

Lys Arg Lys Tyr Asn Trp Ser Ala Lys Ala Lys Arg Arg Asn Thr Thr
50 55 60

Gly Thr Gly Arg Met Arg His Leu Lys Ile Val Tyr Arg Arg Phe Arg
65 70 75 80

His Gly Phe Arg Glu Gly Thr Thr Pro Lys Pro Lys Arg Ala Ala Val
85 90 95

Ala Ala Phe Gln Phe Ile Phe Lys Asn Val Asn Xaa Phe Ser His Ala
100 105 110

1645

Ile Xaa Cys Xaa Gly Val Leu Lys Asn
 115 120

<210> 1577

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (57)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (59)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (61)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1577

Gly Ile Val Gly Lys Tyr Gly Thr Arg Tyr Gly Ala Ser Leu Arg Lys
 1 5 10 15

Met Val Lys Lys Ile Glu Ile Ser Gln His Ala Lys Tyr Thr Cys Ser
 20 25 30

Phe Cys Gly Lys Thr Lys Met Lys Arg Arg Ala Val Gly Ile Trp His
 35 40 45

Cys Gly Ser Cys Met Lys Thr Val Xaa Gly Xaa Ala Xaa
 50 55 60

<210> 1578

<211> 74

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals any of the naturally occurring L-amino acids

1646

<220>
<221> SITE
<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (51)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (63)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1578
Glu Leu Gly Lys Gly Lys Met Glu Lys Pro Ser Pro Tyr Pro Ala Gln
1 5 10 15
Gly Pro Cys Ile Ile Tyr Asn Glu Asp Asn Gly Ile Ile Lys Ala Phe
20 25 30
Gln Lys His Pro Trp Asn Tyr Ser Ala Xaa Met Xaa Ser Lys Leu Lys
35 40 45
His Phe Xaa Ser Leu Leu Pro Gly Gly Ala Cys Gly Asp Val Xaa Gly
50 55 60
Ile Gly Xaa Glu Met Ala Phe Pro Gly Xaa
65 70

<210> 1579
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)

1647

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (81)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (87)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (91)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1579

Ser	Xaa	Met	Ala	Cys	Ala	Arg	Pro	Leu	Ile	Ser	Val	Tyr	Ser	Glu	Lys
1				5				10						15	

Gly	Glu	Ser	Ser	Gly	Lys	Asn	Val	Thr	Leu	Pro	Ala	Val	Phe	Lys	Ala
			20					25					30		

Pro	Ile	Arg	Pro	Asp	Ile	Val	Asn	Phe	Val	His	Thr	Asn	Leu	Arg	Lys
		35				40						45			

Asn	Asn	Arg	Gln	Pro	Tyr	Ala	Val	Ser	Glu	Leu	Ala	Gly	His	Gln	Thr
	50					55					60				

Ser	Ala	Glu	Ser	Trp	Gly	Thr	Gly	Arg	Ala	Val	Ala	Arg	Ile	Pro	Arg
65					70					75				80	

Xaa	Arg	Gly	Gly	Gly	Thr	Xaa	Arg	Ser	Gly	Xaa	Gly	Ala	Phe	Gly	Asn
			85						90					95	

Met Cys

<210> 1580

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

1648

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (50)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (64)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (71)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1580
Leu Ser Leu Xaa Gly Lys Lys Lys Lys Arg Leu Arg Val Asp Lys Trp
1 5 10 15
Trp Gly Xaa Arg Lys Glu Leu Ala Thr Val Arg Thr Ile Cys Ser His
20 25 30
Val Gln Asn Met Ile Lys Gly Val Thr Leu Gly Phe Arg Tyr Lys Met
35 40 45
Arg Xaa Val Tyr Ala His Xaa Pro Ile Asn Val Val Ile Gln Glu Xaa
50 55 60
Gly Ser Ile Val Glu Ile Xaa Xaa
65 70

<210> 1581
<211> 153
<212> PRT

1649

<213> Homo sapiens

<400> 1581

Ala Ile Met Gly Arg Met His Ala Pro Gly Lys Gly Leu Ser Gln Ser
1 5 10 15

Ala Leu Pro Tyr Arg Arg Ser Val Pro Thr Trp Leu Lys Leu Thr Ser
20 25 30

Asp Asp Val Lys Glu Gln Ile Tyr Lys Leu Ala Lys Lys Gly Leu Thr
35 40 45

Pro Ser Gln Ile Gly Val Ile Leu Arg Asp Ser His Gly Val Ala Gln
50 55 60

Val Arg Phe Val Thr Gly Asn Lys Ile Leu Arg Ile Leu Lys Ser Lys
65 70 75 80

Gly Leu Ala Pro Asp Leu Pro Glu Asp Leu Tyr His Leu Ile Lys Lys
85 90 95

Ala Val Ala Val Arg Lys His Leu Glu Arg Asn Arg Lys Asp Lys Asp
100 105 110

Ala Lys Phe Arg Leu Ile Leu Ile Glu Ser Arg Ile His Arg Leu Ala
115 120 125

Arg Tyr Tyr Lys Thr Lys Arg Val Leu Pro Pro Asn Trp Lys Tyr Glu
130 135 140

Ser Ser Thr Ala Ser Ala Leu Val Ala
145 150

<210> 1582

<211> 129

<212> PRT

<213> Homo sapiens

<400> 1582

Gly Pro Ala Asn Met Gly Arg Val Arg Thr Lys Thr Val Lys Lys Ala
1 5 10 15

Ala Arg Val Ile Ile Glu Lys Tyr Tyr Thr Arg Leu Gly Asn Asp Phe
20 25 30

His Thr Asn Lys Arg Val Cys Glu Glu Ile Ala Ile Ile Pro Ser Lys
35 40 45

Lys Leu Arg Asn Lys Ile Ala Gly Tyr Val Thr His Leu Met Lys Arg

1650

50 55 60
 Ile Gln Arg Gly Pro Val Arg Gly Ile Ser Ile Lys Leu Gln Glu Glu
 65 70 75 80
 Glu Arg Glu Arg Arg Asp Asn Tyr Val Pro Glu Val Ser Ala Leu Asp
 85 90 95
 Gln Glu Ile Ile Glu Val Asp Pro Asp Thr Lys Glu Met Leu Lys Leu
 100 105 110
 Leu Asp Phe Gly Ser Leu Ser Asn Leu Gln Ser Leu Ser Leu Gln Leu
 115 120 125

Gly

<210> 1583
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1583
 Asn Asn Gly Arg Ala Lys Lys Gly Arg Gly His Val Gln Pro Ile Arg
 1 5 10 15
 Cys Thr Asn Cys Ala Arg Cys Val Pro Lys Asp Lys Ala Ile Lys Lys
 20 25 30
 Phe Val Ile Arg Asn Ile Val Glu Ala Ala Ala Val Arg Asp Ile Ser
 35 40 45
 Glu Ala Ser Val Phe Asp Ala Tyr Val Leu Pro Lys Leu Tyr Val Lys
 50 55 60
 Leu His Tyr Cys Val Thr Val Pro Ser Ile Ala Arg Leu Leu Gly Ile
 65 70 75 80
 Asp Pro Ala Lys Pro Gly Arg Thr Glu His Pro His His Asp Ser Asp
 85 90 95
 Leu Leu Ala Leu His Leu Arg Pro Pro Pro Lys Pro Met
 100 105

<210> 1584
 <211> 119
 <212> PRT

1651

<213> Homo sapiens

<220>

<221> SITE

<222> (60)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (99)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (118)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1584

Val	Gln	Arg	Phe	Ile	Lys	Ile	Asp	Gly	Lys	Val	Arg	Thr	Asp	Ile	Thr
1				5					10					15	

Tyr	Pro	Ala	Gly	Phe	Met	Asp	Val	Ile	Ser	Ile	Asp	Lys	Thr	Gly	Glu
			20					25					30		

Asn	Phe	Arg	Leu	Ile	Tyr	Asp	Thr	Lys	Gly	Arg	Phe	Ala	Val	His	Arg
		35					40						45		

Ile	Thr	Pro	Glu	Glu	Ala	Lys	Tyr	Lys	Leu	Cys	Xaa	Val	Arg	Lys	Ile
	50					55					60				

Phe	Val	Gly	Thr	Lys	Gly	Ile	Pro	His	Leu	Val	Thr	His	Asp	Ala	Arg
65					70					75				80	

Thr	Ile	Arg	Tyr	Pro	Asp	Pro	Leu	Ile	Lys	Val	Asn	Asp	Pro	Phe	Ile
			85						90					95	

Leu	Ile	Xaa	Arg	Leu	Ala	Arg	Leu	Leu	Ile	Ser	Ser	Ile	Ser	Thr	Leu
			100					105					110		

Val	Thr	Cys	Val	Trp	Xaa	Leu
			115			

<210> 1585

<211> 81

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

1652

<222> (14)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (26)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (41)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (53)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (67)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (72)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (74)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1585

Gly Arg Tyr Ala Ala Lys Arg Phe Arg Lys Ala Gln Cys Xaa Ile Val
1 5 10 15

Glu Arg Leu Thr Asn Ser Met Met Met Xaa Gly Arg Asn Asn Gly Lys
20 25 30

Lys Leu Met Thr Val Arg Ile Val Xaa His Ala Phe Glu Ile Ile Arg
35 40 45

Leu Leu Thr Gly Xaa Glu Pro Ser Ala Gly Pro Gly Glu Arg His His
50 55 60

Gln His Xaa Ser Pro Gly Arg Xaa His Xaa His Trp Ala Arg Arg Asp
65 70 75 80

Cys

1653

<210> 1586
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 1586
 Lys Asn Cys Ile Val Leu Ile Asp Ser Thr Pro Tyr Arg Gln Trp Tyr
 1 5 10 15
 Glu Ser His Tyr Ala Leu Pro Leu Gly Arg Lys Lys Gly Ala Lys Leu
 20 25 30
 Thr Pro Glu Glu Glu Ile Leu Asn Lys Lys Arg Ser Lys Lys Ile
 35 40 45
 Gln Lys Lys Tyr Asp Glu Arg Lys Lys Asn Ala Lys Ile Ser Ser Leu
 50 55 60
 Leu Glu Glu Gln Phe Gln Gln Gly Lys Leu Leu Ala Cys Ile Ala Ser
 65 70 75 80
 Arg Pro Gly Gln Cys Gly Arg Ala Asp Gly Tyr Val Leu Glu Gly Lys
 85 90 95
 Glu Leu Glu Phe Tyr Leu Arg Lys Ile Lys Ala Arg Lys Gly Lys
 100 105 110

<210> 1587
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (105)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (117)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1587
 Arg Thr Met Pro Gly Val Thr Val Lys Asp Val Asn Gln Gln Glu Phe
 1 5 10 15

1654

Val Arg Ala Leu Ala Ala Phe Leu Lys Lys Ser Gly Lys Leu Lys Val
 20 25 30
 Pro Glu Trp Val Asp Thr Val Lys Leu Ala Lys His Lys Glu Leu Ala
 35 40 45
 Pro Tyr Asp Glu Asn Trp Phe Tyr Thr Arg Ala Ala Ser Thr Ala Arg
 50 55 60
 His Leu Tyr Leu Arg Gly Gly Ala Gly Val Gly Ser Met Thr Lys Ile
 65 70 75 80
 Tyr Gly Gly Arg Gln Arg Asn Gly Val Met Pro Ser His Phe Ser Arg
 85 90 95
 Gly Ser Lys Ser Val Ala Arg Arg Xaa Leu Gln Ala Leu Gly Gly Ala
 100 105 110
 Glu Asn Gly Gly Xaa Gly Pro Arg Trp Arg Pro Ala Asn
 115 120 125

<210> 1588

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (29)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (33)

1655

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (35)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1588

Cys Met Leu Xaa Leu Val Leu Xaa Leu Leu Ser Ser Ser Ser Ala Glu
1 5 10 15

Glu Tyr Xaa Gly Leu Ser Ala Asn Gln Cys Ala Val Xaa Ala Lys Asp
20 25 30

Xaa Val Xaa Cys Gly Tyr
35

<210> 1589

<211> 55

<212> PRT

<213> Homo sapiens

<400> 1589

Gly Thr Ala Thr Gln Gly Leu Ser Pro Val His Thr Pro Gly Asp Gly
1 5 10 15

Arg Leu His Lys Ala Val Ser Val Gly Pro Arg Val His Ile Ile Glu
20 25 30

Glu Leu Gln Ile Phe Ser Ser Gly Gln Pro Val Ala Glu Ser Ala Pro
35 40 45

Gly Thr Pro Thr Gly Gly Leu
50 55

<210> 1590

<211> 92

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (15)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1590

Leu Glu Asp Gly Phe Gly Glu His Pro Phe Tyr His Cys Leu Xaa Ala

1656

1 5 10 15
Glu Val Pro Lys Glu His Trp Thr Pro Glu Gly His Ser Ile Val Gly
 20 25 30
Phe Ala Met Tyr Tyr Phe Thr Tyr Asp Pro Trp Ile Gly Lys Leu Leu
 35 40 45
Tyr Leu Glu Asp Phe Phe Val Met Ser Asp Tyr Arg Gly Phe Gly Ile
 50 55 60
Gly Ser Glu Ile Leu Lys Asn Leu Ser Gln Val Ala Met Arg Cys Arg
 65 70 75 80
Cys Ser Ser Met His Phe Phe Gly Ser Arg Met Glu
 85 90

<210> 1591

<211> 139

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (56)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1657

<222> (114)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (117)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (125)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (133)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1591

Xaa	Gly	Gly	Phe	Xaa	Ile	Thr	Xaa	Gly	Xaa	Asp	Glu	Gly	Lys	Leu	Val
1				5					10					15	

Thr	Pro	Ala	Gly	Asp	Arg	Ser	Gly	Ile	Pro	Gly	Ser	Thr	His	Ala	Ser
			20					25					30		

Gly	Arg	Asp	Val	Ser	Gln	Lys	Val	Leu	Arg	Ser	Gln	Thr	Trp	Val	Pro
		35					40					45			

Arg	Leu	Pro	Ala	Ser	Glu	Ala	Xaa	Ser	Arg	His	Arg	Gly	Lys	Val	Lys
	50						55					60			

Ser	Phe	Pro	Lys	Asp	Asp	Pro	Ser	Lys	Pro	Val	His	Leu	Thr	Ala	Phe
	65				70					75					80

Leu	Gly	Tyr	Lys	Ala	Gly	Met	Thr	His	Ile	Val	Arg	Glu	Val	Asp	Arg
			85						90					95	

Pro	Gly	Ser	Lys	Val	Asn	Lys	Lys	Glu	Gly	Gly	Gly	Gly	Cys	Asp	His
			100					105					110		

Cys	Xaa	Asp	Thr	Xaa	His	Gly	Gly	Leu	Trp	Ala	Leu	Xaa	Ala	Thr	Leu
		115						120				125			

Glu	Asn	Pro	Arg	Xaa	Leu	Arg	Asn	Phe	Lys	Asn
	130						135			

<210> 1592

<211> 42

<212> PRT

1658

<213> Homo sapiens

<400> 1592

Ala Glu His Gly Asp Gln Asp Tyr Ile Trp His Cys Ile Asp Leu Phe
1 5 10 15

Leu Asp Phe Ile Thr Val Phe Arg Lys Leu Met Met Ile Leu Ala Met
20 25 30

Asn Glu Lys Asp Lys Lys Lys Glu Lys Lys
35 40

<210> 1593

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (25)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (31)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (33)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (47)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (56)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1659

<222> (60)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (62)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (79)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1593

Trp	Ile	Pro	Arg	Ala	Ala	Gly	Ser	Leu	Ser	Leu	Ala	Gln	Arg	Arg	Gly
1				5				10						15	

Xaa	Thr	Lys	Thr	Tyr	Thr	Val	Gly	Xaa	Glu	Glu	Cys	Thr	Val	Xaa	Pro
			20					25					30		

Xaa	Leu	Ser	Ile	Pro	Cys	Lys	Leu	Gln	Ser	Gly	Thr	His	Cys	Xaa	Trp
		35					40					45			

Thr	Asp	Gln	Leu	Leu	Gln	Gly	Xaa	Glu	Lys	Gly	Xaa	Gln	Xaa	Arg	His
	50					55						60			

Leu	Ala	Cys	Leu	Pro	Arg	Glu	Pro	Gly	Leu	Gly	Thr	Trp	Gln	Xaa	Leu
65					70					75					80

Arg	Ser	Gln	Ile	Ala
				85

<210> 1594

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (80)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (107)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1660

<222> (122)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (136)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (151)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (152)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (160)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1594

Ala	Ala	Arg	Gly	Ala	Gln	Arg	Asp	Thr	Arg	Glu	Pro	Thr	Met	Ala	Pro
1				5					10					15	

Phe	Glu	Pro	Leu	Ala	Ser	Gly	Ile	Leu	Leu	Leu	Leu	Trp	Leu	Ile	Ala
			20					25					30		

Pro	Ser	Arg	Ala	Cys	Thr	Cys	Val	Pro	Pro	His	Pro	Gln	Thr	Ala	Phe
		35					40					45			

Cys	Asn	Ser	Asp	Leu	Val	Ile	Arg	Ala	Lys	Phe	Val	Gly	Thr	Pro	Glu
	50						55					60			

Val	Asn	Gln	Thr	Thr	Leu	Tyr	Gln	Arg	Tyr	Glu	Ile	Lys	Met	Thr	Xaa
65					70					75					80

Met	Tyr	Lys	Gly	Phe	Gln	Ala	Leu	Gly	Asp	Ala	Ala	Asp	Ile	Arg	Phe
				85					90					95	

Val	Tyr	Thr	Pro	Ala	Met	Glu	Ser	Val	Cys	Xaa	Tyr	Phe	His	Arg	Ser
			100					105						110	

His	Asn	Arg	Ser	Glu	Glu	Phe	Leu	Ile	Xaa	Gly	Lys	Leu	Gln	Asp	Gly
	115						120						125		

Leu	Leu	His	Ile	Thr	Thr	Cys	Xaa	Phe	Val	Ala	Pro	Trp	Asn	Ser	Leu
						130		135				140			

1661

Ser Leu Ala Gln Arg Arg Xaa Xaa Thr Lys Thr Tyr Thr Val Gly Xaa
 145 150 155 160

Glu Glu Met His Lys Cys Phe Pro Val Tyr Pro Ser Pro Ala Asn Cys
 165 170 175

Arg Val Gly Thr His Cys Leu
 180

<210> 1595
 <211> 153
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (143)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (151)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1595
 Ser Thr Cys Pro Asp Glu Gln Cys Val Asn Ser Pro Gly Ser Tyr Gln
 1 5 10 15

Cys Val Pro Cys Thr Glu Gly Phe Arg Gly Trp Asn Gly Gln Cys Leu
 20 25 30

Asp Val Asp Glu Cys Leu Glu Pro Asn Val Cys Ala Asn Gly Asp Cys
 35 40 45

Ser Asn Leu Glu Gly Ser Tyr Met Cys Ser Cys His Lys Gly Tyr Thr
 50 55 60

Arg Thr Pro Asp His Lys His Cys Arg Asp Ile Asp Glu Cys Gln Gln
 65 70 75 80

Gly Asn Leu Cys Val Asn Gly Gln Cys Lys Asn Thr Glu Gly Ser Phe
 85 90 95

Arg Cys Thr Val Asp Arg Gly Tyr Gln Leu Ser Ala Ala Lys Asp Gln
 100 105 110

Phe Glu Asp Ile Asp Glu Cys His Thr Val Ile Ser Val Ala His Gly
 115 120 125

1662

His Ala Arg Thr Leu Lys Leu Phe Ser Met Cys Phe Leu Thr Xaa Val
130 135 140

Thr Glu His Leu Gly Leu Xaa Thr Leu
145 150

<210> 1596

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (102)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1596

Leu Gly Ser Ser Ala Met Ala Pro Ser Arg Lys Phe Phe Val Gly Gly
1 5 10 15

Asn Trp Lys Met Asn Gly Arg Lys Gln Ser Leu Gly Glu Leu Ile Gly
20 25 30

Thr Leu Asn Ala Ala Lys Val Pro Ala Asp Thr Glu Val Val Cys Ala
35 40 45

Pro Pro Thr Ala Tyr Ile Asp Phe Ala Arg Gln Lys Leu Asp Pro Lys
50 55 60

Ile Ala Val Ala Ala Gln Asn Cys Tyr Lys Val Thr Asn Gly Ala Phe
65 70 75 80

Thr Gly Glu Ile Ser Pro Gly Met Ile Lys Asp Cys Gly Pro Arg Gly
85 90 95

Trp Ser Trp Gly Thr Xaa Arg Glu Ala Cys Leu Trp Gly Ile Arg
100 105 110

<210> 1597

<211> 82

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

1663

<220>
 <221> SITE
 <222> (71)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (79)
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<220>
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 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1597
 Ile Phe Glu Asp Ser Asp Ser Leu Arg Leu Arg Arg Asp Val Leu Pro
 1 5 10 15
 Ala Ala Xaa Val Gln Ala Ala Leu Pro Ala Thr Ser Cys Val Pro His
 20 25 30
 Ala Lys Val Pro Lys Ser His Val His Pro Arg Ser Ala Leu Ser Leu
 35 40 45
 Thr Cys Leu Leu Leu Val His Leu Ser Ile Ala His Leu His Leu Ala
 50 55 60
 Ser Ile Asn Ala Leu Leu Xaa Gln Pro Tyr His Pro Gly Ser Xaa Xaa
 65 70 75 80
 Ser Pro

<210> 1598
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
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<220>
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 <223> Xaa equals any of the naturally occurring L-amino acids

1664

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 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (49)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1598
 Xaa Lys Xaa Gly Arg Asn Lys Ala Arg Pro Leu Thr Ser Leu Arg Xaa
 1 5 10 15
 Thr Phe Xaa Ala Thr Phe Cys Pro Val Xaa Gly Thr Tyr Ile Leu Asn
 20 25 30
 Asp Cys Pro Xaa Thr His Ser Gly Ile Phe Phe Phe Leu Lys Xaa Xaa
 35 40 45
 Xaa Lys Ala Phe
 50

1665

<210> 1599
<211> 32
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1599
Ala Phe Asn Xaa Ser Tyr Arg Lys Xaa Val Xaa Ala Val Arg Xaa Glu
1 5 10 15
Phe Arg Val Thr Gln Arg Pro Gly Leu Xaa Xaa Leu Gly Leu Glu Phe
20 25 30

<210> 1600
<211> 19
<212> PRT
<213> Homo sapiens

1666

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 <222> (12)
 <223> Xaa equals any of the naturally occurring L-amino acids

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 <222> (13)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (15)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1600
 Ala Arg Gly Phe Phe Phe Phe Phe Phe Phe Xaa Xaa Phe Xaa Phe
 1 5 10 15
 Phe Lys Lys

<210> 1601
 <211> 22
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (20)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (22)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1601
 Arg Xaa Asn Arg Val Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
 1 5 10 15
 Phe Phe Phe Xaa Pro Xaa
 20

1667

<210> 1602
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (98)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1602
Asp Phe Gly Arg Ser Phe Leu Leu Trp Phe Ser Leu Phe Phe Leu Pro
1 5 10 15
Phe Tyr Ser Ala Arg Ile Ser Gly Gly Leu Met Val Gly Tyr Asn Val
20 25 30
Ser Val Leu Leu Gln Ile Gly Leu Lys Gly Tyr Pro Ala Glu Ser Pro
35 40 45
Ala Phe Leu Ser Ser Ile Tyr Phe Ser Gly Lys Leu Phe Phe Leu Phe
50 55 60
Phe Phe Lys Val Asn Leu Cys Ile Glu Leu Asn Cys Ile Ser Val Phe
65 70 75 80
Pro Ala Tyr Val Tyr Ile Ile Pro Met Ile Pro Asn Ser Tyr Leu Tyr
85 90 95
Phe Xaa Thr Asn Ser Gln Ser Glu
100

<210> 1603
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (30)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (45)
<223> Xaa equals any of the naturally occurring L-amino acids

1668

<220>
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 <222> (62)
 <223> Xaa equals any of the naturally occurring L-amino acids

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 <222> (63)
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 <222> (73)
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 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (81)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1603
 Phe Leu Met Leu Ser Phe Met Gly Ile Val Thr Phe Leu Phe Ser Lys
 1 5 10 15
 Ser His Cys Trp Asn His Gln Gly Cys Gly Met Ser Leu Xaa Val Leu
 20 25 30
 Phe Met Gln Val Thr Val Thr Phe Ala Ile Met Ala Xaa Phe Glu Thr
 35 40 45
 Leu Ile Met Cys Phe Tyr Phe Phe Ile Pro Val Lys Met Xaa Xaa Lys
 50 55 60
 Arg Lys Lys Val Val Ile Ala Pro Xaa Ile Ser Gly Ser Lys Leu Xaa
 65 70 75 80
 Xaa Lys Phe Pro Lys Lys
 85

<210> 1604
 <211> 34
 <212> PRT
 <213> Homo sapiens

1669

<400> 1604

Ser Asp Glu Ile Ile Tyr Asn Phe Ile Val Thr Ser Ser Val Phe Pro
1 5 10 15

Phe Glu Arg Cys Met Asn Ser Leu His Phe Tyr Ser Asn Val Leu Ser
20 25 30

Val Asp

<210> 1605

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (30)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (37)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (43)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (45)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (48)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1605

Leu Leu Val Trp Ser Glu Tyr Asn Thr Ser Ile Ile Thr Tyr Asn Ser
1 5 10 15

1670

Xaa Pro Gly Thr Gly Gly Tyr Lys Tyr Asn Phe Phe Lys Xaa Asn Ser
20 25 30

Trp Leu Ser Thr Xaa Leu Gln Val Pro Leu Xaa Gly Xaa Leu Trp Xaa
35 40 45

Ile Thr Leu Gly Lys
50

<210> 1606

<211> 32

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (15)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

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<222> (20)

<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (22)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (23)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (28)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (31)

<223> Xaa equals any of the naturally occurring L-amino acids

1671

<400> 1606

Asp Ala Trp Ala Asp Ala Trp Gly Lys Val Ser Ser Ser Leu Xaa Ser
1 5 10 15

Xaa Ile Cys Xaa Leu Xaa Xaa Arg Lys Val Arg Xaa Gly Gln Xaa Met
20 25 30

<210> 1607

<211> 31

<212> PRT

<213> Homo sapiens

<220>

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<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (28)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (30)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1607

Leu Ile Met Asp Thr Ile Leu Asn Lys Xaa Ile Gln Val Lys Pro Val
1 5 10 15

Lys Glu Lys Glu Ile Lys Val Ser Gly Ser Cys Xaa Ser Xaa Val
20 25 30

<210> 1608

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (24)

<223> Xaa equals any of the naturally occurring L-amino acids

1672

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<222> (34)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (38)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (97)
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<222> (101)
<223> Xaa equals any of the naturally occurring L-amino acids

1673

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 <222> (102)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (103)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (104)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (107)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1608
 Asp Pro Gln Gly Ile Arg His Pro His Ile Val Gln Leu Lys Asp Phe
 1 5 10 15
 Gln Cys Glu Leu Gly Ala Gly Xaa Leu Pro Lys Gly Val Glu Lys Asp
 20 25 30
 Ile Xaa Phe Arg Pro Xaa Leu Cys Leu Leu Lys Gln Gln Leu Gly Thr
 35 40 45
 Val Glu Pro Ile Asn Leu Xaa Phe Asn Pro Leu Gly Ser Phe Phe Ala
 50 55 60
 Gly Gln Gly Gly Gly Arg Lys Pro Trp Xaa Phe Xaa Xaa Phe Xaa Ser
 65 70 75 80
 Gln Leu Asn Pro Gly Gln Xaa Asn Phe Leu Gly Pro Leu Lys Glu Lys
 85 90 95
 Xaa Phe Gly Pro Xaa Xaa Xaa Xaa Leu Ser Xaa
 100 105

<210> 1609
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE

1674

<222> (51)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1609

Arg Gln Thr Ser Thr Ala Lys Leu Gln Lys Gly Gly Phe Cys Ser Arg
1 5 10 15

Arg Lys Glu Asp Val Tyr Leu Gln Gly Ala Lys Gln Gly Glu Leu Gly
20 25 30

Ser Ser Cys Leu Arg Pro Asn Leu His Asp Asp Leu Gln Ala Arg Val
35 40 45

Phe Lys Xaa Ser Gly Lys Phe Pro Gly Lys Pro Glu Val Lys Gly Gln
50 55 60

Asn Cys Lys Ser Val Glu Ile Gly
65 70

<210> 1610

<211> 77

<212> PRT

<213> Homo sapiens

<400> 1610

Leu Tyr Arg Gly Ser Val Gln Gly Arg Val Glu Leu Leu Ser Glu Gly
1 5 10 15

Ser Leu Gly Gly Pro Leu Arg Pro Gly Pro Asp Pro Val Leu Gln Gly
20 25 30

Leu Ser Gln Gly Gln Val His Gly Glu Thr Met Gly Cys Leu Ser Asp
35 40 45

Thr Asp Leu Ala Leu Leu Ser Pro Pro Ile Arg Leu Ser Phe Leu Cys
50 55 60

Ser Glu Cys Leu Gln Gly Leu Asp Pro Gly Lys Glu Phe
65 70 75

<210> 1611

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

1675

<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (25)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (38)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (58)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (66)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (71)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1611
Glu Asn Leu Pro Ser Gln Xaa Ala Pro Ala Gly Leu Pro Lys Xaa Xaa
1 5 10 15

1676

Gln Pro Cys Leu Tyr Phe Tyr Gly Xaa Asn Gly His Lys Ile Ile Ile
20 25 30

Asn Leu Thr Lys Thr Xaa Leu Phe Ser Xaa Phe Leu Glu Leu Ser Trp
35 40 45

Ser Phe Leu Ile Leu Xaa Phe Gly Asn Xaa Arg Leu Phe Leu Lys Cys
50 55 60

Phe Xaa Asp Val Lys Ile Xaa Tyr
65 70

<210> 1612

<211> 63

<212> PRT

<213> Homo sapiens

<220>

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<222> (11)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (16)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (25)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (34)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (47)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (52)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1677

<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1612
Arg Glu Ser Glu Met Leu Cys Asn Leu Leu Xaa Gln Leu Lys His Xaa
1 5 10 15
Met Leu Arg Gly Arg Asn Tyr Lys Xaa Cys Ser Asn Leu Phe Trp Val
20 25 30
Ile Xaa Met Tyr Leu Trp Val Gln Ala Leu Phe Gly Gly Phe Xaa Phe
35 40 45
Gln Arg Asn Xaa Xaa Lys Val Xaa Leu Leu Ile Lys Lys Arg Lys
50 55 60

<210> 1613
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (12)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1613
Lys Ser Xaa Ser Xaa Thr Ala Gly Asp Arg Xaa Xaa Thr Ser Gly Ser

1678

1 5 10 15

Pro Gly Leu Gln Glu Phe
20

<210> 1614

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (14)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (15)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (20)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (51)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (63)

<223> Xaa equals any of the naturally occurring L-amino acids

1679

<220>
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 <222> (75)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (78)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (83)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (85)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1614
 Asp Gly Gly Phe Xaa Xaa Phe Phe Phe Phe Phe Phe Xaa Xaa Phe
 1 5 10 15
 Phe Phe Tyr Xaa Trp Val Ile Ser Thr Cys Phe Ile Pro Ala Ile Lys
 20 25 30
 Ile Ile Lys Asn Ile Ser Asn Tyr Tyr Thr His Thr Lys Xaa Val Gln
 35 40 45
 Ser Leu Xaa Leu Pro Pro Thr Arg Gly Lys Asn Cys Phe Xaa Leu
 50 55 60
 Trp Glu Val Val Ser Glu Thr Arg Gly Gln Xaa Thr Gln Xaa Arg Leu
 65 70 75 80
 Gly Gly Xaa Arg Xaa
 85

<210> 1615
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 1615
 Tyr Ala Val Pro Cys Ser Gly Ile Gln Gly Arg Phe Ser Pro Leu Ser
 1 5 10 15

1680

Phe Leu Leu Ala Gly Asp Ser Cys Thr Cys Ala Gly Ser Cys Lys Cys
20 25 30

Lys Glu Cys Lys Cys Thr Ser Cys Lys Lys Ser Lys Trp Asp Pro Leu
35 40 45

Phe Pro Leu Pro Leu Pro Val Leu Gln Pro Val Pro Ser Ser Pro Ser
50 55 60

Ser Gly Glu Leu Lys Gln Val Trp Gly Cys Pro Ile Ala Pro Gly Asn
65 70 75 80

Trp Trp Pro Pro Gln
85

<210> 1616

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (25)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (26)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (28)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (29)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1616

Ala Glu Gly Asn Ile Arg Xaa Ala Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

1681

Lys Lys Lys Lys Lys Lys Lys Lys Xaa Xaa Lys Xaa Xaa
 20 25

<210> 1617
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (4)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (11)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (20)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (26)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (36)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1617
 Gly Pro Ala Xaa Trp Arg Glu Thr Pro Pro Xaa Leu Tyr Lys Glu Phe
 1 5 10 15

Pro Gly Val Xaa Gly Ser Phe Ser Leu Xaa Ser Glu Trp Gly Ala Gln
 20 25 30

Ile Trp Ala Xaa Cys
 35

<210> 1618
 <211> 22
 <212> PRT
 <213> Homo sapiens

1682

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1618
Gly Xaa Gly Phe Xaa Pro Ser Pro Ser Cys Phe Pro Gln Cys Leu Lys
1 5 10 15
Xaa Leu Asp Gly Leu Xaa
20

<210> 1619
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1619
Gln Ser Ile Ser Leu Asn Arg Asp Gly Val Glu Glu Leu Lys Val Gly
1 5 10 15
Ile Cys Ser Leu Met Thr Thr Met Phe Thr Ile Cys Cys Gly Leu Val
20 25 30
Gly Ala Leu Arg Gln Glu Asn His Val Glu Pro Thr Gly Ser Arg Pro
35 40 45
Ala Trp Glu Thr
50

<210> 1620

1683

<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (28)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1620
Pro Thr Glu Gln Val Thr Leu Gly Ile Thr Ala Gln Ser Tyr Ser Arg
1 5 10 15
Val His Ile Asn Asn Arg Val Tyr Asp Leu Asp Xaa Gly Ser Gly His
20 25 30
Pro Asp Xaa Ala Ala Ala Ile Lys Gly Ser Phe Val Gln Arg Leu Lys
35 40 45
Ser Tyr Val Ile
50

<210> 1621
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (87)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (112)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1621
Leu Phe Pro Ala Pro Ala Pro Pro Ala Pro Ala Phe Ala Pro Pro

1684

1 5 10 15
 Pro Lys Val Pro Ser Pro Glu Arg Ser Ala Pro Arg Val Pro Leu Pro
 20 25 30
 Ser Pro Gln Pro Ser Tyr Pro Phe Arg Pro Ala Ala Ser Gly Gly Thr
 35 40 45
 Pro Pro Pro Ala Cys Leu Pro Pro Ala Gln Pro Cys Gln Val Pro Pro
 50 55 60
 Ala Met Asn Leu Phe Arg Phe Leu Gly Lys Leu Ser Gln Leu Leu Ala
 65 70 75 80
 Ile Ile Leu Leu Leu Leu Xaa Ile Trp Asn Ser Arg Ser Cys Ala Glu
 85 90 95
 Ile Gln Glu Lys Asn Ser Pro Val Trp Cys Gly Xaa Phe Asn Gly Xaa
 100 105 110

Ile

<210> 1622

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1622

Val Phe Lys Thr Met Xaa Gln Val Ser Asn Asp Glu Ile Lys His Leu
 1 5 10 15

Phe Val Leu Tyr Gln
 20

<210> 1623

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

1685

<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<400> 1623
Leu Arg Thr Ser Cys Phe Xaa Leu Asn Xaa Met Ile His Phe Ile Lys
1 5 10 15
Val Pro Val Ile Lys Tyr Xaa Val Lys Tyr Leu Leu Xaa Trp Thr Ile
20 25 30
Xaa Cys Lys Leu Pro Phe Xaa Xaa
35 40

<210> 1624
<211> 95
<212> PRT
<213> Homo sapiens

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1686

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 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1624
 Ile His Pro Xaa Leu Ala Ser Gln Val Ala Gly His Tyr Arg Arg Glu
 1 5 10 15
 His Ser Arg Pro Arg Leu Lys Xaa Ala Tyr Ser Lys Lys Gln Phe Gln
 20 25 30

Phe	Leu	Ser	Lys	Leu	Cys	Xaa	Xaa	Arg	Gly	Ser	Thr	Asp	Phe	Leu	Gly
		35					40					45			
Pro	Val	Asn	Leu	Asn	Gln	Ser	Leu	Arg	Phe	Cys	Gln	Glu	Ser	Ser	Leu
	50					55					60				
Leu	Ser	Lys	Trp	Val	Phe	Pro	Asn	Gly	His	Asn	Gly	Lys	Xaa	Xaa	Arg
65					70					75					80
Gly	Xaa	Asn	Ile	Lys	Lys	Xaa	Lys	Lys	Asn	Leu	Gly	Gly	Gly	Xaa	
				85					90					95	

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<210> 1625
<211> 40
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<400> 1625
Ala Arg Ala Thr Met Ala Leu Trp Thr Xaa Val Ser Phe Ala Glu Xaa
 1             5             10             15
Leu Glu Arg Gly Ser Asp Glu Lys Val Xaa Leu Lys Arg Leu Ala Arg
      20             25             30
Leu Leu Gly Leu Ile Thr Ala Pro
      35             40

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<210> 1626
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1688

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<400> 1626
Ala Arg Ala Gly Ile Val Pro Xaa His Ser Ser Leu Gly Asp Arg Ala
1 5 10 15
Arg Leu His Leu Lys Lys Lys Lys Lys Xaa
20 25

<210> 1627
<211> 171
<212> PRT
<213> Homo sapiens

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<400> 1627

Glu	Leu	Gln	Ala	Ser	Glu	Asn	Gln	Pro	Cys	Ser	Arg	His	Ala	Arg	Pro
1				5				10						15	

Arg	Leu	Pro	Ser	Ser	Leu	Phe	Pro	Leu	Pro	Ala	Gln	Pro	Ser	Leu	Pro
			20					25						30	

Ser	Ser	Ala	Gly	Lys	Ala	Gly	Thr	His	Ser	Gly	Cys	Leu	Pro	Pro	Gly
		35					40					45			

Gly	Lys	Glu	Arg	Glu	Gly	Gly	Trp	Val	Gly	Xaa	Gly	Leu	Pro	Pro	Gly
	50					55						60			

Asn	Val	Thr	Leu	Pro	Gly	Pro	Arg	Ile	Ala	Pro	Gly	Pro	Lys	Pro	Lys
65					70					75					80

Ala	Gln	Pro	Gly	Thr	Lys	Leu	Arg	Xaa	Ser	Ala	Gly	Arg	Ser	Tyr	Phe
				85					90					95	

Tyr	Leu	Pro	Pro	Pro	Leu	Leu	Val	Pro	Pro	Pro	Gly	Arg	Leu	Ala	Ala
		100						105					110		

Glu	Ser	Asp	Thr	Gly	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Glu	Pro	Trp	Tyr	Pro
		115					120						125		

Ile	Leu	Gly	Pro	Gly	Pro	Xaa	Leu	Gly	Pro	Asn	Pro	Ser	Ser	Val	Asp
	130					135								140	

Asn	Gly	Val	Trp	Asn	Lys	Cys	Cys	Leu	Ser	Xaa	Gln	Gln	Lys	Lys	Lys
145					150					155					160

Lys	Arg	Gly	Gly	Arg	Phe	Arg	Gly	Phe	Lys	Ala
					165				170	

1690

<210> 1628
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<400> 1628
Arg Pro Ala Arg Ser Pro Ala Glu Val Gly Ser Arg Gly Leu Ser Ser
1 5 10 15
Pro Pro Arg Ala His His Arg Pro Val Ser Pro Ala Ala Pro Gly Arg
20 25 30
Trp Ser Thr Ser Ala Arg Val Arg Thr Arg Lys Met Val Asn Tyr Ala
35 40 45
Trp Ala Gly Arg Xaa Arg Arg Lys Leu Trp Trp Arg Ser Val Ala Val
50 55 60
Leu Thr Cys Lys Ser Val Val Arg Pro Gly Tyr Arg Gly Glu Arg Leu
65 70 75 80
Asn Arg Thr Ile Leu Val Ser Trp Phe Pro Ser Glu Xaa Phe Pro Gln
85 90 95

1691

Asp Lys Leu Gly Ala Leu Ala Arg Pro Arg Arg Asn Pro Xaa Xaa Gly
100 105 110

Ile Phe Ile Arg Xaa Lys Arg Ile
115 120

<210> 1629

<211> 86

<212> PRT

<213> Homo sapiens

<400> 1629

Asn Leu Val Pro Gly Ser Ser Ala Thr Tyr Ile Ser Leu Ser Ser Cys
1 5 10 15

Cys Phe Val Lys Arg Lys Arg Lys Lys Lys Pro Lys Leu Val Arg Val
20 25 30

Ile Ser Asn Tyr Leu Ile Phe Cys Arg Ser Val Ile Lys Asn Leu Val
35 40 45

Ile Pro Ser Thr Ser Tyr Cys Glu Glu Gln Thr Leu Gly Pro Thr Leu
50 55 60

Lys Ser Pro Leu Val Thr His Ser His Pro Pro Gly Ser Cys Leu Pro
65 70 75 80

Gly Arg Gly Cys Arg Lys
85

<210> 1630

<211> 35

<212> PRT

<213> Homo sapiens

<220>

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1630

Leu Lys Lys Lys Phe Pro Glu Glu Glu Lys Lys Thr Thr Lys Asn Lys
1 5 10 15

Thr Leu Lys Val Asp Ile Leu Cys Gly Xaa Thr Phe Glu Leu Asn Ser
20 25 30

1692

Glu Phe Phe
35

<210> 1631
<211> 40
<212> PRT
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<222> (31)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1631
His Glu Gln Pro Thr Ala Ala Cys Ile Cys Ile Xaa Arg Gln Val Pro
1 5 10 15

Pro Val Pro Ala Ala Arg Xaa Pro Gln Ser Arg Thr Xaa Ser Xaa Gln
20 25 30

Ala Lys Leu Ala Leu Thr Met Pro
35 40

<210> 1632
<211> 97
<212> PRT
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<222> (95)

<223> Xaa equals any of the naturally occurring L-amino acids

1694

<400> 1632

Xaa Ser Gly Ser Pro Gly Pro Ala Gly Pro Arg Gly Pro Val Gly Pro
1 5 10 15

Xaa Gly Pro Pro Gly Lys Asp Gly Thr Xaa Gly His Pro Gly Ala Ile
20 25 30

Gly Pro Pro Gly Pro Arg Gly Asn Xaa Gly Glu Xaa Gly Ser Xaa Gly
35 40 45

Ser Pro Gly Pro Xaa Arg Ala Thr Arg Ala Leu Leu Xaa Pro Pro Gly
50 55 60

Ala Pro Gly Pro Cys Cys Gly Gly Val Xaa Ala Ala Ala Ile Ala Gly
65 70 75 80

Ile Gly Arg Leu Lys Lys Leu Gly Arg Phe Xaa Pro Arg Val Xaa Trp
85 90 95

Gly

<210> 1633

<211> 43

<212> PRT

<213> Homo sapiens

<220>

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1633

Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 1 5 10 15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Arg Pro Phe Xaa Arg
 20 25 30

Ile Gln Xaa Tyr Val Xaa Xaa Xaa Ala Thr Ser
 35 40

<210> 1634

<211> 88

<212> PRT

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1634

Ala Arg Ala Ala Leu Ser Ala Thr Lys Thr Cys Arg Pro Ala Phe Arg
 1 5 10 15

Gly Ala Ser Ala Ala Pro Arg Gly Gly Gly Pro Ala Arg Ser Pro Gly
 20 25 30

Arg Val Leu Gly Arg His Ala Ala Gly Ser Leu Ala Arg Leu Val Gly
 35 40 45

Arg Ser Arg Gly Phe Trp Leu Leu Gly Gly Glu Val Lys Ser Phe Cys
 50 55 60

Arg Cys Trp Gly Arg Arg Thr Arg Arg Glu Arg Lys Lys Lys Lys Lys
 65 70 75 80

Lys Xaa Leu Gly Lys Tyr Phe Xaa
 85

1696

<210> 1635
<211> 105
<212> PRT
<213> Homo sapiens

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<400> 1635
Tyr Ser His Ser Gly Phe Cys Ser Pro Thr Asp Glu Asp Arg Cys Thr
1 5 10 15
Asn Glu Ala Asp Gly Asn His Pro Val Glu Val His Leu Arg Ser Asp
20 25 30
Pro Asp Asp Ala Arg Ala Met Thr Gly Pro Ala Gly Val Ala Pro Arg
35 40 45
Gly Asp Gln Pro Trp Ser Ser His Arg Arg Lys Pro Leu Arg Ser Gly
50 55 60
Lys Arg Arg Arg Lys Xaa Lys Trp Gln Lys Gln Lys Glu Pro Gln Ser
65 70 75 80
Ser Ile Gly Asp His Ser Met His Phe Leu Pro Ala Ala Thr Gln Thr
85 90 95
Leu Pro Glu Leu Leu Xaa Asn Leu Met
100 105

<210> 1636
<211> 47
<212> PRT
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<400> 1636
Gln Arg Pro Arg Xaa Xaa Gly Thr Gly Ser Gly Pro Pro Gly Pro Gly
1 5 10 15
Lys Ala Ser His Gly Gly Gly Ala Pro Val Ser Arg Ser Gly Thr Gly
20 25 30
Ser Glu Asp Gly Arg Glu Ser Arg Ala Thr Val Val Xaa Cys
35 40 45

<210> 1637
<211> 55
<212> PRT
<213> Homo sapiens

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<400> 1637
Gly Asp Pro Pro Glu Gly Pro Ala Thr Ser Pro Leu Thr Asn Ser Xaa
1 5 10 15
His Pro Xaa Ser Xaa Gly Thr Ala Ala Thr Gln Arg Arg Xaa Ser
20 25 30
Glu Gln Gly Gly Arg Xaa Thr Cys Gly Pro Ala Gly Ala Gly Ser Pro
35 40 45
Xaa Xaa Pro Pro Arg Ala Xaa
50 55

<210> 1638
<211> 55
<212> PRT
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<221> SITE

<222> (49)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1638

Ile	Arg	Xaa	His	Ala	Thr	Xaa	Tyr	Arg	Gly	Xaa	Phe	Cys	Xaa	Arg	Arg
1				5					10					15	

Thr	Xaa	Xaa	Xaa	Leu	His	Ser	Ala	Asn	Val	Thr	Thr	Xaa	Xaa	Leu	Leu
				20				25						30	

Leu	Xaa	Xaa	Phe	Tyr	Xaa	Xaa	Arg	Xaa	Xaa	Ala	Xaa	Val	Asn	Ile	Ser
			35				40						45		

Xaa	Val	Pro	His	Cys	Pro	Ile
	50					55

<210> 1639

<211> 58

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1639

Ile	Cys	Pro	Gln	Asn	Pro	Leu	Asn	Pro	Leu	Val	Asn	Leu	Thr	Xaa	Ser
1				5					10					15	

1701

Pro Lys Arg Asn Ser Ser Leu Asp Thr Arg Lys Lys Pro Cys Arg Glu
 20 25 30

Ser Lys Lys Phe Asn Thr His Ser Arg Pro Lys Ser Ser His Gln Leu
 35 40 45

Arg Lys Arg Ser Ser Xaa Thr Pro Thr Thr
 50 55

<210> 1640
 <211> 37
 <212> PRT
 <213> Homo sapiens

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<400> 1640
 Met Cys Val Asp Cys Met Asn Asp Leu Glu Lys Lys Lys Lys Lys Lys
 1 5 10 15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Xaa Pro Xaa
 20 25 30

Gly Xaa Pro Xaa Pro
 35

<210> 1641
 <211> 41

1702

<212> PRT

<213> Homo sapiens

<400> 1641

Tyr Val Trp Leu Gly His Phe Val Ala Lys Val Arg Thr Cys Leu Trp
1 5 10 15

Lys Thr Ser Leu Trp Leu Gly Glu Ser Val Trp Pro Ala Ala Ser Asp
20 25 30

Leu Cys Arg Val Leu Thr Cys Gln Gly
35 40

<210> 1642

<211> 99

<212> PRT

<213> Homo sapiens

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<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

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<220>
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 <222> (95)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 1642
 Xaa Pro Ala Ala Ser Tyr Leu Met Thr Leu Met Glu Pro Leu Ser Leu
 1 5 10 15
 Ile Xaa Xaa Xaa Leu Ser Pro Pro Leu Xaa Xaa Ser Lys Glu Asn His
 20 25 30
 Phe Asp Ala Arg Ser Cys Leu Xaa Ser Xaa Pro Lys Cys Ser Cys Ser
 35 40 45
 Xaa Pro Xaa Pro Gly Ile Ser Leu Pro Arg Asp Lys Ser Ala Ser Glu
 50 55 60
 Ile Leu His Asp Ser Leu Cys Phe Gln Asn Pro Gly Leu Phe Cys Ile
 65 70 75 80
 Ser Ser Phe Leu Gly Pro Ala Ser Cys Val Pro Leu Lys Gly Xaa Trp
 85 90 95
 Ala Lys Thr

<210> 1643
 <211> 42
 <212> PRT

1704

<213> Homo sapiens

<220>

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<220>

<221> SITE

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1643

Lys Xaa Pro Xaa Asn Leu Gly Lys Ala Arg Leu Gln Val Pro Val Arg
1 5 10 15

Asn Ser Arg Val Asp Leu Arg Val Phe Ile Tyr Ile Asp Ile Tyr Ile
20 25 30

Asp Ile Tyr Arg Tyr Ile Tyr Arg Tyr Ile
35 40

<210> 1644

<211> 46

<212> PRT

<213> Homo sapiens

<220>

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<222> (11)

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<221> SITE

<222> (26)

<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (43)

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<400> 1644

Arg Val Gly Val Arg Leu Ala Gln Val Pro Xaa His Leu Thr Ser Arg
1 5 10 15

Ser His His Pro His Pro Val Phe His Xaa Arg Leu Lys Ala Thr Met
20 25 30

Arg Met Xaa His Thr Glu Ala Xaa Met Xaa Xaa Asn His Leu
35 40 45

<210> 1645

<211> 69

<212> PRT

<213> Homo sapiens

<400> 1645

His Val Arg Leu Lys Pro Ile Phe Ser Pro Phe Phe Leu Leu Phe Ser
1 5 10 15

Leu Ala Ala His Ile Val Pro Leu Phe Tyr Glu Pro Gln Phe Ser Gly
20 25 30

Leu Ser Leu Lys Lys Lys Ser Ser Leu Asn Ile Ala Phe Arg Lys Leu
35 40 45

Leu Phe Leu Asp Lys Lys Ser Tyr Thr Leu Lys Lys Lys Lys Thr Phe
50 55 60

Ser Arg Lys Ile Tyr
65

<210> 1646

<211> 78

<212> PRT

<213> Homo sapiens

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<222> (42)

1706

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (77)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1646

Ile	Ile	Cys	Phe	Val	Leu	Ser	Phe	Ile	Tyr	His	Phe	Phe	Leu	Tyr	Lys
1				5					10					15	

Ser	Ile	Ile	Ser	Arg	Phe	Leu	Tyr	Tyr	Met	Ile	Asp	Ile	Asn	Trp	Val
			20					25					30		

Ile	Ser	Ser	Arg	Gln	Phe	Val	Phe	Ser	Xaa	Xaa	Pro	Pro	Ser	Thr	Val
			35					40					45		

Ser	Gln	Arg	Pro	Asp	Xaa	Val	Gly	Lys	Val	Phe	Phe	Leu	Arg	Ile	Val
	50					55						60			

Lys	Gly	Ser	Xaa	Gln	Leu	Gly	Leu	Ile	Lys	Ala	Xaa	Xaa	Pro
65					70					75			

<210> 1647

<211> 58

<212> PRT

<213> Homo sapiens

<400> 1647

1707

Ile Cys Pro Gln Asn Pro Leu Asn Pro Leu Val Asn Leu Thr Val Ser
1 5 10 15

Pro Lys Arg Asn Ser Ser Leu Asp Thr Arg Lys Lys Pro Cys Arg Glu
20 25 30

Ser Lys Lys Phe Asn Thr His Ser Arg Pro Lys Ser Ser His Gln Leu
35 40 45

Arg Lys Arg Ser Ser Ser Thr Pro Thr Thr
50 55

<210> 1648

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1648

Cys Leu Phe Leu Leu Pro Val Met Leu Leu Gln Ile His Ile Ser Arg
1 5 10 15

Ser Thr Val Asn Val Ser Thr Ser Arg Gly Thr Pro Pro Ser Thr Leu
20 25 30

Ser Val Lys Gly Gln Asn Glu Thr Val Arg Val Lys Gly Thr Gly Arg
35 40 45

Lys Phe Ala Cys Leu Gln Val Thr Arg Ile Arg
50 55

<210> 1649

<211> 110

<212> PRT

<213> Homo sapiens

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1708

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (94)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1649

Val Pro Pro Pro Val Pro Trp Gly Gly Pro Xaa Arg Glu Gly Glu Val
1 5 10 15

Ser His Thr Lys Ala Asp Ala Pro Leu Val Gly Gly Xaa Trp Pro Gly
20 25 30

Lys Ile Glu Gly Cys Ala Gly Leu Pro Leu Arg Ala Ala Gln Thr Ala
35 40 45

Leu Met Cys Gly Gly Xaa Ala Arg Trp Val Arg Ala Gln Glu Val Ala
50 55 60

Pro Xaa Thr Val Ala Asp Xaa Leu Pro Arg Val Pro Gly Ser Ser Leu
65 70 75 80

Tyr Pro Trp Tyr Ala Xaa Asn Xaa Trp Phe Pro His Pro Xaa Ala Ala
85 90 95

Lys Ser Leu Phe Pro Trp Ile Ser Gln Ala Lys Leu Gly Leu
100 105 110

1709

<210> 1650
<211> 74
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1650
Ser Pro Glu Gly Leu Ser Leu Leu Ala Pro Xaa Pro Gly Arg Ala Pro
1 5 10 15
Ala Gly Pro Thr Pro Leu Arg Gly Gln Cys Gln Xaa Gly Ser Leu Thr
20 25 30
Gly Ala Val His Leu Ser Asn Gly Asn Ala Gly Val Leu Arg Arg Ala
35 40 45
Gln Gly Gly Gln Lys Pro Pro Val Glu Gln Lys Gly Lys Ser Ser Leu
50 55 60
Asp Leu His Phe Gln Tyr Glu Tyr Arg Pro
65 70

<210> 1651
<211> 83
<212> PRT
<213> Homo sapiens

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1710

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1651

Asn	Lys	Gly	Gly	Gly	Arg	Met	Met	Thr	Tyr	Pro	Glu	Val	Leu	Pro	Leu
1				5					10				15		

Thr	Ala	Arg	Thr	Gly	Ala	Cys	Ser	Val	Pro	Trp	Glu	His	Xaa	Ala	Gln
	20						25						30		

Leu	Ser	Gly	Val	Gln	Ala	Val	Gly	Ser	Phe	Pro	Asn	Xaa	Ser	Ile	Ser
	35						40					45			

Xaa	Pro	Xaa	Xaa	Leu	Lys	Pro	Val	Gly	Gln	Ile	Ser	Lys	Xaa	Leu	Xaa
	50					55						60			

Xaa	Arg	Xaa	Pro	Phe	Thr	Asn	Pro	Arg	Phe	Cys	Gly	Gln	Cys	Pro	Lys
	65					70				75					80

Gly Val Gly

1711

<210> 1652
<211> 90
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (89)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1652
Phe Phe Phe Phe Leu Asp Val Lys Gly Ile Xaa Phe Gln Arg Leu Leu
1 5 10 15

1712

Glu Ser Leu Val Tyr Thr Asp Glu Gly Val Arg Cys Cys Phe Pro Ser
20 25 30

Glu Ser Ser Ala Ser Thr Glu Ile Xaa Leu Xaa Leu Ile Phe Asp Ile
35 40 45

Leu His Cys Leu Leu Xaa Xaa Xaa Arg Ser Phe Leu Pro Phe Thr Ser
50 55 60

Pro Ser Asn Tyr Val Gln Met Cys Arg Leu Leu Xaa Ser Gly Leu Ser
65 70 75 80

Pro Lys Ala Leu Thr Leu Gly Leu Xaa Phe
85 90

<210> 1653

<211> 55

<212> PRT

<213> Homo sapiens

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<222> (48)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (49)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1653

Lys Leu Trp Phe Val Phe Val Phe Cys Leu Phe His Leu Phe Pro Ser
1 5 10 15

1713

Gln Pro Gln Thr Phe Cys Ser Leu Arg Glu Leu Thr Phe Pro Phe Phe
20 25 30

Phe Leu Phe Phe Phe Phe Gly Xaa Leu Xaa Val Xaa Asn Lys Ile Xaa
35 40 45

Xaa Ala Ile Lys Lys Lys Lys
50 55

<210> 1654

<211> 61

<212> PRT

<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<220>

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<222> (58)

<223> Xaa equals any of the naturally occurring L-amino acids

1714

<220>

<221> SITE

<222> (60)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1654

Val Xaa Ala Thr Asn Leu Pro Ser Leu Val Ile Ala Xaa Cys Ser Xaa
1 5 10 15

Ile Glu Ser Leu Val Pro Leu Leu Ile Trp Pro Gln Lys Pro Pro Asn
20 25 30

Ser Pro Trp Leu Ile Leu Thr Val Xaa Pro Lys Lys Gly Thr Xaa Ser
35 40 45

Leu Gly Pro Leu Xaa Lys Lys Thr Leu Xaa Lys Xaa Asn
50 55 60

<210> 1655

<211> 20

<212> PRT

<213> Homo sapiens

<220>

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<222> (17)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

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<222> (18)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (20)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1655

Ala Ala Val Leu Gln Thr Ala Arg Arg Ala Arg Ser Ala Cys Arg Leu
1 5 10 15

Xaa Xaa Xaa Xaa

1715

20

<210> 1656
<211> 24
<212> PRT
<213> Homo sapiens

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1656
Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Xaa Xaa Thr Ile Phe
1 5 10 15

Xaa Asn Xaa Lys Arg Val Leu Leu
20

<210> 1657
<211> 34
<212> PRT
<213> Homo sapiens

<220>
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<222> (10)
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1716

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (34)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1657

Ala	Ala	Cys	Leu	Pro	Ala	Thr	Glu	Xaa	Ser	Gln	His	His	Glu	Gly
1				5				10					15	

Leu	Asp	Leu	Leu	Ser	Pro	Leu	Pro	Gly	Arg	Glu	Gly	Leu	Gly	Xaa	Pro
			20					25						30	

Ser Xaa

<210> 1658

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1658

Cys	Lys	Gln	Tyr	Leu	Thr	Asn	Pro	Gln	Val	Leu	Asn	Tyr	Gln	Thr	Cys
1				5					10					15	

Ile	Lys	Asn	Phe	Gly	Trp	Gly	Asp	Leu	Gly	Ala	Glu	Pro	Asn	Leu	Arg
			20					25						30	

Ala	Val	His	Ala	Lys	Thr	Ser	Pro	Val	Lys	Ala	Asn	Tyr	Tyr	Thr	Gln
			35					40					45		

Leu	Ile	Gln
		50

<210> 1659

<211> 166

<212> PRT

<213> Homo sapiens

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<222> (50)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

1717

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

1719

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1659

Ser Thr His Ala Ser Gly His Ser His Ser Gln Ala Ser Leu Ala Gly
1 5 10 15

Ser Arg Val Ala Arg Val Arg Cys Leu Leu Gln Leu Gln Asp Asp Arg
20 25 30

Pro Glu Asp Ala Leu Leu Leu Phe Leu Pro Gln Pro Arg Gln Glu Ala
35 40 45

Thr Xaa Pro Gln Xaa Pro Ser Arg Pro Ser Arg Gly Pro Xaa Trp Leu
50 55 60

Gly Leu Leu Lys Lys Ala Glu Xaa Gly Gly His Pro Ser Gln Glu Xaa
65 70 75 80

Pro Gly Trp Xaa Gly Glu Xaa Xaa Glu Arg Arg Pro Pro Trp Xaa Leu
85 90 95

Asn Xaa Arg Thr Phe Trp Asn Arg Ile Pro Glu Glu Gln Arg Ala Arg
100 105 110

Gly Pro Xaa Leu Xaa Xaa Arg Gly Pro Xaa Xaa Val Xaa Pro Trp Gly
115 120 125

Phe Leu Glu Xaa Xaa Pro Gly Lys Glu Ser Xaa Leu Arg Gly Gly Xaa
130 135 140

Phe Arg Gly Lys Xaa Leu Phe Leu Ile Lys Ala Lys Leu Gly Ile Xaa
145 150 155 160

Phe Xaa Lys Arg Lys Gly
165

<210> 1660

<211> 68

<212> PRT

<213> Homo sapiens

<220>

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<222> (9)

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1720

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1721

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<400> 1660
Ser Pro Gly Leu Gln Glu Phe Gly Xaa Arg Gly Xaa Arg Asn Arg Leu
1 5 10 15
Asn Tyr Ala Xaa Xaa His His Xaa Xaa Pro His Arg Xaa Ser Ile Pro
20 25 30
Thr His Ala Leu His Ser Xaa Arg Gly Asp Asp Ala Xaa Leu Thr Ile
35 40 45
Lys Ile Xaa Xaa Pro Pro Met Val Leu Glu Pro Thr Ser Thr Pro Asp
50 55 60
His Xaa Val Asp
65

<210> 1661
<211> 61
<212> PRT
<213> Homo sapiens

<220>
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<222> (47)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (48)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1661
Leu Asn Ala Asp Thr Leu Met Asn Asp Gln Gln Gln Leu Ser Ala Leu
1 5 10 15
Lys Lys Thr Leu Ile Phe Glu Phe Thr Cys Trp Val Pro Gly Ser Asn
20 25 30
Gly Gly Lys Arg Pro Leu Phe Ile Lys Arg Gly Pro Pro Phe Xaa Xaa

1722

	35		40		45
Pro	Lys	Asp	Phe	Leu	Xaa
	50		55		60
			Phe	Gln	Ile
			Gly	Lys	Gly
					Thr

<210> 1662

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (3)

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<220>

<221> SITE

<222> (19)

<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE

<222> (22)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (27)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (47)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1662

Thr	Val	Xaa	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Asn	Leu
1			5				10						15	

Glu	Val	Xaa	Gly	Ile	Xaa	Asn	Leu	Asp	Ile	Xaa	Phe	Gly	Thr	Ser	Asn
			20				25						30		

Pro	His	Ser	Pro	Thr	His	Ala	Gly	Gly	Cys	Ala	Cys	Arg	Thr	Xaa	Leu
		35					40						45		

Thr	Asp	Trp	Trp	Ile	Leu
	50				

1723

<210> 1663

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1663

Ala Arg Glu Lys Leu Cys Val Arg Gly Arg Gly Leu Phe Arg Cys Arg
1 5 10 15
Val Ser Ser Ser Cys Thr Leu Phe Lys Ser Leu His Trp Arg Asn Ser
20 25 30
Ala Ile Thr Ser Ser Leu Val Ala Glu Gly Arg Gly Asn Ile His Leu
35 40 45
Phe Met Pro Val Cys Cys Met Gln Ala Phe Trp Leu Pro Thr Leu Gln
50 55 60
Gln Asn Asn Cys Thr Asn Ser Leu Val Pro Ile Pro Pro Thr Glu Ser
65 70 75 80
Pro Gly Ala Thr Val Phe Phe Ala Leu His Cys Lys Glu Arg Asp
85 90 95

<210> 1664

<211> 100

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (70)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (85)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

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<222> (90)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (91)

<223> Xaa equals any of the naturally occurring L-amino acids

1724

<400> 1664

Val Asn Gln Glu Thr Thr Pro Val Asp Cys Gly Ala Leu Glu Gly Leu
1 5 10 15

Val Gly Val Asn Leu Pro Thr Pro Tyr Asn Cys Gly Arg Ile Gln Lys
20 25 30

Ser Leu Ser Phe Tyr Ile His Ser Leu Asp Val Ile Gly Pro Leu Pro
35 40 45

Pro Ile Ser Leu Arg Cys His Ala Ser Met Gly Ser Gly Val Val Arg
50 55 60

Lys Asn Lys Arg Arg Xaa Asp Ser Leu Val Met Asp Lys Ile Leu Thr
65 70 75 80

Thr Val Phe Pro Xaa Gly Ile Pro Tyr Xaa Xaa Phe Asn Phe Phe Phe
85 90 95

Ser Leu Lys Asn
100

<210> 1665

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (11)

<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>

1725

<221> SITE

<222> (26)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1665

Ser Ala Pro Gly Gly Ser Cys Tyr Ser Gly Xaa Pro Arg Val Pro Lys
 1 5 10 15

Cys Xaa Ile Gln Xaa Asp Pro Xaa Ser Xaa Pro Pro Cys Leu Gln Leu
 20 25 30

Val

<210> 1666

<211> 47

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (26)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (37)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (39)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1666

Gly Arg Val Gly Gly Arg Val Gly Gly Arg Val Gly Arg Glu Pro Gln
 1 5 10 15

Val Tyr Thr Leu Pro Pro Ser Arg Glu Xaa Met Thr Lys Lys Gln Ser
 20 25 30

Ala Glu Leu Pro Xaa Ser Xaa Gly Phe Tyr Pro Thr Lys Ser Pro
 35 40 45

<210> 1667

<211> 34

<212> PRT

1726

<213> Homo sapiens

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<400> 1667

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1 5 10 15

Glu Arg Ala Thr Leu Glu Gln Leu Lys Glu His Thr Pro Leu Phe Leu
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Pro Xaa

<210> 1668

<211> 41

<212> PRT

<213> Homo sapiens

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<400> 1668

Ile Cys Pro Gln Asn Pro Leu Asn Pro Leu Val Asn Leu Thr Val Xaa

1727

1	5	10	15												
Pro	Lys	Arg	Asn	Lys	Leu	Phe	Gly	His	Xaa	Glu	Lys	Thr	Leu	Tyr	Arg
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Glu	Glu	Xaa	Xaa	Phe	Xaa	Asn	Pro	Tyr							
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Thr Phe Val Xaa Asn Gly Thr Val Leu Leu Ala Pro Pro Arg Gly Gly
 20 25 30

Pro Leu Val Ser Pro Leu Pro Ala Arg Arg Arg Cys Val Trp Glu Gly
 35 40 45

Val Gly Cys Gly Pro Arg Pro Asp Leu Ala Val Pro Pro Ala Ala Phe
 50 55 60

Cys Val Ala Gly Ala Gly Arg Arg Gly Pro Leu Thr Xaa Gln Thr Ala
 65 70 75 80

1728

Leu Ala Val Xaa Ser Ser Gly Xaa Arg Leu Ala Gly Gly Thr Pro Thr
 85 90 95

<210> 1670

<211> 140

<212> PRT

<213> Homo sapiens

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<400> 1670

Gly Ser Thr His Ala Ser Gly Ser Thr Glu Lys Glu Gly Leu Leu His
 1 5 10 15

Glu Ala Thr Leu Ser Val His Gln Gly Leu Gly Leu Arg Gly Pro Trp
 20 25 30

Ser Ser Cys Ser Ser Pro Ala Pro Pro Trp Met His Cys Cys Arg Ala
 35 40 45

Glu Xaa Pro Leu Pro Gly Pro Ala Leu Gly Phe Leu Glu Thr Ser Phe
 50 55 60

Ser Phe Ala Ile Phe Phe Lys Trp Glu Lys Gly Gly Gln Leu Ser Leu
 65 70 75 80

Gly Lys Arg Gly Pro Ala Thr Cys Pro Ala Trp Ala Pro Glu Pro Ser
 85 90 95

1729

Ser Leu Thr Gly Gln Ser Leu Val Gly Lys Ala Ala Ser Trp Pro Xaa
 100 105 110

Ser Leu Leu Met Phe Leu Val Ser Arg Val Gln Ser Gln Leu Phe Xaa
 115 120 125

Phe Leu Val Val Pro Val Xaa Glu Ala Phe Gln Asn
 130 135 140

<210> 1671

<211> 34

<212> PRT

<213> Homo sapiens

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<400> 1671

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Arg Leu Ser Xaa His Glu Gly Cys Ser Ala Xaa Cys Ile Ser Val Tyr
 20 25 30

Val Val

<210> 1672

<211> 113

1730

<212> PRT

<213> Homo sapiens

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<400> 1672

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Ser	Gly	Ile	Pro	Gly	Gly	Ile	Pro	Leu	Ser	Pro	Arg	Asp	Pro	Thr	Leu
		20						25					30		

Ala	Ser	Trp	Pro	Thr	Arg	Ser	Arg	Glu	Ser	Leu	Arg	Glu	Arg	Arg	Arg
	35						40					45			

Ser	Arg	Ala	Ala	Ser	Gly	Leu	Gly	Ile	Arg	Pro	Leu	Gly	Pro	Pro	Leu
	50					55						60			

Val	Ser	Arg	Val	Gly	Arg	Asn	Arg	Arg	Leu	Ala	His	Leu	Ala	Trp	Val
	65				70					75				80	

Cys	Pro	His	Val	Val	Ile	Val	Gln	Ile	Asn	Ala	His	Ser	Glu	Leu	Ala
			85						90					95	

Val	Tyr	Phe	Leu	Lys	Phe	Asn	Ile	Val	Phe	Val	Ile	Leu	Lys	Tyr	Leu
			100				105						110		

Leu

<210> 1673

<211> 86

<212> PRT

<213> Homo sapiens

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1731

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<400> 1673

Pro Ala Phe Asn Phe Asp Pro Leu Phe Phe Leu Phe Val Arg Cys Thr
1 5 10 15

Arg Leu Pro Ser Cys Phe Ser Leu Leu Ser Cys His Gln Pro Phe Leu
20 25 30

Leu Gly Gly His Val Leu Gly Lys Arg Pro His Asp Leu Ser Gly Ser
35 40 45

Thr Gln Cys Leu Arg His Pro Ala Ser Phe Ala Cys Ile Pro Gln Thr
50 55 60

Ile Ser Leu Ile Leu Phe Thr Ala Ala Asn Leu Ser Leu Val Asp Glu
65 70 75 80

Thr Val Phe Ile Xaa Leu
85

<210> 1674

<211> 56

<212> PRT

<213> Homo sapiens

<400> 1674

Ser Asp Tyr Glu Leu Leu Phe Lys Arg Lys Met Leu Phe Ile His Ala
1 5 10 15

Glu Val Ile Gln Phe Pro Pro Ser Tyr Arg Ser Ile Leu Ile His Pro
20 25 30

Thr Leu Glu Met Gln His Leu Cys Gly Arg Leu Phe His Lys Pro Pro
35 40 45

Arg Leu Leu Arg Leu Gly Arg Tyr
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<210> 1675

<211> 65

<212> PRT

<213> Homo sapiens

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 <222> (43)
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 Leu Val Cys Ile Leu Pro Lys Val Arg Xaa Pro Thr Leu Gly Ile Thr
 1 5 10 15
 Leu Leu Ile Val Ile Leu Val Xaa Ile Leu Pro Gly Val Met Tyr Ser
 20 25 30
 Leu Lys Ala Leu Asn Val Cys Ile Ala Thr Xaa His Gln Ile Leu Asn
 35 40 45
 Gly Leu Ser Phe Gly Trp Asn Tyr Lys Leu Lys Lys Cys Phe Ser Gly
 50 55 60

Lys
 65

<210> 1676
 <211> 52
 <212> PRT
 <213> Homo sapiens

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<400> 1676
 Pro Thr Glu Gln Val Thr Leu Gly Ile Thr Ala Gln Ser Tyr Ser Arg
 1 5 10 15
 Val His Ile Asn Asn Arg Val Tyr Asp Leu Asp Val Gly Ser Gly His
 20 25 30
 Pro Asp Gly Ala Ala Ala Ile Lys Gly Ser Phe Xaa Gln Arg Leu Lys
 35 40 45

1733

Ser Tyr Val Ile
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<210> 1677
<211> 40
<212> PRT
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<400> 1677
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1 5 10 15

Lys Lys Lys Lys Lys Lys Gly Gly Arg Xaa Lys Gly Ser Lys Leu Thr

1734

20 25 30

Tyr Xaa Cys Met Xaa Arg Xaa Ser
35 40

<210> 1678
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1678
Thr Ala Ala Met Ser Ile Phe Thr Pro Thr Asn Gln Ile Arg Leu Thr
1 5 10 15
Asn Val Ala Val Val Arg Met Lys Arg Ala Arg Lys Arg Phe Glu Ile
20 25 30
Ala Cys Tyr Arg Asn Lys Ser Ser Ala Gly Gly Gly Leu Trp Lys Lys
35 40 45
Thr

<210> 1679
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1679
Ala Ala Ala Gln Gln Val Val Asp Gln Ala Thr Glu Ala Gly Gln Lys
1 5 10 15
Ala Met Asp Gln Leu Ala Lys Thr Thr Gln Glu Thr Ile Asp Lys Thr
20 25 30
Ala Asn Gln Ala Ser Asp Thr Phe Ser Gly Ile Gly Lys Lys Phe Gly
35 40 45
Leu Leu Lys
50

<210> 1680
<211> 41
<212> PRT
<213> Homo sapiens

1735

<400> 1680

Ala Phe Asn Arg Ser Gln Arg Gly Ser Cys Ser Ala Thr Tyr Glu Thr
1 5 10 15

Pro Thr Gln Lys Gln Val Val Tyr Glu Trp Phe Ser Ala Arg Phe Pro
20 25 30

Thr Asn Val Arg Cys Val Thr Gly Glu
35 40

<210> 1681

<211> 34

<212> PRT

<213> Homo sapiens

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<400> 1681

Gly Xaa Gly Val Arg Val Asn Val Arg Thr Ser Ala Gly Cys Ser Pro
1 5 10 15

His Pro Asn Pro Leu Pro Lys Gly Arg Arg Gly Pro Val Thr Gln Phe
20 25 30

Ala Leu

<210> 1682

<211> 85

<212> PRT

<213> Homo sapiens

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 1 5 10 15

Gln Thr Ile Ser Tyr Glu Val Thr Leu Ala Ile Ile Pro Thr Ile Asn
 20 25 30

Ile Thr Asn Xaa Leu Ala Pro Leu Thr Ser Pro Pro Leu Ser Gln His
 35 40 45

Lys Asn Thr Pro Glu Tyr Pro Ala Ile Ile Thr Leu Trp Pro Tyr Xaa
 50 55 60

Ile Ile Phe His Thr Arg Xaa Asn Asn Glu Pro Pro Ser Xaa Leu Xaa
 65 70 75 80

Lys Gly Asn Phe Xaa
 85

<210> 1683

<211> 53

<212> PRT

<213> Homo sapiens

<400> 1683

Val Gly Leu Glu Ile Asn Met Leu Ala Phe Ile Pro Val Leu Thr Lys
 1 5 10 15

Lys Ile Asn Pro Arg Ser Thr Glu Ala Ala Ile Lys Tyr Phe Leu Thr
 20 25 30

1737

Gln Ala Thr Ala Ser Ile Ile Leu Leu Ile Ala Ile Leu Phe Asn Asn
 35 40 45

Ile Leu Ser Gly Gln
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<210> 1684

<211> 169

<212> PRT

<213> Homo sapiens

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 1 5 10 15

Asp Gly Arg Val Ser Val Ser Ala Arg Ile Asp Arg Lys Gly Phe Cys
 20 25 30

Glu Gly Asp Glu Ile Ser Ile His Ala Asp Phe Glu Asn Thr Cys Ser
 35 40 45

Arg Ile Val Val Pro Lys Ala Ala Ile Val Ala Arg His Thr Tyr Leu
 50 55 60

1738

Ala Asn Gly Gln Thr Lys Val Leu Thr Gln Lys Leu Ser Ser Val Arg
65 70 75 80

Gly Asn His Ile Ile Ser Gly Thr Cys Ala Ser Trp Arg Gly Lys Ser
85 90 95

Leu Arg Val Gln Lys Ile Arg Pro Ser Ile Leu Gly Cys Asn Ile Leu
100 105 110

Arg Val Glu Tyr Ser Leu Leu Ile Tyr Val Ser Val Pro Gly Ser Lys
115 120 125

Lys Val Ile Leu Asp Leu Pro Leu Val Ile Gly Ser Arg Ser Gly Leu
130 135 140

Ser Xaa Arg Thr Ser Ser Trp Xaa Ala Xaa Thr Xaa Ser Glu Asp Glu
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Xaa Gly Arg Ser Glu His Pro Asp Thr
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<212> DNA
<213> Homo sapiens

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tctcccgac tcctgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctcca acccccatcg 360
agaaaacccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tccgacggt ccttcttct ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggaacgtct tctcatgtc cgtgatgcat gaggtctctg 660
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gactctagag gat 733

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<212> PRT
<213> Homo sapiens

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<210> 1687

<211> 86

<212> DNA

<213> Homo sapiens

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cccgaatat ctgccatctc aattag 86

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<213> Homo sapiens

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<210> 1689

<211> 271

<212> DNA

<213> Homo sapiens

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gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
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<212> DNA

<213> Homo sapiens

<400> 1690

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1740

<210> 1691
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<400> 1691
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<210> 1692
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12

<210> 1693
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ccatctcaat tag 73

<210> 1694
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<212> DNA
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cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180
ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240
cttttgcaaa aagctt 256

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/05882

A. CLASSIFICATION OF SUBJECT MATTER IPC(7) : C12P 19/34 US CL : 435/91.1 According to International Patent Classification (IPC) or to both national classification and IPC														
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/91.1 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) MEDLINE, SCISEARCH, GenEmbl Database														
C. DOCUMENTS CONSIDERED TO BE RELEVANT														
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.												
Y	Database GenEmbl on STN. KELKER, W. 'Sequence of human E-cadherin cDNA', GenEmbl Database, Accession Z18923.1, Version Z18923.1 GI:31074, 04 December, 1992 (04.12.1992), see nucleotide position 456-1007.	1-12, 14-16, and 21 for SEQ ID NO:1												
Y	BANERJI, J. A gene pair from the human major histocompatibility complex encodes large proline-rich proteins with multiple repeated motifs and a single ubiquitin-like domain, Proc. Natl. Acad. Sci. USA, 1990, Vol 87, pages 2374-2378, see entire document.	1-12, 14-16, and 21 for SEQ ID NO:2												
Y	Database GenEmbl on STN. SKUCE, C. 'Homo sapiens chromosome 20 clone RP4-661120 map q11.23-12', GenEmbl Database, Accession AL031669, Version AL031669.18 GI:6983365, 11 FEBRUARY, 2000 (04.02.2000), see nucleotide position 63147-63482.	1-12, 14-16, and 21 for SEQ ID NO:3												
Y	Database GenEmbl on STN. RAKER, V.A. 'Human SnRNP core protein Sm D2 mRNA, complete cds', GenEmbl Database, Accession U15008, Version U15008.1 GI:600747, 10 December, 1994 (10.12.1994), see nucleotide position 23-479	1-12, 14-16, and 21 for SEQ ID NO:4												
Y	Database GenEmbl on STN. ELLER et al. 'Cellular retinoic acid-binding protein [human, skin, mRNA, 735 nt]', GenEmbl Database, Accession S74445, Version S74445.1, GI:241541, 7 May, 1993 (07.05.1993), see nucleotide position 7-733.	1-12, 14-16 and 21 for SEQ ID NO:6												
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.														
<table border="0"><tr><td>* Special categories of cited documents:</td><td>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td></tr><tr><td>"A" document defining the general state of the art which is not considered to be of particular relevance</td><td>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td></tr><tr><td>"E" earlier application or patent published on or after the international filing date</td><td>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td></tr><tr><td>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td><td>"A" document member of the same patent family</td></tr><tr><td>"O" document referring to an oral disclosure, use, exhibition or other means</td><td></td></tr><tr><td>"P" document published prior to the international filing date but later than the priority date claimed</td><td></td></tr></table>			* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"E" earlier application or patent published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"A" document member of the same patent family	"O" document referring to an oral disclosure, use, exhibition or other means		"P" document published prior to the international filing date but later than the priority date claimed	
* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention													
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone													
"E" earlier application or patent published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art													
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"A" document member of the same patent family													
"O" document referring to an oral disclosure, use, exhibition or other means														
"P" document published prior to the international filing date but later than the priority date claimed														
Date of the actual completion of the international search 03 May 2000 (03.05.2000)		Date of mailing of the international search report 26 JUL 2000												
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230		Authorized officer Michael Woodward Telephone No. (703) 308-0196												

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/05882

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^o	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Database GenEmbl on STN. SHARMA et al 'Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds.', GenEmbl Database, Accession M30471, Version M30471.1 GI:178133, 5 October, 1995 (05.10.1997), see nucleotide position 2-2277.	1-12, 14-16, and 21 for SEQ ID NO:8
Y	Database GenEmbl on STN. ABEDINIA, M. 'Human transketolase (TKT) mRNA, complete cds.', GenEmbl, Accession U55017 M86521, Version U55017.1 GI:1297296, 6 May, 1996 (05.05.1996), see nucleotide position 687-2038.	1-12, 14-16, and 21 for SEQ ID NO:10

Form PCT/ISA/210 (continuation of second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/05882

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-12, 14-16, and 21 for the first 10 sequences in Table 1

Remark on Protest

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☐

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/05882

BOX III. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1.

Group 1, claims 1-12, 14-16, and 21 in so far as they are drawn to the first ten polynucleotides of Table 1 (pages 12-118), protein, vector, gene, method of making host cell, recombinant host cell, method of producing the protein of SEQ ID NO:61.

Groups 2-209, claims 1-12, 14-16, in so far as they are drawn to the next 208 polynucleotide groups (any four sequences constitute a single group) and encoded proteins listed in Table 1.

Groups 210-418, claim 13, in so far as they are drawn to isolated antibodies that bind to any one group of the next 208 polypeptide sequence groups listed in Table 1.

Groups 419-627, claims 15-16, in so far as they are drawn to a method of making any one group of the next 208 polypeptide sequence groups listed in Table 1.

Groups 628-836, claim 17, in so far as they are drawn to a method of treatment by administration any one group of the next 208 polypeptide sequence groups listed in Table 1.

Groups 837-1045, claim 18, in so far as they are drawn to a method of diagnosing a pathological condition by determining a presence or absence of a mutation in any one group of the next 208 polypeptide sequence groups listed in Table 1.

Groups 1046-1255, claim 19, in so far as they are drawn to a method of diagnosing a pathological condition by determining the presence or amount of any one group of the next 208 polypeptide sequence groups listed in Table 1.

Groups 1256-1465, claims 20 and 23, in so far as they are drawn to a method of identifying any one group of the next 208 polypeptide sequence groups listed in Table 1, and the product produce by the same method.

Group 1466-1675, claim 22, in so far as they are drawn to a method of identifying an activity in a biological assay by expression of any one group of the next 208 polypeptide sequence groups listed in Table 1.

The inventions not elected, do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT rule 13.2, the non-elected groups lack the same or corresponding technical features for the following reasons: Group 1 corresponds to the first invention wherein the first product is the polynucleotide, and the first method of use is the method of using the polynucleotide to make the protein, and the protein. Note, there is no method of making the polynucleotide. Each of groups 2-1675 does not share the same or corresponding special technical feature because, each group is drawn to different polynucleotide or encoded protein. Additionally, each of groups 210-1675 does not share the same or corresponding technical feature because, each group is drawn to different compounds or methods of using any of the fifty polynucleotides and encoded proteins listed in Table 1. The Authority therefore considers that the several inventions do not share a special technical feature within the meaning of PCT Rule 13.2 and thus do not relate to a single general inventive concept within the meaning of PCT Rule 13.1.